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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:41:58 ; Search time 34.2113 Seconds  
(without alignments)  
3179.172 Million cell updates/sec

Title: US-09-887-669-1

Perfect score: 7809

Sequence: 1 MDVAAALPAFVALWLLYPW.....EAPQYRVCYDVALEYLESS 1457

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7809	100.0	1457	2	US-08-652-971-3
2	7809	100.0	1457	2	US-08-449-644-1
3	7809	100.0	1457	2	US-08-087-244A-1
4	7809	100.0	1457	2	US-08-991-258A-3
5	7809	100.0	1457	2	US-08-769-399-3
6	7809	100.0	1457	2	US-08-991-953A-3
7	7586	97.1	1439	2	US-08-449-644-2
8	7586	97.1	1439	2	US-08-087-244A-2
9	4812.5	61.6	1452	2	US-08-449-644-8
10	4812.5	61.6	1452	2	US-08-087-244A-8
11	4793.5	61.4	1452	2	US-08-652-971-4
12	4793.5	61.4	1452	2	US-08-991-258A-4
13	4793.5	61.4	1452	2	US-08-769-399-4
14	4793.5	61.4	1452	3	US-08-991-953A-4
15	4575	58.6	1436	2	US-08-652-971-2
16	4575	58.6	1436	2	US-08-991-258A-2
17	4575	58.6	1436	2	US-08-769-399-2
18	4575	58.6	1436	3	US-08-991-953A-2
19	4063	52.0	777	4	US-09-949-016-7158
20	3732	47.8	1075	4	US-09-949-016-8308
21	1514.5	19.4	1501	2	US-08-447-464-3
22	1514.5	19.4	1501	2	US-08-716-679-3
23	1480	19.0	1911	1	US-08-348-006B-5
24	1480	19.0	1911	2	US-08-800-825A-5
25	1480	19.0	1911	3	US-09-158-657-5
26	1480	19.0	1911	5	PCT-US94-10166-5
27	1170.5	15.0	793	1	US-08-015-985-3

28	1170.5	15.0	793	4	US-09-280-597-3	Sequence 3, Appli
29	1155	14.8	802	1	US-08-015-985-1	Sequence 1, Appli
30	1155	14.8	802	4	US-09-280-597-1	Sequence 1, Appli
31	1155	14.8	807	4	US-09-949-016-7356	Sequence 7356, Ap
32	1153	14.8	538	4	US-09-743-492A-9	Sequence 9, Appli
33	1142	14.6	699	1	US-08-348-006B-7	Sequence 7, Appli
34	1142	14.6	699	2	US-08-800-825A-7	Sequence 7, Appli
35	1142	14.6	699	3	US-09-158-657-7	Sequence 7, Appli
36	1096	14.0	249	2	US-08-685-992-8	Sequence 8, Appli
37	1096	14.0	249	2	US-09-144-925-8	Sequence 8, Appli
38	1073.5	13.7	560	4	US-09-949-016-10786	Sequence 10786, A
39	1019	13.0	2314	4	US-09-816-703A-2	Sequence 2, Appli
40	1018	13.0	2308	1	US-08-015-973-1	Sequence 1, Appli
41	1018	13.0	2308	2	US-08-448-164-1	Sequence 1, Appli
42	1018	13.0	2308	3	US-08-081-929-2	Sequence 2, Appli
43	1018	13.0	2308	4	US-10-000-954-2	Sequence 2, Appli
44	1009	12.9	1442	1	US-08-015-986A-3	Sequence 3, Appli
45	1009	12.9	1442	2	US-08-446-363-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-08-652-971-3  
; Sequence 3, Application US/08652971  
; Patent No. 5814507  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd.  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,971  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: P1033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 225-3216  
; TELEFAX: (415) 952-9881  
; TELEX: 910 371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1457 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-652-971-3

Query Match 100.0%; Score 7809; DB 2; Length 1457;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MDVAAALPAFVALWLLYPWLLGSAIGQFSAGCTFDDGFGACDYHQDLYDDPEWVHVS 60  
Sequence 5, Appli  
Db 1 MDVAAALPAFVALWLLYPWLLGSAIGQFSAGCTFDDGFGACDYHQDLYDDPEWVHVS 60  
Sequence 3, Appli

QY 61 AQEPHYLPPEMPOGSMYVDSNNDPGEKARLOLPMTKENDTHCIDFSYLLYSQKGLNPG 120  
Db 61 AQEPHYLPPEMPOGSMYVDSNNDPGEKARLOLPMTKENDTHCIDFSYLLYSQKGLNPG 120  
QY 121 TLNLIIVRNKGPFLANPIWNVTGFTGRDMLRAELAVSTFWPNEYQVIFAEAVSGGRSGYIA 180  
Db 121 TLNLIIVRNKGPFLANPIWNVTGFTGRDMLRAELAVSTFWPNEYQVIFAEAVSGGRSGYIA 180  
QY 181 IDDIQVLSYPCDKSPHFRLGLGDEVEVAGNATFQCIATGRDAVHNKMLQRRNGEDIPVA 240  
Db 181 IDDIQVLSYPCDKSPHFRLGLGDEVEVAGNATFQCIATGRDAVHNKMLQRRNGEDIPVA 240  
QY 241 QTKNINRRFAASFLQVTKTDQDLRYCVTQSERGSGVSNFAQLIVREPRPIAPPOLL 300  
Db 241 QTKNINRRFAASFLQVTKTDQDLRYCVTQSERGSGVSNFAQLIVREPRPIAPPOLL 300  
QY 301 GVGPTYLLIQLNANSIIGDPTIILKEVEYRMTSGSWTETHAVNAPTYKMLHLPDPTYEI 360  
Db 301 GVGPTYLLIQLNANSIIGDPTIILKEVEYRMTSGSWTETHAVNAPTYKMLHLPDPTYEI 360  
QY 361 RVLTRPCEGGTGLPGPLITRTKCAEPMRTPTKLKIAEIQARRIAVDWESLGYNITRCH 420  
Db 361 RVLTRPCEGGTGLPGPLITRTKCAEPMRTPTKLKIAEIQARRIAVDWESLGYNITRCH 420  
QY 421 TFNVITICHYFRGHNESADCLMDPKAPQHVNNHLPPTYTNVLSKMLITNPEGRKESEET 480  
Db 421 TFNVITICHYFRGHNESADCLMDPKAPQHVNNHLPPTYTNVLSKMLITNPEGRKESEET 480  
QY 481 IIQTDDEVPVGVKSLQGTSPENKI FLNWKPELPNGII IQEYVSYSSIRSFDPAPVA 540  
Db 481 IIQTDDEVPVGVKSLQGTSPENKI FLNWKPELPNGII IQEYVSYSSIRSFDPAPVA 540  
QY 541 GPPQTVSNLWNSHTHVFHMLPGTITTYFFIRASTVKFGPATAINVTNINSAPSLPDYEG 600  
Db 541 GPPQTVSNLWNSHTHVFHMLPGTITTYFFIRASTVKFGPATAINVTNINSAPSLPDYEG 600  
QY 601 VDASLNETAITITVLLRPAQAAGAPISAYQIIVVEQLHPHRTKREAGAMECYQVPVYQNA 660  
Db 601 VDASLNETAITITVLLRPAQAAGAPISAYQIIVVEQLHPHRTKREAGAMECYQVPVYQNA 660  
QY 661 LSGGAPYFAELPPGNLPEPAPFTVGDNRVTYKGFNPNPLAPRKGYNIYFOAMSSVEKET 720  
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Db 781 KKRKDMGNTRQEMTHMUNAMDRSVADOSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPTA 840  
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Db 841 VLDEHNSATAESRLLDVPYLCESPTESPYQGLHPAIRVADLLQHLNLMKTSYSGFK 900  
QY 901 EYESFFEGQSASWDVAKKQDNKRNKRYGNIILAYDHSRVILQPVDEDDPSSDYINANYIDI 960  
Db 901 EYESFFEGQSASWDVAKKQDNKRNKRYGNIILAYDHSRVILQPVDEDDPSSDYINANYIDI 960  
QY 961 WLYRQGYQPSHYIATQGVHETVYDFWFMVWQBSACIWMVTNLVEGRVKCYKWPDD 1020  
Db 961 WLYRQGYQPSHYIATQGVHETVYDFWFMVWQBSACIWMVTNLVEGRVKCYKWPDD 1020  
QY 1021 TEVYGDVKVTCVEMPEPLAEBYVVRTFTLRRRGYNEIREVKQPHFTGWPDHGVPHYATGLLS 1080  
Db 1021 TEVYGDVKVTCVEMPEPLAEBYVVRTFTLRRRGYNEIREVKQPHFTGWPDHGVPHYATGLLS 1080  
QY 1081 FIRRVKLSNPPSAGPIVWHCSAGAGRTGCIYIVIDIMLDMAREGVVDIYNCVKALRSRRI 1140  
Db 1081 FIRRVKLSNPPSAGPIVWHCSAGAGRTGCIYIVIDIMLDMAREGVVDIYNCVKALRSRRI 1140

QY 1141 NMVOTESQYIFIHDAILEACLCGETAIPVCBEKAAAYFDMIRIDSQTNSSHLKDBEQTLNS 1200  
Db 1141 NMVOTESQYIFIHDAILEACLCGETAIPVCBEKAAAYFDMIRIDSQTNSSHLKDBEQTLNS 1200  
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Db 1201 VTPRLQAEDECSIACLPRNHDKNRPMFMDLPPDRCLPFLITIDGESSNYINAAALMDSYRQPA 1260  
QY 1261 AFIVTQYPLPNTVKDFWRLVVDYDCTSIUMLNEVDLSQGCCQYWPPEEGMLRYGPIQVECM 1320  
Db 1261 AFIVTQYPLPNTVKDFWRLVVDYDCTSIUMLNEVDLSQGCCQYWPPEEGMLRYGPIQVECM 1320  
QY 1321 SCSDMDCDVINRIFRICNLTRPOEGYLMVQOQFYILGWASHREVPVGSKRSLKLILQVEKWQ 1380  
Db 1321 SCSDMDCDVINRIFRICNLTRPOEGYLMVQOQFYILGWASHREVPVGSKRSLKLILQVEKWQ 1380  
QY 1381 ECEGEGRITIIHCLNGGGRSGMFCAGIIVVEMVKRQNVVDVFFHAVKTLRNSKPNMVEAP 1440  
Db 1381 ECEGEGRITIIHCLNGGGRSGMFCAGIIVVEMVKRQNVVDVFFHAVKTLRNSKPNMVEAP 1440  
QY 1441 EQYRFDVDALEYLESS 1457  
Db 1441 EQYRFDVDALEYLESS 1457

## RESULT 2

US-08-449-644-1  
; Sequence 1, Application US/08449644  
; Patent No. 5856162  
; GENERAL INFORMATION:  
; APPLICANT: Schlössinger, Joseph  
; APPLICANT: Sap, Jan M.  
; APPLICANT: Ullrich, Axel  
; APPLICANT: Vogel, Wolfgang  
; APPLICANT: Fuchs, Miriam  
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
; TITLE OF INVENTION: PHOSPHATASE-KAPPA  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,644  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/087,244  
; FILING DATE: 01-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7683-042  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1457 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-449-644-1

Query Match 100.0%; Score 7809; DB 2; Length 1457;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDVAAALPAFVALWLLYPWLLSALGQFSGAGCTFDDGPGACDYHQDLDDFEWVHVS 60  
Db 1 MDVAAALPAFVALWLLYPWLLSALGQFSGAGCTFDDGPGACDYHQDLDDFEWVHVS 60

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Db 61 AQEHPYLPPEMPOGSMYVDSNHDGPKARLQIPTWKENDTHCIDPSYLLYSOKGLNPG 120

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Db 121 TLNLIVRVNKGPLANPTWNTGTRDWLRAELAVSTFWPNEYQVIFEAEVSGRSGVIA 180

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Db 181 IDDIQVLSYPCDKSPHFLRGDVEVNAGQATFOCIATGRDAVHNKWLQORNGEDIPVA 240

Qy 241 QTKNINRRFAASPRLOEVTKTDQDLYRCVTSQSERGSGVSNFAQLIVREPPRIAPPQLL 300  
Db 241 QTKNINRRFAASPRLOEVTKTDQDLYRCVTSQSERGSGVSNFAQLIVREPPRIAPPQLL 300

Qy 301 GVGPYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKWLHLPDPTYEI 360  
Db 301 GVGPYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKWLHLPDPTYEI 360

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Db 361 RVLLITRPEGGTGLPGPLITRTKCAEPMRTPTKLTAEIQARRIAVDWESLGNITRCH 420

Qy 421 TFNVTCIYHFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEET 480  
Db 421 TFNVTCIYHFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEET 480

Qy 481 IIQTDEDPVGPVKSLQGSTFENKIFLNWKEPLEPNGIITQYEVSVSSIRSPDPAPVPA 540  
Db 481 IIQTDEDPVGPVKSLQGSTFENKIFLNWKEPLEPNGIITQYEVSVSSIRSPDPAPVPA 540

Qy 541 GPPQTVSNLWNSTHHVFMLHPGTYQFFIRASTVKGFGPATANVTNINISAPSLPDYEG 600  
Db 541 GPPQTVSNLWNSTHHVFMLHPGTYQFFIRASTVKGFGPATANVTNINISAPSLPDYEG 600

Qy 601 VDSLNSTATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQNA 660  
Db 601 VDSLNSTATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQNA 660

Qy 661 LSGGAPYFAELPPGNLPEPAPTVGDNRTYKGFWMPPPLAPRGYNIYFOAMSSVEKET 720  
Db 661 LSGGAPYFAELPPGNLPEPAPTVGDNRTYKGFWMPPPLAPRGYNIYFOAMSSVEKET 720

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Db 721 KTCQVRIATKAAATEEPEVDPAPAKOTDRVVKIAGISAGILVTLILLVIVIVKSKLA 780

Qy 781 KKRKDMAGNTQEMTHVMNANDRSYADQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPTA 840  
Db 781 KKRKDMAGNTQEMTHVMNANDRSYADQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPTA 840

Qy 841 VLNDHSAATESSRLLDVPRYLCGTSPTQGLHPAIRVADLLQHINLMKTSDSYGFK 900  
Db 841 VLNDHSAATESSRLLDVPRYLCGTSPTQGLHPAIRVADLLQHINLMKTSDSYGFK 900

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Db 901 EYESFPFEGOSASWDVAKQONRAKNYGNIIAYDHSRVILQPVEDDPSDYNINAYIDI 960

Qy 961 WLVRDGYQRSHYIATQGVHETVYDFWRVWQSQSACIIVMTNLVWGRVKCYKWPDD 1020  
Db 961 WLVRDGYQRSHYIATQGVHETVYDFWRVWQSQSACIIVMTNLVWGRVKCYKWPDD 1020

Qy 1021 TEVYDGFVKTCVMEPLAEYVVRTFTLERRGYNEIREVKQFHTGWPDHGVPVYHATGLLS 1080

Db 1021 TEVYDGFVKTCVMEPLAEYVVRTFTLERRGYNEIREVKQFHTGWPDHGVPVYHATGLLS 1080

Qy 1081 FIRVKLSNPPSAGPIVVHCSAGAGRTGCTYVIDIMLDMAREGVDVIYNCVKALRSRRI 1140  
Db 1081 FIRVKLSNPPSAGPIVVHCSAGAGRTGCTYVIDIMLDMAREGVDVIYNCVKALRSRRI 1140

Qy 1141 NMVQTEQYFIHDAILEACLCGETAIPVCEFFKAAAFDMIRIDSQTNSSHLKDBFQTLNS 1200  
Db 1141 NMVQTEQYFIHDAILEACLCGETAIPVCEFFKAAAFDMIRIDSQTNSSHLKDBFQTLNS 1200

Qy 1201 VTPRLQADCSIACLPRNHDKNRPMDLPPDRCLPFLITIDGESSNINAAALMDSYQPA 1260  
Db 1201 VTPRLQADCSIACLPRNHDKNRPMDLPPDRCLPFLITIDGESSNINAAALMDSYQPA 1260

Qy 1261 AFIVQYPLPNTVKDFWRLVYDYGCTSIVMNLNEVDLSQGCPCQYWPPEEGMLRYGPIQVECM 1320  
Db 1261 AFIVQYPLPNTVKDFWRLVYDYGCTSIVMNLNEVDLSQGCPCQYWPPEEGMLRYGPIQVECM 1320

Qy 1321 SCNSMCDVINRIFRICNLTRPQEGYLMVQOQFYILGWASHREVPGSKRSFLKLILQVEKMQ 1380  
Db 1321 SCNSMCDVINRIFRICNLTRPQEGYLMVQOQFYILGWASHREVPGSKRSFLKLILQVEKMQ 1380

Qy 1381 ECEEGEGRTIIHCLNGGSGRGMFCATGIUVWVKRONVVDVPHAVKTLRNSKKNMVEAP 1440  
Db 1381 ECEEGEGRTIIHCLNGGSGRGMFCATGIUVWVKRONVVDVPHAVKTLRNSKKNMVEAP 1440

Qy 1441 EQYRFCYDVALEYLESS 1457  
Db 1441 EQYRFCYDVALEYLESS 1457

RESULT 3  
US-08-087-244A-1  
; Sequence 1, Application US/08087244A  
; Patent No. 5863755  
; GENERAL INFORMATION:  
; APPLICANT: Schliesinger, Joseph  
; APPLICANT: Sap, Jan M.  
; APPLICANT: Ullrich, Axel  
; APPLICANT: Vogel, Wolfgang  
; APPLICANT: Fuchs, Miriam  
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/087,244A  
; FILING DATE: 01-JUL-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7683-042  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1457 amino acids  
; TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-087-244A-1

Query Match 100.0%; Score 7809; DB 2; Length 1457;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDVAAAALPAFVALMLLPWLLGALQGFAGGCTFDDGACDYHQDLYDDFEWVHVS	60
DB	1	MDVAAAALPAFVALMLLPWLLGALQGFAGGCTFDDGACDYHQDLYDDFEWVHVS	60
QY	61	AOEHPYLPPEPQGSVMVDSNSHDPGEKARLQLPTMKENDTHCIDFSYLLYSQKGLNPG	120
DB	61	AOEHPYLPPEPQGSVMVDSNSHDPGEKARLQLPTMKENDTHCIDFSYLLYSQKGLNPG	120
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DB	121	TLNIIIVRNKGPLANPIWVGTGRDMLRAELAVSTFWPNEYQVIFEAESVSGRSGYIA	180
QY	181	IDDIQVLSYPCDKSPHFRLGDEVNAGNATFQCIATGRDAVHNKMLQRRNGEDIPVA	240
DB	181	IDDIQVLSYPCDKSPHFRLGDEVNAGNATFQCIATGRDAVHNKMLQRRNGEDIPVA	240
QY	241	QTKNINHRFAASFLQEVTKTDQDLRYCVTQSERGSGVSNFAQLIVREPRTIAPPOLL	300
DB	241	QTKNINHRFAASFLQEVTKTDQDLRYCVTQSERGSGVSNFAQLIVREPRTIAPPOLL	300
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DB	301	GVGPTYLLIQLNANSIIGDPTILKEVEYRMTSGSWTETHAVNAPTYKMLHLDPDTEYEI	360
QY	361	RVLITRPGEGGTGLPGPLITRTKCAEPMRTPTKLIAEIQARRIAVDWESLGYNITRCH	420
DB	361	RVLITRPGEGGTGLPGPLITRTKCAEPMRTPTKLIAEIQARRIAVDWESLGYNITRCH	420
QY	421	TENVTICVHYFRGHNESRADCLMDPKAPQHVHNLPPYTNVSLKMLITNPEGRKSEET	480
DB	421	TENVTICVHYFRGHNESRADCLMDPKAPQHVHNLPPYTNVSLKMLITNPEGRKSEET	480
QY	481	IIQTDVDPGPVVKSLQTSFENKI FLNWKLEPENGII IQEYVSYSIRSFDPAVPA	540
DB	481	IIQTDVDPGPVVKSLQTSFENKI FLNWKLEPENGII IQEYVSYSIRSFDPAVPA	540
QY	541	GPQTVSNLWNSHTHVPFHLHGTTTQFFIRASTVKGFAPATINVTNISAPSLPDYEG	600
DB	541	GPQTVSNLWNSHTHVPFHLHGTTTQFFIRASTVKGFAPATINVTNISAPSLPDYEG	600
QY	601	VDASLNETATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQNA	660
DB	601	VDASLNETATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQNA	660
QY	661	LSGGAPYFAALPPGNLPEPAPFTVGNRTYKGFNPPPLAPRKGYNIYFOAMSSVEKET	720
DB	661	LSGGAPYFAALPPGNLPEPAPFTVGNRTYKGFNPPPLAPRKGYNIYFOAMSSVEKET	720
QY	721	KTCQVRIATKAAATEEPIVDPKQTRVVKIAGISAGILVIFILLLVIVIVVKSKLA	780
DB	721	KTCQVRIATKAAATEEPIVDPKQTRVVKIAGISAGILVIFILLLVIVIVVKSKLA	780
QY	781	KKRDAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSLTFMDQHNFPRLNDPLVPTA	840
DB	781	KKRDAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSLTFMDQHNFPRLNDPLVPTA	840
QY	841	VLDENHSATAESRLLDVPRYLCEGTESPYQGLHPAIRVADLLQHLNLMKTSYSGFK	900
DB	841	VLDENHSATAESRLLDVPRYLCEGTESPYQGLHPAIRVADLLQHLNLMKTSYSGFK	900
QY	901	EYESFFEQSASWDVAKQDNRAKNRYGNIITAYDHSRVILQPVDDPSSDYINANYIDI	960
DB	901	EYESFFEQSASWDVAKQDNRAKNRYGNIITAYDHSRVILQPVDDPSSDYINANYIDI	960
QY	961	WLYRDGYQRP SHYIATQGPVHETVDFWRVMWQOSACIVMVTNLVEGRVKCYKYWDD	1020

DB	961	WLYRDGYQRP SHYIATQGPVHETVDFWRVMWQOSACIVMVTNLVEGRVKCYKYWDD	1020
QY	1021	TEVYDGFKVTCEMEPLAEYVVRFTTLERRGYNIREVKQPHFTGWPDPHGYVYHATGLLS	1080
DB	1021	TEVYDGFKVTCEMEPLAEYVVRFTTLERRGYNIREVKQPHFTGWPDPHGYVYHATGLLS	1080
QY	1081	FIRRVKLSNPPSAGPIVHCSAGAGRTGCIYIIVIMLDMABREGVVDIYNCVKALRSRI	1140
DB	1081	FIRRVKLSNPPSAGPIVHCSAGAGRTGCIYIIVIMLDMABREGVVDIYNCVKALRSRI	1140
QY	1141	NMVTQEQYIFIHDAILEACLCGETAIPVCEFKAAYPDMIRIDISQTNSSHLKDEFQTLNS	1200
DB	1141	NMVTQEQYIFIHDAILEACLCGETAIPVCEFKAAYPDMIRIDISQTNSSHLKDEFQTLNS	1200
QY	1201	VTPLQAEDECSIACLPRNHDKNRMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPA	1260
DB	1201	VTPLQAEDECSIACLPRNHDKNRMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPA	1260
QY	1261	AFIVTQVPLENTVKDFWRLVVDYDCTSIWMLNEVDLSQCCPYWPEEGMLRYGPIQVECM	1320
DB	1261	AFIVTQVPLENTVKDFWRLVVDYDCTSIWMLNEVDLSQCCPYWPEEGMLRYGPIQVECM	1320
QY	1321	SCSMDCDVINRIFRICNLTRPOEGYLMVQOQYILGWASHREVPGSKRSFLKLILOVEKWQ	1380
DB	1321	SCSMDCDVINRIFRICNLTRPOEGYLMVQOQYILGWASHREVPGSKRSFLKLILOVEKWQ	1380
QY	1381	EECEGEGRITIIHCLNGGSGRMFCAGIIVVEMVKRQNVVDVFAVKTLRNSKPNMVEAP	1440
DB	1381	EECEGEGRITIIHCLNGGSGRMFCAGIIVVEMVKRQNVVDVFAVKTLRNSKPNMVEAP	1440
QY	1441	EQYRFCYDVALEYLESS 1457	
DB	1441	EQYRFCYDVALEYLESS 1457	

RESULT 4  
US-08-991-258A-3  
; Sequence 3, Application US/08991258A  
; Patent No. 5928887  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991,258A  
; FILING DATE: 17-DEC-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/652,971  
; FILING DATE: 24-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX:

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1457 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-991-258A-3

Query Match 100.0%; Score 7809; DB 2; Length 1457;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDVAAAALPAFVALWLLYPWLLGSLGALQFSGAGCTFDDGPGACDYHQDLYDDFEWVHVS	60
Db	1	MDVAAAALPAFVALWLLYPWLLGSLGALQFSGAGCTFDDGPGACDYHQDLYDDFEWVHVS	60
Qy	61	AOEPHYLPPEMPOGYSVMVDSNSHDGPKARLQLPWKENDTHCIDFSYLLYSOKGLNPG	120
Db	61	AOEPHYLPPEMPOGYSVMVDSNSHDGPKARLQLPWKENDTHCIDFSYLLYSOKGLNPG	120
Qy	121	TLNLIVRVNKGPLANPIWNVGTFGRDWLRAELAVSTFWPNEYQVIFEAESVSGRSGVIA	180
Db	121	TLNLIVRVNKGPLANPIWNVGTFGRDWLRAELAVSTFWPNEYQVIFEAESVSGRSGVIA	180
Qy	181	IDDIQVLVSYPCDKSPHFLRLGDEVVNAGQATFQCIATGRDAVHNKWLQRRNGEDIPVA	240
Db	181	IDDIQVLVSYPCDKSPHFLRLGDEVVNAGQATFQCIATGRDAVHNKWLQRRNGEDIPVA	240
Qy	241	QTKNINHRRAAFASPRLOEVTKTDQDLVRCVTSQSRGSGVSNFAOLIIVREPPRIAPQLL	300
Db	241	QTKNINHRRAAFASPRLOEVTKTDQDLVRCVTSQSRGSGVSNFAOLIIVREPPRIAPQLL	300
Qy	301	GVGPTYLLIQLNANSIIGDGPILKEVEYRMTSGTETHAVNAPTYKWLHLDPTDEYEI	360
Db	301	GVGPTYLLIQLNANSIIGDGPILKEVEYRMTSGTETHAVNAPTYKWLHLDPTDEYEI	360
Qy	361	RVLLTRPEGGTGLPGLPILTRTKCAEPMRTPKTKIAEQARRIAVDWESLGNITRCH	420
Db	361	RVLLTRPEGGTGLPGLPILTRTKCAEPMRTPKTKIAEQARRIAVDWESLGNITRCH	420
Qy	421	TENVTCIYHFRGHNESRADCLMDPKAPQVHVNHLPPYTNVSLKMLITNPEGRKSEET	480
Db	421	TENVTCIYHFRGHNESRADCLMDPKAPQVHVNHLPPYTNVSLKMLITNPEGRKSEET	480
Qy	481	IIQTDVDPGVPVVKSLQGTGFENKIFLNWKEPLEPNGIITQYEVSYSSIRSDPAVPVA	540
Db	481	IIQTDVDPGVPVVKSLQGTGFENKIFLNWKEPLEPNGIITQYEVSYSSIRSDPAVPVA	540
Qy	541	GPQTVSNLWNSHHVFMHLHPGTTYQFFIRASTVKGFPGPATAINVTTNISAPSLPDYEG	600
Db	541	GPQTVSNLWNSHHVFMHLHPGTTYQFFIRASTVKGFPGPATAINVTTNISAPSLPDYEG	600
Qy	601	VDASLNATATITVLLRPAQAKGAPISAYQIVVQLHPHRTKREAGAMECVQVPTVYQNA	660
Db	601	VDASLNATATITVLLRPAQAKGAPISAYQIVVQLHPHRTKREAGAMECVQVPTVYQNA	660
Qy	661	LSGGAPYFAELPPGMLPEPAPTVGDNRTYKGFWMNPPLAPRKGYNIYFOAMSSVEKET	720
Db	661	LSGGAPYFAELPPGMLPEPAPTVGDNRTYKGFWMNPPLAPRKGYNIYFOAMSSVEKET	720
Qy	721	KTCQVRIATKAAATEEPEVIPPDAKQTDVVKVIAIGISAGILVFIILLVWIVIVKSKLA	780
Db	721	KTCQVRIATKAAATEEPEVIPPDAKQTDVVKVIAIGISAGILVFIILLVWIVIVKSKLA	780
Qy	781	KKRKDMGNTRQETHMVMNMDRYADQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPTA	840
Db	781	KKRKDMGNTRQETHMVMNMDRYADQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPTA	840
Qy	841	VLDENHSATAESRLLDVPRVLCGTSPTQGLHPAIRVADLLOHINLMKTSDSYGFK	900
Db	841	VLDENHSATAESRLLDVPRVLCGTSPTQGLHPAIRVADLLOHINLMKTSDSYGFK	900

Qy	901	EYESFPEGQSASWDVAKQONRAKNRYGNIIVDHSRVILQPVDEDDPSSDIYINANYIDI	960
Db	901	EYESFPEGQSASWDVAKQONRAKNRYGNIIVDHSRVILQPVDEDDPSSDIYINANYIDI	960
Qy	961	WLYRDGYQRPSHYIATQGVHETVYDFWRVWQSQSACIIVMTNLVEVGRVKCYKYPDD	1020
Db	961	WLYRDGYQRPSHYIATQGVHETVYDFWRVWQSQSACIIVMTNLVEVGRVKCYKYPDD	1020
Qy	1021	TEVVGDFKVTCEMEPLAEYVVRTFTLERRGYNEIREVKQFPHFTGWDHGVPIYHATGLLS	1080
Db	1021	TEVVGDFKVTCEMEPLAEYVVRTFTLERRGYNEIREVKQFPHFTGWDHGVPIYHATGLLS	1080
Qy	1081	FIRRVKLSNPSPSAGPIVWHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRI	1140
Db	1081	FIRRVKLSNPSPSAGPIVWHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRI	1140
Qy	1141	NMQVTEQYIFIHDALEACLGETAIPVCEFKAAAYFDMIRIDSQTNSSHLKDEFQTLNS	1200
Db	1141	NMQVTEQYIFIHDALEACLGETAIPVCEFKAAAYFDMIRIDSQTNSSHLKDEFQTLNS	1200
Qy	1201	VTPLQAEDECSIACLPRNHDKNRPMMLPPDRCLPFLITIDGESSNYINAALMDSYRQPA	1260
Db	1201	VTPLQAEDECSIACLPRNHDKNRPMMLPPDRCLPFLITIDGESSNYINAALMDSYRQPA	1260
Qy	1261	AFIVTQYPLNTWKDFWRLVYDYGCTSIIVMLNEVDLSQGCPOYWPPEGMLRYGPIQVECM	1320
Db	1261	AFIVTQYPLNTWKDFWRLVYDYGCTSIIVMLNEVDLSQGCPOYWPPEGMLRYGPIQVECM	1320
Qy	1321	SCSMDCDVINRIFRINLTPQEGYLMVQOQFYGLGWASHREVPGSKSFLKLILOVEKQW	1380
Db	1321	SCSMDCDVINRIFRINLTPQEGYLMVQOQFYGLGWASHREVPGSKSFLKLILOVEKQW	1380
Qy	1381	EECEEGEGRTIIHCLNGGSGRGMFCATIGIVVMVKRQNVVDVPHAVKTLRNSKENMVEAP	1440
Db	1381	EECEEGEGRTIIHCLNGGSGRGMFCATIGIVVMVKRQNVVDVPHAVKTLRNSKENMVEAP	1440
Qy	1441	EQYRFCYDVALEYLESS 1457	
Db	1441	EQYRFCYDVALEYLESS 1457	

## RESULT 5

US-08-769-399-3  
; Sequence 3, Application US/08769399  
; Patent No. 5976852  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd.  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08769,399  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: P1033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 225-3216

```
;
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-769-399-3

Query Match      100.0%; Score 7809; DB 2; Length 1457;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDVAAAALPAFVALWLLYPWPLGSGALGQFSGAGCTFDDGPGACDYHQDLYDDFEWVHVS 60
DB 1 MDVAAAALPAFVALWLLYPWPLGSGALGQFSGAGCTFDDGPGACDYHQDLYDDFEWVHVS 60
QY 61 AQEPHYLPPEMPQGSYMWVDSNNDHPGKARLQLPTMKENDTHCIDPSYLLYSQKGLNPG 120
DB 61 AQEPHYLPPEMPQGSYMWVDSNNDHPGKARLQLPTMKENDTHCIDPSYLLYSQKGLNPG 120
QY 121 TLNIIIVRNKGPLANPINNVGTGCRDMLRAELAVSTFWPNEYQVIFPAEYSGGRSGYIA 180
DB 121 TLNIIIVRNKGPLANPINNVGTGCRDMLRAELAVSTFWPNEYQVIFPAEYSGGRSGYIA 180
QY 181 IDDIQVLSYPCDKSPHFLRLGDLGVEVNAGONATFQCIATGRDAVHNKMLQRRNGSDIPVA 240
DB 181 IDDIQVLSYPCDKSPHFLRLGDLGVEVNAGONATFQCIATGRDAVHNKMLQRRNGSDIPVA 240
QY 241 QTKNINHRFAAFSLQEVTKTDQDLYRCVQTSERGSVSNFAQLIVREPPRTAPPOLL 300
DB 241 QTKNINHRFAAFSLQEVTKTDQDLYRCVQTSERGSVSNFAQLIVREPPRTAPPOLL 300
QY 301 GVGPTYLLIQLNANSIIGDGPITILKEVEYRMTSGSWTETHAVNAPTYKWLHLDPDTEYEI 360
DB 301 GVGPTYLLIQLNANSIIGDGPITILKEVEYRMTSGSWTETHAVNAPTYKWLHLDPDTEYEI 360
QY 361 RVLVLRPGEGGTGLPGPLITRKAEMRTPKTLKIAEIQARRIAVDWESLGYNITRCH 420
DB 361 RVLVLRPGEGGTGLPGPLITRKAEMRTPKTLKIAEIQARRIAVDWESLGYNITRCH 420
QY 421 TENVTICHYFRGHNESRADCLMDPKAPQHVVNHLPPYTNVSLKXVILTNPEGRKESSET 480
DB 421 TENVTICHYFRGHNESRADCLMDPKAPQHVVNHLPPYTNVSLKXVILTNPEGRKESSET 480
QY 481 IITQDDEVPGVPVKSLOQTSFENKIFLNWKEPLSPNGIITQVEYSYSIRSFDPAVPA 540
DB 481 IITQDDEVPGVPVKSLOQTSFENKIFLNWKEPLSPNGIITQVEYSYSIRSFDPAVPA 540
QY 541 GPPQTVSNLWNSTHVFVHLHPGTTTQFFIRASTVKFGPATAINVTNISAPSPDYEG 600
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DB 601 VDASLNETHATTTVLLRPAQAAGAPISAYQIIVVEQLHPHRTKREAGAMECYQVPVYQNA 660
QY 661 LSGGAPYFAAELPGNLPPEPAPFTVGDNRTYKGFNPNPLAPRKGVNIYFQAMSSVEKET 720
DB 661 LSGGAPYFAAELPGNLPPEPAPFTVGDNRTYKGFNPNPLAPRKGVNIYFQAMSSVEKET 720
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DB 721 KTQCVRIATKAAATEEPIPDPAKQTRVVKIAGISAGILVIFILLVLIIVIVKSKLA 780
QY 781 KKRKQAMGNTRQEMTHVNMADRSYADQSTLHABDPLSLTFMDQHNFSRPLNDPLVPTA 840
DB 781 KKRKQAMGNTRQEMTHVNMADRSYADQSTLHABDPLSLTFMDQHNFSRPLNDPLVPTA 840
QY 841 VLDEHNSATAESRLLDVPVRYLCBGTSPYQGLHPAIRVADLLQHLINLMKTSYSGFK 900
DB 841 VLDEHNSATAESRLLDVPVRYLCBGTSPYQGLHPAIRVADLLQHLINLMKTSYSGFK 900
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DB 841 VLDEHNSATAESRLLDVPVRYLCBGTSPYQGLHPAIRVADLLQHLINLMKTSYSGFK 900
QY 901 EYESPEFGOSASWDVAKKQONRAKNRYGNIITADHSRVILQPVDEDDPSSDIYINANYIDI 960
DB 901 EYESPEFGOSASWDVAKKQONRAKNRYGNIITADHSRVILQPVDEDDPSSDIYINANYIDI 960
QY 961 WLYRDGYQRPSHYIATQGPVHETVYDFWRVWVQSQSACIIVMVTNLVEVGRVKCYKWPDD 1020
DB 961 WLYRDGYQRPSHYIATQGPVHETVYDFWRVWVQSQSACIIVMVTNLVEVGRVKCYKWPDD 1020
QY 1021 TEVYGDFKVTCEVMEPLAEYVVRTFTLERRGYNEIREVKQPHFTGWDPHGVYHATGLLS 1080
DB 1021 TEVYGDFKVTCEVMEPLAEYVVRTFTLERRGYNEIREVKQPHFTGWDPHGVYHATGLLS 1080
QY 1081 FIRVKLSNPPSAGPIVWHCSAGAGRTGCTYIIVIMLDMAREGVDVIYNCVKALRSRI 1140
DB 1081 FIRVKLSNPPSAGPIVWHCSAGAGRTGCTYIIVIMLDMAREGVDVIYNCVKALRSRI 1140
QY 1141 NMVOTERQYIFIHDAILEACLCGETAIPVCBFKAAYFDMIRIDISQTNSSHLKDEFOTLNS 1200
DB 1141 NMVOTERQYIFIHDAILEACLCGETAIPVCBFKAAYFDMIRIDISQTNSSHLKDEFOTLNS 1200
QY 1201 VTPRLQAEDECSIACLPRNHDKNRPMDMPLPPDRCLPFLITIDGESSNYINAAALMDSYRQPA 1260
DB 1201 VTPRLQAEDECSIACLPRNHDKNRPMDMPLPPDRCLPFLITIDGESSNYINAAALMDSYRQPA 1260
QY 1261 AFIVTQVPLNTVDFWRLVYDYGCTSIVMLENEVDLSQGCQPYWPEEGMLRYGPIQVECM 1320
DB 1261 AFIVTQVPLNTVDFWRLVYDYGCTSIVMLENEVDLSQGCQPYWPEEGMLRYGPIQVECM 1320
QY 1321 SCSDMCDVINRIFRICNLTRPOEGYLMVQQFOYLGWASHREVPGSKRSFLKLILOVEKWQ 1380
DB 1321 SCSDMCDVINRIFRICNLTRPOEGYLMVQQFOYLGWASHREVPGSKRSFLKLILOVEKWQ 1380
QY 1381 ECEGEGRITIIHCLNGGSRGMFCAGIIVVMVKRQNVVDVFAVKTLRNSKPNMVEAP 1440
DB 1381 ECEGEGRITIIHCLNGGSRGMFCAGIIVVMVKRQNVVDVFAVKTLRNSKPNMVEAP 1440
QY 1441 EQYRFDVDALEYLESS 1457
DB 1441 EQYRFDVDALEYLESS 1457

RESULT 6
US-08-991-953A-3
; Sequence 3, Application US/08991953A
; Patent No. 6083748
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ELEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,953A
; FILING DATE: 16-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
```

NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1457 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-991-953A-3

Query Match 100.0%; Score 7809; DB 3; Length 1457;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDVAAALPAFVALWLLYPWLLGSLGQFSAGGCTFDDGFGACDYHQDLYDDFEWVHVS 60  
DB 1 MDVAAALPAFVALWLLYPWLLGSLGQFSAGGCTFDDGFGACDYHQDLYDDFEWVHVS 60  
QY 61 AOEPHYLPPMPQGSYMWVDSNNHDPGEKARLQLPTMKENDTHCIDFSYLLYSOKGLNPG 120  
DB 61 AOEPHYLPPMPQGSYMWVDSNNHDPGEKARLQLPTMKENDTHCIDFSYLLYSOKGLNPG 120  
QY 121 TLNLLVRVNGKPLANPIWNTVGTGRDWRRLAEAVSTFWPNEYOVIFEAEVSGRSGYIA 180  
DB 121 TLNLLVRVNGKPLANPIWNTVGTGRDWRRLAEAVSTFWPNEYOVIFEAEVSGRSGYIA 180  
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DB 181 IDDIQVLSYPCDKSPHFLRGDVEVNAQONATFOCIATGRDAVHNKMLWLRNGEDIPVA 240  
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DB 241 QTKNINRRFAASRLQEVTKTDOLYRCVTSQSRGSGVSNFAOLIIVREPPRIAPQLL 300  
QY 301 GVGPYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKMLHLDPDTEYI 360  
DB 301 GVGPYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKMLHLDPDTEYI 360  
QY 361 RVLLTRPEGGTGLPGPPLITRTKCAEPMRTPTKLKIAEQARIAVDWESLGYNIIRCH 420  
DB 361 RVLLTRPEGGTGLPGPPLITRTKCAEPMRTPTKLKIAEQARIAVDWESLGYNIIRCH 420  
QY 421 TFNVTCIYHVRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKSEET 480  
DB 421 TFNVTCIYHVRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKSEET 480  
QY 481 IIQTDDEVPGVPVKSLOGTSFENKI FLNWKELPENGIIITQYEVSYSSIRSDPAVPVA 540  
DB 481 IIQTDDEVPGVPVKSLOGTSFENKI FLNWKELPENGIIITQYEVSYSSIRSDPAVPVA 540  
QY 541 GPPTVSNLWNSTHVFMHLHPGTYQFFIRASTVKGFGPATAINVTNINSAPSLPDYEG 600  
DB 541 GPPTVSNLWNSTHVFMHLHPGTYQFFIRASTVKGFGPATAINVTNINSAPSLPDYEG 600  
QY 601 VDASLNATATTITVLLRPAQAKGAPI SAYQIVVQQLPHRHTKREAGAMECVQVPVYQNA 660  
DB 601 VDASLNATATTITVLLRPAQAKGAPI SAYQIVVQQLPHRHTKREAGAMECVQVPVYQNA 660  
QY 661 LSGGAPYFAABLPPGNLPEPAPTVGDNRTYKGFWMPPPLAPRGYNIYFOAMSSVEKET 720  
DB 661 LSGGAPYFAABLPPGNLPEPAPTVGDNRTYKGFWMPPPLAPRGYNIYFOAMSSVEKET 720  
QY 721 KTCQVRIATAAAATEEVEVDPDAKQDVRVKIAGISAGILVFLLLLVIVIVVKKSLA 780  
DB 721 KTCQVRIATAAAATEEVEVDPDAKQDVRVKIAGISAGILVFLLLLVIVIVVKKSLA 780  
QY 781 KCKRDAMGNTRQEMTHVMNAMDRSYADQSTLIHABDPLSLTFMDQHNFSRPLPNDPLVPTA 840

Db 781 KCKRDAMGNTRQEMTHVMNAMDRSYADQSTLIHABDPLSLTFMDQHNFSRPLPNDPLVPTA 840  
QY 841 VLDEHSAATAESSRLLDVPRYLCEGTSPYQTGLHPAIRVADLLQHINLMKTSDSYGFK 900  
DB 841 VLDEHSAATAESSRLLDVPRYLCEGTSPYQTGLHPAIRVADLLQHINLMKTSDSYGFK 900  
QY 901 EYESFPPEGQSASWDVAKQONRAKNRYGNI IAYDHSRVILQPVDEDDPSSDIYINANYIDI 960  
DB 901 EYESFPPEGQSASWDVAKQONRAKNRYGNI IAYDHSRVILQPVDEDDPSSDIYINANYIDI 960  
QY 961 WLYRDGYQRPSHYIATQGVHETVYDFWRVWMOEQSACI VMVTNLVSVGRVKCYKWPDD 1020  
DB 961 WLYRDGYQRPSHYIATQGVHETVYDFWRVWMOEQSACI VMVTNLVSVGRVKCYKWPDD 1020  
QY 1021 TEVYGDFKVTCEVMEPLAEYVVRTFTLERRGYNEIREVKQFPHFTGWDHGVPHYHATGLLS 1080  
DB 1021 TEVYGDFKVTCEVMEPLAEYVVRTFTLERRGYNEIREVKQFPHFTGWDHGVPHYHATGLLS 1080  
QY 1081 FIRRVKLSNPPSAGPIVHVCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRI 1140  
DB 1081 FIRRVKLSNPPSAGPIVHVCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRI 1140  
QY 1141 NMVQTEQYIFIHDAILEACLGCETAI PVCEFAAYFDMIRIDSQTNSSHLKDEFOTLNS 1200  
DB 1141 NMVQTEQYIFIHDAILEACLGCETAI PVCEFAAYFDMIRIDSQTNSSHLKDEFOTLNS 1200  
QY 1201 VTPLRLQADCSIAICLPRNHDKNFMDLPPDRCLPFLITIDGESSNVIINAALMDSYQPA 1260  
DB 1201 VTPLRLQADCSIAICLPRNHDKNFMDLPPDRCLPFLITIDGESSNVIINAALMDSYQPA 1260  
QY 1261 AFIVTQYPLENTVKDFMRLVYDYGCTSI VMLNEVDLSQGCQYWPPEGMLRYGPIQVECM 1320  
DB 1261 AFIVTQYPLENTVKDFMRLVYDYGCTSI VMLNEVDLSQGCQYWPPEGMLRYGPIQVECM 1320  
QY 1321 SCSDMCDVINRI FRICNLTRPOEGYLMVQOFOYLGWASHREVPGSKSFLKLILOVEKWQ 1380  
DB 1321 SCSDMCDVINRI FRICNLTRPOEGYLMVQOFOYLGWASHREVPGSKSFLKLILOVEKWQ 1380  
QY 1381 EECBEGBRTIIHCLNGGSGRMFCALGI VVMVKRONVVDVPHAVKTLRNSKPMVVEAP 1440  
DB 1381 EECBEGBRTIIHCLNGGSGRMFCALGI VVMVKRONVVDVPHAVKTLRNSKPMVVEAP 1440  
QY 1441 EQYRCYDVALEYLESS 1457  
DB 1441 EQYRCYDVALEYLESS 1457

## RESULT 7

US-08-449-644-2  
; Sequence 2, Application US/08449644  
; Patent No. 5856162  
; GENERAL INFORMATION:  
; APPLICANT: Schlessinger, Joseph  
; APPLICANT: Sap, Jan M.  
; APPLICANT: Ullrich, Axel  
; APPLICANT: Vogel, Wolfgang  
; APPLICANT: Fuchs, Miriam  
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25



COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/087,244A  
FILING DATE: 01-JUL-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-042  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1439 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-087-244A-2

Query Match 97.1%; Score 7586; DB 2; Length 1439;  
Best Local Similarity 97.5%; Pred. No. 0;  
Matches 1421; Conservative 12; Mismatches 5; Indels 20; Gaps 4;

Qy 1 MD-VAAALPAFVALWLLYPWLLGSAIGQSAGCTFDDGPGACDHYHQDLYDFEWVHV 59  
Db 1 MDTAAAAALPAFVALLLLSPWLLGSAQGFAGCTFDDGPGACDHYHQDLYDFEWVHV 60  
Qy 60 SAQPHYLPPMPGSGYVMDSSNHDGCEKARLQPTMKENDTHCIDFSLYLSQKGLNP 119  
Db 61 SAQPHYLPPMPGSGYVMDSSDHDGCEKARLQPTMKENDTHCIDFSLYLSQKGLNP 120  
Qy 120 GTNLVVRVNGKPLANPWNVTGTRDMLRAELAVSTFWPNEYQVIFAEVSGRSGYI 179  
Db 121 GTNLVVRVNGKPLANPWNVTGTRDMLRAELAVSTFWPNEYQVIFAEVSGRSGYI 180  
Qy 180 AIDDIQVLSYPCDKSPHFLRGDVEVNAQGNATFCIATGRDAVHNKLWLRNGEDIPV 239  
Db 181 AIDDIQVLSYPCDKSPHFLRGDVEVNAQGNATFCIATGRDAVHNKLWLRNGEDIPV 240  
Qy 240 AQTNIHNRPAASFRLOEVTKTDDLYRCVYQTSERGSVSNFAQLIVREPPIAPPOL 299  
Db 241 AQTNIHNRPAASFRLOEVTKTDDLYRCVYQTSERGSVSNFAQLIVREPPIAPPOL 300  
Qy 300 LGVGTLYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 359  
Db 301 LGVGTLYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 360  
Qy 360 IRVLLTRPGEGTGLPGPLTRTKCAEPMPTKTLKIAEQARRIADVMSLGYNITRC 419  
Db 361 IRVLLTRPGEGTGLPGPLTRTKCAEPMPTKTLKIAEQARRIADVMSLGYNITRC 420  
Qy 420 HTFNVTTCYHYFRGHNSRADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEE 479  
Db 421 HTFNVTTCYHYFRGHNSKADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEE 480  
Qy 480 TIITDDEVPQVPVKSLQGTSPFNKIFLNKKEPLEPNGIITQVEVSVSSIRSDPAVPV 539  
Db 481 TIITDDEVPQVPVKSLQGTSPFNKIFLNKKEPLEPNGIITQVEVSVSSIRSDPAVPV 540  
Qy 540 AGPPQTVSNLWNSHHVFMHLHPCGTTQFFIRASTVKFGFPATAINVTNISAPSLDYE 599  
Db 541 AGPPQTVSNLWNSHHVFMHLHPCGTTQFFIRASTVKFGFPATAINVTNISAPSLDYE 600  
Qy 600 GVDASLNETAATTITVLLRPAQAKGAPISAVQIVVEQLHPHRTKREAGAMECYQVPVTVQN 659  
Db 601 GVDASLNETAATTITVLLRPAQAKGAPISAVQIVVEQLHPHRTKREAGAMECYQVPVTVQN 660  
Qy 660 ALSGAPYFAAEELPPGNLPEPAPFTYGDNRITKGFNWNPPPLAPRKGNYIYFOAMSSVEKE 719  
Db 661 AMSGAPYFAAEELPPGNLPEPAPFTYGDNRITKGFNWNPPPLAPRKGNYIYFOAMSSVEKE 720  
Qy 720 TKTCQVRIATKAAATEPEVIPPDAKQTDNRVVKIAGISAGILVILLVIVVKKSKL 779  
Db 721 TKTCQVRIATK-AAATEPEVIPPDAKQTDNRVVKIAGISAGILVILLVIVVKKSKL 779  
Qy 780 AKRDKAMGNTROQWTHVNMADRSYADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPT 839  
Db 780 AKRDKAMGNTROQWTHVNMADRSYADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPT 831  
Qy 840 AVLDENHSATAESSRLLDVPRYLCEGTESPTQQLHPAIRVADLQHLINIMKTSDSYGF 899  
Db 832 ----ENHSATAESSRLLDVPRYLCEGTESPTQQLHPAIRVADLQHLINIMKTSDSYGF 887  
Qy 900 KEYESFEGQSASWDVAKKQONRAKRYGNI IAYDHSRVILQPVEDDPSSDIYNANYID 959  
Db 888 KEYESFEGQSASWDVAKKQONRAKRYGNI IAYDHSRVILQPVEDDPSSDIYNANYI- 946  
Qy 960 IWLRYDGVQRPSPHYIATQGPVHETVDFWRVMWQESACIWMVTNLVVRGKVCYKWPDP 1019  
Db 947 ----DGYQRPSPHYIATQGPVHETVDFWRVMWQESACIWMVTNLVVRGKVCYKWPDP 1001  
Qy 1020 DTEVYGDVKVTCVEMEPLAEYVVRFTTLERRGYNEIREVKQFHFTGMPDHGVPYHATGLL 1079  
Db 1002 DTEVYGDVKVTCVEMEPLAEYVVRFTTLERRGYNEIREVKQFHFTGMPDHGVPYHATGLL 1061  
Qy 1080 SFTRRVKLSNPPSAGPIVHCSAGAGRTGCVIIVDMLDMAEREGVVDIYNCVKALRSRR 1139  
Db 1062 SFTRRVKLSNPPSAGPIVHCSAGAGRTGCVIIVDMLDMAEREGVVDIYNCVKALRSRR 1121  
Qy 1140 INMVQTEEQVIFIHDAILEACLGCTAI PVCEPKAAVFDIMRIDISQTNSSHLKDBFOTLN 1199  
Db 1122 INMVQTEEQVIFIHDAILEACLGCTAI PVCEPKAAVFDIMRIDISQTNSSHLKDBFOTLN 1181  
Qy 1200 SVTPRLQAECDSCIACLPNRHDKNRFMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQP 1259  
Db 1182 SVTPRLQAECDSCIACLPNRHDKNRFMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQP 1241  
Qy 1260 AAFITVQYPLNTVKDFWRLVYDYGCTSI VMLNEVDLSQGPCQYWPBEGMLRYGPIQVEK 1319  
Db 1242 AAFITVQYPLNTVKDFWRLVYDYGCTSI VMLNEVDLSQGPCQYWPBEGMLRYGPIQVEK 1301  
Qy 1320 MSCMDCDVINRIFRICNLTRPOEGYLMVQOQFYLGHASHREVPGSKRSTFLKILQVEKW 1379  
Db 1302 MSCMDCDVINRIFRICNLTRPOEGYLMVQOQFYLGHASHREVPGSKRSTFLKILQVEKW 1361  
Qy 1380 QEECEGEGRITIIHCLNGGSGRMFCAIGIIVEMVKRQNVVDVPHAVKTLRNSKPNMVEA 1439  
Db 1362 QEECEGEGRITIIHCLNGGSGRMFCAIGIIVEMVKRQNVVDVPHAVKTLRNSKPNMVEA 1421  
Qy 1440 PEQYRFCYDVALEYLESS 1457  
Db 1422 PEQYRFCYDVALEYLESS 1439

RESULT 9  
US-08-449-644-8  
Sequence 8, Application US/08449644  
Patent No. 5856162  
GENERAL INFORMATION:  
APPLICANT: Schlössinger, Joseph  
APPLICANT: Sap, Jan M.  
APPLICANT: Ulrich, Axel  
APPLICANT: Vogel, Wolfgang  
APPLICANT: Fuchs, Miriam  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
TITLE OF INVENTION: PHOSPHATASE-KAPPA  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:



APPLICANT: Sap, Jan M.  
 APPLICANT: Ullrich, Axel  
 APPLICANT: Vogel, Wolfgang  
 APPLICANT: Fuchs, Miriam  
 TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
 TITLE OF INVENTION: PHOSPHATASE-KAPPA  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PENNIE & EDMONDS  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/087,244A  
 FILING DATE: 01-JUL-1993  
 CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7683-042  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-790-9090  
 TELEFAX: 212-869-8864/9741  
 TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1452 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 US-08-087-244A-8

Query Match 61.6%; Score 4812.5; DB 2; Length 1452;

Best Local Similarity 61.4%; Pred. No. 0;  
 Matches 891; Conservative 209; Mismatches 322; Indels 29; Gaps 9;

QY 22 LLSALQFSGAGGCTFDGACDYGQDLYDDFEWVHVSAGEPHYLPPMPQGSYMWVDS 81  
 DB 14 LLLTAAGTSGGCLFDEPSTCGYSQSEGGDFNWEQVNTLTKPTSPWPGSLMLVNA 73  
 QY 82 SNHDPGEKARQLPTMKENDTHCIDFSYLLYSQKGLNPGLTILVRVKNKGLANPINVT 141  
 DB 74 SGRPEGQRAHLLLPQLKENDTHCIDFHYFVSSKSNPPGLLVVYKVNNGPLGNPINNIS 133  
 QY 142 GFTGRDLWRLAELAVSTWPNEXYQVIFEAHSVGGSGSYAIDDDIOVLSPCDKSPHFLRG 201  
 DB 134 GDPTRTNWRAELASTWPNFYQVIFEV-ITSGHGYLAIDDEVKVLGHPCPTRTPHFLRIQ 192  
 QY 202 DVEYNAGONATFOCIATGRDAVHKNLQRRNGBDIPVAOTKNIHRRFAASPRLOEVTK 261  
 DB 193 NVEVNAQFATFQCSAGRTVAGDRMLQGLDVRDALFKELKVTSSRRFTASFVNVTK 252  
 QY 262 TDQDLRCVCTQSERGSGVNSFAQLIVREPRPRIAPPQLLGGVPTLLIQLNANSIIGDGP 321  
 DB 253 RDAGKYRCMIRTEGGVIGISNVAELVVKPEVPVPIAPPQLASVATYMLQLNANSINGDP 312  
 QY 322 IILKEVEYRTSGWTETHAVNAPTYKLWHLDPDTEYIRVLLTRPGEGLTLPGLPLIT 381  
 DB 313 IVAREVEYCTASGWNDRQPVDSYSKIGHLDPDTEYISVLLTRPGEGLTSGSPALRT 372  
 QY 382 RTKCAEMRPTKLIKIAEIOARRIADVWESIGYNI TRCHTFNVTCIVHYFRGHNESRAD- 440  
 DB 373 RTKCADPMRGPRLKEVVEVRSQITIRWEPFGYNLTRCHSNLTVHYCYQVGGOEQVREE 432  
 QY 441 -CLDMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEETIIQTDEBDFPVPVKSLOG 499

Db 433 VSMDTENSHPOHTITNLSPTYNVSVKILNMPERKESQELIVQTDLDLPGAVTESIQG 492  
 QY 500 TSPENKIFLNWKEPLEPNGIITOVEVSYSSRDPAPVAGPPQTVSNLWNSHHVFMH 559  
 DB 493 STEEKIFLOWREPTQYVITLYEITYKAVSDFDEIDISNQSQRVSKLGNETHFLPFG 552  
 QY 560 LHPGTTYQFFIRASTVKFGFATAINVTNISAPSLPDYEGVDASLNETATITVLRLPA 619  
 DB 553 LYPGTTYSTIRASTAKGFGPPATNQFTTKISAPMAYE-LETPLNQNTONTVTVMUKPA 611  
 QY 620 QAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTYONALSGAAYVFAAEPLPGNLP 679  
 DB 612 HSRGAPVSVYQIVVEERPRRTKTEILKCYPIHFQNASLINSOYIFAEEFPADSLQ 671  
 QY 680 EPAPFTVGNRTYKGFNPNPLAPRGYNIYFQAMSSVEKETKTCTOCVRIATKAAATEPEV 739  
 DB 672 AAOPTIGDNKTYNGYNTPLLPYKSYRIYFQAASRANGETKIDCVQVATKGAATP-- 729  
 QY 740 IPDPAKQTDVRVKIAGISAGILVFIILLVIVIVVKSKLAKRKDKAMGNTRQEMTHVN 799  
 DB 730 VPPEKQTDHTVKIAGVIAGILLFVIFLGVLMVKRKLAKRKETMSSTRQEMTVMN 789  
 QY 800 AMDRSYADQSTLHAEDPLSLTFMDQHNFSPRLNDP-----LVPATVL-DENH 846  
 DB 790 SMDKSYAEQGTNCDE--AFSMDTHNLGRSVSSPSFTMTKNTLTSTSPNSYYPDETH 846  
 QY 847 SATAESRLADVPRY-LCEGTESPYQTGQLHPAIRVADLLQHLNLMKTSYSGPKEEVES 905  
 DB 847 TMASTSSSLVQSHYTKREPADVPYQTGQLHPAIRVADLLQHLQTMKCAEGYKPEYES 906  
 QY 906 FFEQASASMDVAKQONRAKNRYGNIITAYDHSRVILQFVEDDSSDYINANYIDILYRD 965  
 DB 907 FFEQASAPWDSAKDENRMKNRYGNIITAYDHSRVILQFIEDGTDNSYINGNYI-----D 960  
 QY 966 GYORPSHYIATQPVHETVDFWRMWQEOSACIVMTNLVEVGRVKCYKWPDDTEVYG 1025  
 DB 961 GYHRPNHYIATQGPQMOETIYDFWRMWVENTASTIIMVTNLVEVGRVCKYWPDDTEYIK 1020  
 QY 1026 DEKVTQVMEPLAEYVVRTFLRRRGYNEIREVKQFHFTGWPDPHGVPHYATGLLSFIRRV 1085  
 DB 1021 DIKVTLETLLAEYVIRTFAVEKRGVHEIREIQFHFTGWPDPHGVPHYATGLLGFRVQV 1080  
 QY 1086 KLSNPSAGIIVVHCSAGAGRTGCIYIDIMLMAEREGVVVDIYNCVKALRSRRINMVQT 1145  
 DB 1081 KSKSPSAGIIVVHCSAGAGRTGCFIVIDIMLMAEREGVVVDIYNCVRELRSRVNMVQT 1140  
 QY 1146 EQYIFIHDAILEACLCGETAIPVCEPKAAYFDMIRIDSQTNSSHLDKDEFTQNSVTPRL 1205  
 DB 1141 EQYVTFHDAILEACLCGDTSPASQVRSLYYDMNKLDPQTNSSQIKEBFRTLMNVPTL 1200  
 QY 1206 QAEDCSFACILPRNHNKRMMLPPORCLPLITIDGESNNYNAALMDSYVROPAAFIVT 1265  
 DB 1201 RVBDCSALLPRNHNKRMMLPPORCLPLITIDGESNNYNAALMDSYVROPAAFIVT 1260  
 QY 1266 QYELPNTVKDFWRLVDYDCTSIWMLNEVDLSQCPQYWPPEEGMLRYGPIQVECMSCMD 1325  
 DB 1261 QHPLPNTVKDFWRLVDYDCTSIWMLNEVDLSQCPQYWPPEEGMLRYGPIQVECMSCMD 1320  
 QY 1326 CDVINRIFRICNTRPOEGLYMQOYQYLGWASHREVPVSGSKRFLKLILOVEKMQEESCE 1385  
 DB 1321 EDIISRIFRIYNAARPDQGRVYMQOYQYLGWASHREVPVSGSKRFLKLILOVEKMQEES 1380  
 QY 1386 GEGRTIHLCLNGSGRGMFCAIGIVEMVKRONVDFHVAVKTLRNSKPNVPEAQRFP 1445  
 DB 1381 GEGRTIHLCLNGSGRGMFCAIGIVEMVKRONVDFHVAVKTLRNSKPNVPEAQRFP 1440  
 QY 1446 CYDVALEYLES 1456  
 DB 1441 CYEVALEYLNS 1451

RESULT 11

US-08-652-971-4

; Sequence 4, Application US/08652971  
 ; Patent No. 5814507  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheng, Jill  
 ; APPLICANT: Lasky, Laurence A.  
 ; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
 ; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd.  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/652,971  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dregler, Ginger R.  
 ; REGISTRATION NUMBER: 33,055  
 ; REFERENCE/DOCKET NUMBER: P1033  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 225-3216  
 ; TELEFAX: (415) 952-9881  
 ; TELEX: 910 371-7168  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1452 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-652-971-4

Query Match 61.4%; Score 4793.5; DB 2; Length 1452;  
 Best Local Similarity 61.3%; Pred. No. 0;  
 Matches 889; Conservative 208; Mismatches 325; Indels 29; Gaps 9;

QY	22	LLGSALGQPSAGGCTFDGPGACDYHQDLYDDFEVWHVSAQBPHYLPPEMPOGSGYMWVDS	81
DB	14	LLLTAAGETFSGGLFDFEPYSTCGYSQADEDDFNHEQVNTLTKPTSDPWPFGSGFVLNT	73
QY	82	SNHDPGEKARLQLPWKENDTHCIDFSYLLYSQKGLNPGTLMILVRVKNKGPLANPWNT	141
DB	74	SKPEGORAHLLLPQKENDTHCIDFHYFVSSKNAAPGLLNVVYKVNNGPLGNPWNTS	133
QY	142	GTGRDLRAELAVSTFWNEVQVIFEAHSVSGRGYTAIDDIQVLSYPCDKSPHFLRLG	201
DB	134	GDPTTRHRAELAISTFWNFYQVIFEV-VTSGHQGLAIDEVKVLGHPCFCTETPHFLRIQ	192
QY	202	DVEVNAGQATFOCIATGDADAHNKLWLRORRGEIDIPVAQTKNINHRRAAFSFRQEVTK	261
DB	193	NVEVNAGQATTFQCSAIGTAVAGRLWLOGIDVRDAPLKEIKVTSRRPIASFNVNTTK	252
QY	262	TQDLYRCVTSQBSGVSFNQAQLIVREPPRIAPQLLGVTGYLLIQLNANSITGDGP	321
DB	253	RDAGKYRCMCTEGGVGISNAELVVKPEPVIAPQLASVGATVLIQLNANSINGDGP	312
QY	322	IILKEVEYRMTSGSWTEHAVNAPTYKLMHLDDPDTEYEIRVLLTRPEGGTLGCPPLIT	381
DB	313	IVAREVEYCTASGSMNDROQFVDSYKIGHLDPDTEYEISVLLTRPEGGSGSPGPAURT	372
QY	382	RTKCAEPMRTPTKIAETQARRIAVDWESLGNITRCHTFNVTICYHYFRGHNSRAD-	440
DB	373	RTKCADPMRGPKLEVVVEVVKSRQITIRWEPFGYNTVTRCHSYNLTIVHYGYOVGGQVREE	432

QY	441	-CLDMDPKAQHVHNLPPYTNVSLKMLTNPEGRKESEETIIQTDREDVPGVPVKSIQG	499
DB	433	VSWDTDNSHPQHTITNLSPYTNVSVKILMNPGRKESQELTVQTDPLGAVPTESIQG	492
QY	500	TSPENKIFLWKEPLEPNGIITQYEVSYSSIRSFPDPAVPVAGPPQTVSNLWNSTHHVPMH	559
DB	493	SAFEKIFLOWREPTQYGVITLYEITYKAVSSFPDIDLSNQSGRVSKLGNETHFLFFG	552
QY	560	LHPGTTYOFFIRASTVKGPGATAINTVWISAPSLPDYEGVDASLNETATTITVLRLPA	619
DB	553	LYPGTYSFTIRASTAKGFGPPATNQFTTKISAPSDPAYE-FETPLNQTDNTVTVMLKPA	611
QY	620	QAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTYONALSGAPYFAELPPGNLP	679
DB	612	QSRGAPVSVOIVVEEERPRRTKTTILKCYPIPIHFQNASILNSQYFAAEFPADSLQ	671
QY	680	EPAPPTVGDNRITYKGFWNPPPLAPRKGNYIYFOAMSSVEKETKTCQVRIATKAAATEPEV	739
DB	672	AAQFTTIGDNKTYNGYWNTPLLPHKSYRIYQAASRANGEIKIDCVRVATKGVTPKP--	729
QY	740	IPDPAKQTRVVKIAGISAGILVFILLVIVIVVKSKLAKKRDAMGNTRQEMTHMVN	799
DB	730	VPEPEKQTDHTVKIAGVIAGILLFVIIPLGVVLVWKKRKLAKRKTMSSTRQEMTMVN	789
QY	800	AMDRSYADOSTLHAEDPLSLTFMDQHNFSPLNDP-----LVPTAVL-DENH	846
DB	790	SMDXSAYEQGTNCDE--AFSFMGTNLNGRSVSPSFTMKTNTLTSTSVNSVYPPDTH	846
QY	847	SATAESSRLLDVPRY-LCEGTESPYQTQLHPALRVADLLQHLINLMKTSDSYKPEEYES	905
DB	847	TMASDTSSLAQPHYTKREAADVYQTQLHPALRVADLLQHLITQMKCAEGYKPEEYES	906
QY	906	FFEGQSASWDVAKKQDNRAKNRYGNIIAYDSHRVILQVEDDPSPDSYINANYIDILWYRD	965
DB	907	FFEGQSAPWDSAKKQDNRMKNRYGNIIAYDSHRVRLQMLEGDNNSDYINGNYI-----D	960
QY	966	GYQRPISHYIATQGPVHETVDFPWRMVQESACIWMVNLVEVGRVKYKYPDDTVEYG	1025
DB	961	GYHRPNHYIATQGPVHETVDFPWRMVHENTASIMVNLVEVGRVKCKWPDDTEYK	1020
QY	1026	DFKVTCEMEPLAEVYVTRFTLERRGYNEIREVKQFHTGWPDPHGVPYHATGLLSFIRRV	1085
DB	1021	DIKVTLDITELLAEYVIRTFAVEKRGHIEIREIQFHTGWPDPHGVPYHATGLLGFVRQV	1080
QY	1086	KLSPPSAGPTVHVHCSAGAGTCYIVIDIMLMAEREGVVDIYNCVKALSRRLNMVQT	1145
DB	1081	KSQPPNAGPLVHCSAGAGTCGCFIVIDIMLMAEREGVVDIYNCVRELASRRVNMVQT	1140
QY	1146	BEQYIFHDAILEACLGETAIPVCEPKAAYPDMIRIDSTNSSHLKDFOTLNSVTPL	1205
DB	1141	BEQYVFHDAILEACLQGDTSIPASQVRSLYDMNKLDPQTNSSQIKKEEFTLNMVTP	1200
QY	1206	QAECSIACLPRNHDKNRMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAFIVT	1265
DB	1201	RVEDCSIALPRNHEKRCMDILLPPDRCLPFLITIDGESSNYINAAALMDSYKQPSAFIVT	1260
QY	1266	QYPLNTVKDFWRLVYDGYCTSI VMLNEVDLSQGCQYWPBEGMLRGP IQVECMSCSD	1325
DB	1261	QHPLENTVKDFWRLVLDVHCTSVVMLNDVDAQLCFQYWPENGVRHHP IQVEFVSADLE	1320
QY	1326	CDVINRIPICNLIRPQEGYLMVQOQYGLWASHREVFGSKRSFLKLLIQVEKQWEECEE	1385
DB	1321	EDIISIRPRIYNASRPQDGRMVQOQFGLGPMVREDTVPVSKRSFLKLLIQVDKQWEEYNG	1380
QY	1386	GEGRTHICLNGGGRSGMFCAGIIVEMVKNQVVDVFAVKTILNSKPNMVAEAEQYRF	1445
DB	1381	GEPTVIVHCLNGGGRSGTFCALISIVCEMLRHQRTVDVFAVKTILNNKPNMVDLDDQYKF	1440
QY	1446	CYDVALEYLES 1456	
DB	1441	CYVALEYLNS 1451	

## RESULT 12

US-08-991-258A-4  
; Sequence 4, Application US/08991258A  
; Patent No. 5928887  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT, LLP  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991,258A  
; FILING DATE: 17-DEC-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/652,971  
; FILING DATE: 24-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-63478-3/WH/MTK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1452 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-991-258A-4

Query Match 61.4%; Score 4793.5; DB 2; Length 1452;

Best Local Similarity 61.3%; Pred. No. 0;

Matches 889; Conservative 208; Mismatches 325; Indels 29; Gaps 9;

QY	22	LLGSALQFSAGGCTFDGACDYGHDLYDDFEWVHSAQEPHYLPPEMPQGSYMWVDS	81
DB	14	LLTAAGETSGGCLFDEPYSTCGYSQADEDFNWEQVNTLTPTSDPMPGSGFMLVNT	73
QY	82	SNHDPGEKARLQLPTMKENDTHCIDFSLYSQKGLNPGTLNILVRVYKGLPANIWNVT	141
DB	74	SGRPEGORALLLPQAKENDTHCIDFHYFVSSKSNAPGLLVVYKVNGLNPNWIS	133
QY	142	GFTGRDMLRAELAVSTFWPNEYQVIFAEVSGRSGVIAIDDTQVLSYPCDKSPHFLRLG	201
DB	134	GDPTRTWRAELAISTFWPNFYQVIFEV-VTSGHQGYLAIDEVKVLGHPCTRTPHFLRIQ	192
QY	202	DVEVNAGNATFOCIATGRDAVHNKWLQRNGEDIIVAQTKNINRRFAASERLQEVTK	261
DB	193	NVEVNAGQFATFCSAIGRTVAGRLWLGQIDVRDAPLKEIKVTSRRFIAFENVNTTK	252
QY	262	TDQDLYRCVTSQSRGSGVSNFAQLIVREPPRIAPPOLLGVGPTYLILQNLANSIIIGDGP	321
DB	253	RDAGYRCMCTEGGVGINSVAELVKEPVPVPIAPPOLASVATYLIQLNANSINGDGP	312
QY	322	ILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYERVLTRPGEGTGLPGPPLIT	381

DB	313	IVAREVEYCTASGSWMDRQVDSSTVKIGHLDPDTEYEVISVLLTRPGEGTGSGPPALRT	372
QY	382	RTKCAEPMRTPKTKIAEIQARRIAVDWESLGNITRCHTFNVTICVHYFRGNESRAD-	440
DB	373	RTKCADPMRGPRKLEVVVEKSRQITIRWEPFGNVTRCHSYNLTVHYGYVGQEQVREE	432
QY	441	-CLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGRKSEETIIQTDEDDVPGVPVKSLQ	499
DB	433	VSWDTDNHSHQHTITNLSPYTNVSKLILNMPGRKESQELTVQTDSDLCAVPTESIQ	492
QY	500	TSFENKIFLNKEPLSPNGIITQVEYSYSSIRSFDDPAVPVAPPPQTVSNLWNSTHVPMH	559
DB	493	SAFEKIFLOWREPTQTYGVITIEYIKAVSFDPEIDLSQSGRVSUKLGNETHFIFPG	552
QY	560	LHPGTTYQFFIRASTVKGFGPATAINVNTNISAPSLPDYEGVDASLNETATTTVLRLPA	619
DB	553	LYPGTIVSFTIRASTAKGFGPPATNQFTTKISAPSMPAYE-FETPLNQTONTVTMLKPA	611
QY	620	OAKGAPISAYQIVVEQLHPHRTYKREAGAMECYQVPTYQNALSGGAPYYFAELPPGNLP	679
DB	612	QSRGAPVSVYQIVVEBERPRRTKTTIELKCYVPPIHFQNASILNSQYFPAEFPADSLQ	671
QY	680	EPAPFTVGDNRITYKGFNWPPLAPRGVNIYFOAMSSVEKETKTCQVRIATAKAAATEPEV	739
DB	672	AAQFTTIGDNKTYGNTWNTPLLPKHSYRIYQAASRANGETKIDCVKATKGAVTAP--	729
QY	740	IPDPAKQTRVVKIAGISAGILVPIILLVIVIVVKSKLAKRKAQMGNTROBMTMVN	799
DB	730	VPEPEKQDHTVKIAGIAGILVFIIFLGVLMVKRKLAKRKTETMSSTROBMTMVN	789
QY	800	AMDRSVADQSTLHAEDPLSLTTFMDQHNFSRLNDP-----LPTAVL-DENH	846
DB	790	SMDKSYAEQGTNCDE--AFSFMGTNLNGRSVSSPSTFTMKTNTLSTVSPNSYYPDETH	846
QY	847	SATAESSRLLDVPRY-LCEGTSPYQGLHPAIRVADLLQHLNLMKTSYSGPKEEVES	905
DB	847	TMASTSSSLAQPHTYKKEAADVPYQGLHPAIRVADLLQHLQTMKCAEGYKPEEVES	906
QY	906	FFEQSASMDVAKQDNRAKNRYCNIIAYDHSRVILQPVDEDDPSSDYINANYIDIMLYRD	965
DB	907	FFEQSAPWDSACKDENMKRNGNIIAYDHSRVRLQMLSGDNNSDYINGNYI-----D	960
QY	966	GYORPSHYIATQGVHETVDFWRMVWQEOSACIMVNTNLVEVGRVKCYKWPDDTEVYG	1025
DB	961	GYHRPNHYIATQGMQETIYDFWRMVWMENTASIIMVNTNLVEVGRVKCYKWPDDTEIYK	1020
QY	1026	DFKVTCTVEMEPLAEYVVRFTFLERRGYNIEVREKQHFHTGPDHGVPHATGLLSFTRV	1085
DB	1021	DIKVTLTIDTELLAEYVIRTEFAVEKRGHIEIREIQHFHTGMPDHGVPHATGLLGFRQV	1080
QY	1086	KLNSPPSAGPIVVHCSAGAGRTGCIYVIDIMLMAEREGVVDIYNCVKALRSRRINNMQT	1145
DB	1081	KSKSPNAGPLVVHCSAGAGRTGCFIVIDIMLMAEREGVVDIYNCVRELSRRVNMVQT	1140
QY	1146	EEQYIFIHDAILEACLGCTAIPVCBFKAAAYFDMIRIDSQTNSSHLEKDEFQTLNSVTPRL	1205
DB	1141	EEQYVFHDAILEACLGCTSIIPASQVRSLYDMNKLDPQTNSSQIKEEPFTLNMTPTL	1200
QY	1206	QAECSIAIACLRNHNKRPMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFIVT	1265
DB	1201	RVEDCSIALPRNHNKRCMDILPPDRCLPFLITIDGESSNYINAAALMDSYKQPSAFIVT	1260
QY	1266	QYPLPNTVKDFWRLVVDYGCSTIVMLNEVDLSQCPQYWPBEEGMLRYGPIQVECMCSMD	1325
DB	1261	QHPPLNTVKDFWRLVLDYHCTSVMLNDVDPAQLCFQYWFENGVRHGRGPIQVEFVSADLE	1320
QY	1326	CDVINRIFRICNLTRPQEGYLMVQQFOYLGWASHREVPGSKRSLKLILQVEKMQBCEE	1385
DB	1321	EDIISRIFRIYNASRRQDGRWVQQFQFLCPWYRDPFVSKRSLKLIRQVDKMQEYNG	1380
QY	1386	GEORTIHLCLNGGGRSGMFCAGIIVEMVGRQNVVDVFAVKTILRNSKPNMVEAPEQYRP	1445
DB	1381	GEFTVWHCLNGGGRSGTFCASIVCEMLRHQRTVDVFAVKTILRNNKPNMVDLLDQYKF	1440

QY 1446 CYDALEYLELES 1456  
DB 1441 CYDALEYLELNS 1451

RESULT 13  
US-08-769-399-4  
; Sequence 4, Application US/08769399  
; Patent No. 5976852  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Laaky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd.  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/769,399  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: P1033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 225-3216  
; TELEFAX: (415) 952-9881  
; TELEX: 910 371-7168  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1452 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-769-399-4

Query Match 61.4%; Score 4793.5; DB 2; Length 1452;  
Best Local Similarity 61.3%; Pred. No. 0;  
Matches 889; Conservative 208; Mismatches 325; Indels 29; Gaps 9;

QY 22 LIGSALGQFSAGGCTFDGPGACDYHQLYDDFEVWHVSAQEPHYLPPEMPOGSMYVDS 81  
DB 14 LLTLAGETFGGCLFDEPYTCGYSQADEDDFNQEVNLTLYKPSDPMPPSGSMLVNT 73

QY 82 SNHDPCEKARLQPTMKENDTHCIDFSYLLYSQKGLNPGTLNLRVKNKGPPLANIPWNT 141  
DB 74 SKPEGORAHLLLPQLKENDTHCIDFHYFVSKSNAAFGLLNVYKVNNGPLGNFANIS 133

QY 142 GFTGRDLWRAELAVSTFWNEVQVIFAEVSGRSGYIAIDIQVLSVPCDKSPHFLRIG 201  
DB 134 GDTTRTHRAELAISTFWNPNFYQVIFEV-VTSGHQYLAIDVKVGLGHPCTRTPHFLRIQ 192

QY 202 DVEVNAQONATQCCTATGDAVHKLWLRNGEDIPVAQTKNINHRRAFAASFRLEQVTK 261  
DB 193 NVEVNAQOPATFCQGAIGTAVAGRLWLGQIDVRDAPLKEIKVTSRRFIASFNVVNTTK 252

QY 262 TQDLYRCVTSQSGVSNFAQLIVREPPRIAPQLLGVGPTVILLIQLNANSIIGDGP 321  
DB 253 RDAGKYRCMCTEGGVGISNYAEVLVKEFPVPIAPQLASVGATYLIQLNANSINGDGP 312

QY 322 IILKEVEYRMTSGSWTETHAVNAPTYKILWHLDPDTEYEIRVLLTRPBGSGTGLPGPPLIT 381  
DB 313 IVAREVEYCTASGWNDRQPDVSTSYKIGHLDPDTEYEISVLLTRPBGSGTSGPGLART 372

QY 382 RTKCAEPMRTPKTLKIAEIQARRIAVDWESLGYNITRCHTFNVITICVHYFRGHNESRAD- 440  
DB 373 RTKCADPMRGPRLKLEVVVEKSRQITIRWEPGYNVTRCHSYNLTVHYGYVGQEQVREE 432

QY 441 -CLDMDPKAFOHVVNHLPPYTNVSLKMLITNPGRKESSEETIQTDEVDVPPVPVKSLOG 499  
DB 433 VSWDTNSHPQHTITNLSPYTNVSVKLLMNPGRKESQELTVQTDLPDPAVPTESIQ 492

QY 500 TSEFNKJFLNWKPLENGIITQVEVSVSSRSRDPRAVPVAGPPQTVSNLWNSHTHVPMH 559  
DB 493 SAFBEKIFLOWRSEPTQYGVITLYEITYKAVSSFDPELDLSNQSGRVSUKGNETHFLPFG 552

QY 560 LHPGTTYQFFETIRASTVKGFGPATAINVTNINISAPSLPDYEGVDASLNATATTITVLLRPA 619  
DB 553 LYPGTTYFTIRASTAKGFGPPATNQFTTKISAFSPAYE-FETPLNQTDNTVTVMKXPA 611

QY 620 QAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQNALSGGAPYFPAELPPGNLP 679  
DB 612 QSRGAPSVYQIVVEEERPRRTKTKTEILKCYVPVPIHFQNASILNSQYFPAEFPADSLQ 671

QY 680 EPAPFTVGDNRTYKGFWNPLAPRKGYNIYFQAMSSVEKETKTCQVRIATKAAATEPEV 739  
DB 672 AAQPTTIGDNKTYNGYWNTPLLPHKSYRIYQAAASRANGETKIDCVRVATKAVTPKE-- 729

QY 740 IPDPAKQTDNRVVKIAGISAGILVFILLVIVIVVVKSKLAKGRKADMGNTQEMTHVN 799  
DB 730 VPEPEKQTDHTVKIAGVIAGILLFVILFGLVVLVWKKEKLAKRKETMSSTRQEMTMVN 789

QY 800 AMDSYADQSTLHAEDPLSLTFMDQHNPSPLNDP-----LVPTAVL-DENH 846  
DB 790 SMDKSYAEQGTNCDE--AFSFMGTHNLNGRSVSSPSFTMKTNTLSTSPNSVYYPDETH 846

QY 847 SATAESRLLDVPRY-LCEGTESPVOTGOLHAPRAVADLLOHINLMKTSDSYGRKEEYES 905  
DB 847 TMSADTSLAOPHTYKKREAADVPYQGLHAPRAVADLLOHI TOMKCAEGYGFKEEYES 906

QY 906 FPEGQASWDVAKKDONRAKNRYGNI IAYDHSRVILQPVEDDPSPSDYINANYIDILWYRD 965  
DB 907 FPEGQASAPWDSAKDENEMKNRYGNI IAYDHSRVLRQLMLEGDNNSDYINGNYI-----D 960

QY 966 QYRPSHYIATQGPVHETVYDFWRMVWQESACIMVMTNLVEVGRVKCYKWPDDTEVYG 1025  
DB 961 GYHRPNHYIATQGPWQETIYDFWRMVWHENTASIIIMVTNLVEVGRVKCYKWPDDTEIYK 1020

QY 1026 DFKVTCVEMEPLAEVYVTRFTLEBRGYNEIREVQFHTGWPDHGVPVYHATGLLSFIRRV 1085  
DB 1021 DIKVTLIDTELLAEYIKHTFAVEKRGHIEIREIKQFHTGWPDPDHGVPVYHATGLLGFVQV 1080

QY 1086 KLSNPPSAGPIVHVHCSAGAGRTGCYIVIVIDIMLDAEREGVVDIYNCVKALRSRRINMVT 1145  
DB 1081 KSKSPPNAGPLVHCSAGAGRTGCYIVIVIDIMLDAEREGVVDIYNCVKALRSRRINMVT 1140

QY 1146 EQYFIFHDAILEACLCGETAIPVCEFKAAVDMIRIDSQNTSSHLKDBEQFTLNSVTPRL 1205  
DB 1141 EQYVFIHDAILEACLCGETSIPASQVRSVLYYDNKLDLPQNTSSQIKBEFRTLNMTPTL 1200

QY 1206 QAEDCSIACLRNHDKRPFMDLPPDRCLPLITIDGESSNYINALMDSYRQPAFIVT 1265  
DB 1201 RVEDCSIALPRNHEKNKCMIDLPPDRCLPLITIDGESSNYINALMDSYRQPAFIVT 1260

QY 1266 QYPLPNTVKDFWRLVYDYGCTSI VMLNEVDLSQGCQYWPBEGMLRYGPIQVECMSCSD 1325  
DB 1261 QHPLPNTVKDFWRLVLDVHCTSVMLNDVDPALQCPQWPENGVRHGHGPIQVEFVSADLE 1320

QY 1326 CDVINRIFRI CNLTRPQEGYLMVQQOYGLGWASHREVPGSKRSFKLILQVKEWEECEB 1385  
DB 1321 EDIISRIFRINASRPQDHRMVQQOFLGMPWYRDTTPVSKRSFKLIRQVDKWBEYNG 1380

QY 1386 GEGRTIIHCLNGGGRSGMFCAGIIVEMVKRQNVVDVFAVKTLRNSKPNMWEAPQYRF 1445

Db 1381 GEGTVHCLNGGSGTFCALISVCEMLRHQRTVDVFAVKTLLNNKPNMVDLLDQYKF 1440  
Qy 1446 CYDVALEYLES 1456  
Db 1441 CYEVALEYLNS 1451  
RESULT 14  
US-08-991-953A-4  
; Sequence 4, Application US/08991953A  
; Patent No. 6083748  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT, LLP  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991.953A  
; FILING DATE: 16-DEC-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/652,971  
; FILING DATE: 24-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-63478-3/WHD/WTK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1452 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-991-953A-4  
Query Match 61.4%; Score 4793.5; DB 3; Length 1452;  
Best Local Similarity 61.3%; Pred. No. 0;  
Matches 889; Conservative 208; Mismatches 325; Indels 29; Gaps 9;  
Qy 22 LLGSAFGSAGGCTFDDPGACDQHDLYDDFEMVHVSQAQEPHYLPMPQGSVMVYDS 81  
Db 14 LLLTAAGETSGGCLFDEPYSTCGYSQADEDDFNWQVNTLTUKTSDPMPGSGFMLVNT 73  
Qy 82 SNHDPGKARLQLPTMKENDTHCIDFSYLLYSQKGLNPGTLNILVRNKGKPLANPIWNVT 141  
Db 74 SKRPEGORAHLLLPQKENDTHCIDFHYFVSSKSNAPGLLVVYKVNNGPLGNPINIS 133  
Qy 142 GFTGRDMLRAELAVSTFWPNEYQVIFEAESVGGSGYIAIDDIQVLSYPCDKSPHFLRLG 201  
Db 134 GDPTRTHRAELAISTFWPNFYQVIFEV-VTSGHQGYLAIDVVKVGHPCRTTTHFLRIQ 192  
Qy 202 DVEVNAQONATFOCIATGRDAVHNKMLQRRNGEDIIPVAQTKNINHRFPAAFLQEVTK 261  
Db 193 NVEVNAQOFATFOCSAIGRTVAGDRLWLQGDVDRDAFLKKEIKVTSSRRFTASFNVTTK 252

Qy 262 TDQDLXRCVTSOBSRGSGVSNFAQLIVREPPRIAPPQLLGVGPTYLLQLNANSINGDP 321  
Db 253 RDAGKYRCMCTEGGVGISYAEVLVKEPPVPIAPPQLASVGATVLIQLNANSINGDP 312  
Qy 322 IILKEVEYRMTSGSWTETHAVNAPTYKLWHLDDPTEYEIRVLLTRPGSGTGLPGPLIT 381  
Db 313 IVAREVEYCTASGWNDRQPDVSTSYKIGHLDDPTEYEISVLLTRPGGGTSGPGPALRT 372  
Qy 382 RTKCAEPMRTPKTLKIAEQARRIAVDWESLGYNITRCHTNVNTICHYFRGHNESRAD- 440  
Db 373 RTKCADPMRGPRLKLEVVVEVRSQITIRWEPGYNVTRCHSYNLTVHYGVGGQVREE 432  
Qy 441 -CLMDPKAPOHVVNHLPPYTNVSLKMLITNPEGRKSEETIIOTDEBVPQVPPVKSIOG 499  
Db 433 VSWDTNSHPQHTITNLSPYTNVSVKLLMLNPEGRKESQELTVQTDLPDGAFTESIQG 492  
Qy 500 TSFENKIFLWKEPLENGIITQVEVSYSSTRSDPAVPVAGPPQTVNSLNWNSHHVPMH 559  
Db 493 SAFEKIFLOWREPTQYGVITLYEITYKAVSSPDEIDLSNQSGRVSYKLGNETHFLPFG 552  
Qy 560 LHPGTTYQFFTRASTVKGFGPATVNTNISAPSLPDYEGVDASLNETATTITVLRLPA 619  
Db 553 LYPCTYTSFTIRASTAKFGPPATNQFTTKISAPMPAYE-FETPLAQTDNTVIVMLKPA 611  
Qy 620 QAKGAPISAYQIVVEQLHPHRTKREAGAMBCYQVPTYQNALSGAPYFAAELPPGNLP 679  
Db 612 QSRGAPSVVYQIVVEEERPRRTKTBILKCYPVPIHFQNASILNSQYVFAAEPADSLQ 671  
Qy 680 EPAPFTVDNRITYKGFNWPPLARKGNYIYFOAMSSVEKETKTCVRIATKAAATEPEV 739  
Db 672 AAQPTTIGDNKTYNGYWNTPLLPHKSYRIYYQAAASRANGETKIDCVRVATKGVTPKP- 729  
Qy 740 IPOPAKQTRVVKIAGISAGILVIFILLVIVIVVKSKLAKKRDAMGNTRQENTHVN 799  
Db 730 VPPEKQTDHTVKIAGVIAGILLFVIFLGVLVKMKKLLAKKXKETMSSTRQENTHVN 789  
Qy 800 AMDRSYAQDSTLHAEDPLSLTFMDQHNFSRPLNDP-----LVPTAVL-DBNH 846  
Db 790 SMDKSYAEQGTNCDE---AFSFMGTHNLSRVSVPSSFTMKTNTLSTVSNSVYVDETH 846  
Qy 847 SATAESRLLDVPRY-LCEGTESPYQGLHPAIRVADLLQHLINLMKTSYSGKEEYES 905  
Db 847 TMASDTSSLAQPHYTKKREAADVPYQGLHPAIRVADLLQHLITQMKCAEGYKKEEYES 906  
Qy 906 FFEGQSASWDVAKDONRAKNRYNIIAYDHSRVILOPVEDDPSSDYNNYNIIDLVRD 965  
Db 907 FFEGQSAPWSAKKDNRMKNRYNIIAYDHSRVLQWLEGDNNSDINGNYI-----D 960  
Qy 966 GYORPSHYIATQGPVHETVDFWRMVMQESACIVMVYTNLVVEGRVKCYKWPDDTEYVG 1025  
Db 961 GYHRPNHYIATQGPVHETVDFWRMVMHENTASIIIMVTLNVEGRVKCKYWPDDTEYK 1020  
Qy 1026 DFKVTCTVMEPLAAYVVRTTLERRGYNIREVQKQFHTGWPDPHGVPYHATGLLSFRVR 1085  
Db 1021 DIKVTLLDTELLAAYVIRTEFAVEKRGHIREIRIQFHTGWPDPHGVPYHATGLLGFVRQ 1080  
Qy 1086 KLSNPPSAGPIVHCSAGAGTCGYIVIDIMLDMABREGVVYIYNCVKALRSRRINMVQT 1145  
Db 1081 KKSPPNAGPLVHCSAGAGTCGFIVIDIMLDMABREGVVYIYNCVRELRSRVNMVQT 1140  
Qy 1146 EEQVFIHDAILEACLGCTAIPVCEPKAAYFDMIRIDSQTNSSHLKDEFTOLNSVTPRL 1205  
Db 1141 EEQVFIHDAILEACLGDTISIPASQVRSLYDMNKLDPQTNSSQIKKEEFTLNWVPTL 1200  
Qy 1206 QABDCSIACLPNRHDKNRNFMMLPPDRCLPFLITIDGESSNYINAALMDSYRQPAAFIVT 1265  
Db 1201 RVEDCSIALPRNHEKRNKCMDILPPDRCLPFLITIDGESSNYINAALMDSYKQPSAFIVT 1260  
Qy 1266 QYPLPNTVKDFWRLVVDYDGTSTVLMNEVDLSQGCQYQWEEGMLRGVPTQVECKMSMD 1325  
Db 1261 QHPLPNTVKDFWRLVLDVHCTSVVMLNDVDPAQLCPQYWPENGVRHHRGPIQVEFVSADLE 1320





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:31:52 ; Search time 147.411 Seconds  
(without alignments)  
3822.724 Million cell updates/sec

Title: US-09-887-669-1  
Perfect score: 7809  
Sequence: 1 MDVAAALPAFVALLLYPW.....EAPQYRFCVDVALEYLESS 1457

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7809	100.0	1457	5 ABB57308	Mouse isc
2	7762	99.4	1457	2 AAR63633	Murine re
3	7586	97.1	1439	2 AAR63632	Human rec
4	7582	97.1	1439	7 ADJ68478	Human hea
5	7567.5	96.9	1440	2 AAY29591	Human pro
6	7567.5	96.9	1440	8 ADI23886	Human PTP
7	7412	94.9	1407	2 AAR63631	Murine re
8	4823.5	61.8	1452	4 AAM79159	Human pro
9	4812.5	61.6	1452	6 ABR58629	Human can
10	4812.5	61.6	1452	8 ADI80761	Human pro
11	4789.5	61.3	1452	7 ADJ68277	Human hea
12	4783	61.2	1455	4 AAM80143	Human pro
13	4591	58.8	1436	7 ADB79775	Rat putat
14	4577	58.6	1499	4 AAM25768	Human pro
15	4575	58.6	1436	2 AAM41361	Receptor
16	4545	58.2	1462	5 ABB97521	Human hum
17	4542.5	58.2	1463	6 ABJ37035	Human bre
18	4542.5	58.2	1463	7 ADB75519	Prostate
19	4542.5	58.2	1520	5 ABJ05584	Breast ca
20	4359	55.8	1442	7 ADJ68999	Human hea
21	4271	54.7	1430	2 AAW49907	Human pan
22	2471.5	31.6	623	4 AAM25675	Human pro
23	2216	28.4	815	4 AAM25875	Human pro
24	1514.5	19.4	1501	2 AAR72858	Rat recep
25	1495.5	19.2	1948	7 ADD18742	Human dis

## RESULT 1

\*ABB57308

ID ABB57308 standard; protein; 1457 AA.

XX ABB57308;

XX 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related protein sequence SEQ ID NO:862.

XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
XX vasospastic ischaemia; ischaemic condition; ischaemic disease.

XX Mus musculus.

XX WO200188188-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-JP004192.

XX 18-MAY-2000; 2000JP-00145977.

XX (UYNL-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI; 2002-034733/04.

XX N-PSDB; ABI99774.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes.

XX Claim 2; Page 2155-2161; 2690pp; English.

XX The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or

26 1494.5 19.1 1796 6 AAE37971 Aae37971 Human kin  
27 1494.5 19.1 1949 7 ADE57117 Ade57117 Human pro  
28 1494.5 19.1 1949 7 ADE57121 Ade57121 Human pro  
29 1494.5 19.1 1949 7 ADD47019 Add47019 Human pro  
30 1494.5 19.1 1949 7 ADD47015 Add47015 Human pro  
31 1492.5 19.1 1897 3 AAY81785 Aay81785 Human pro  
32 1492.5 19.1 1897 3 AAY56100 Aay56100 LAR tyros  
33 1492.5 19.1 1897 3 AAB19712 Aab19712 Human pro  
34 1492.5 19.1 1897 7 ADD18740 Add18740 Human dis  
35 1492.5 19.1 1897 8 ADJ33670 Adj33670 Human leu  
36 1492.5 19.1 1907 8 ADP18674 Adp18674 Human pro  
37 1490 19.1 1266 8 ADQ66041 Adq66041 Novel hum  
38 1488.5 19.1 1907 4 AAU14143 Aau14143 Human nov  
39 1485.5 19.0 1254 8 ADN02662 Adn02662 Liver dis  
40 1482.5 19.0 1912 8 ADR40183 Adr40183 Human pro  
41 1480 19.0 1911 2 AAR71726 Aar71726 Human PTP  
42 1480 19.0 1911 2 AAW27225 Aaw27225 Human pro  
43 1480 19.0 1911 2 AAW94027 Aaw94027 Human pro  
44 1480 19.0 1911 4 AAU01459 Aau01459 Human pro  
45 1476 18.9 1495 5 ABB57380 Abb57380 Rat mucoc

## ALIGNMENTS

CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR  
 CC primers for a mouse ischaemic condition related sequence, which are used  
 CC in the exemplification of the present invention  
 XX  
 SQ Sequence 1457 AA;

Query Match 100.0%; Score 7809; DB 5; Length 1457;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDVAAAALPAFVALWLLYPWLLGALGQFSAGGCTFDDGACADYHQDLYDDFEWVHS 60  
 DB 1 MDVAAAALPAFVALWLLYPWLLGALGQFSAGGCTFDDGACADYHQDLYDDFEWVHS 60

QY 61 AQEPHYLPPEMPOGQSYMWVDSNHDPEKARLQLPTMKENDTHC1DPSYLLYSQKGLNPG 120  
 DB 61 AQEPHYLPPEMPOGQSYMWVDSNHDPEKARLQLPTMKENDTHC1DPSYLLYSQKGLNPG 120

QY 121 TLNILLVRNKGFLANPIWNVGTGTRDMLRAELAVSTFWPNEYQVIFPAEVSNGRSGYIA 180  
 DB 121 TLNILLVRNKGFLANPIWNVGTGTRDMLRAELAVSTFWPNEYQVIFPAEVSNGRSGYIA 180

QY 181 IDDIQVLSYPCDKSPHFLRLGDEVEVNAQNATFQCIATGRDAVHNKMLQRRNGEDI 240  
 DB 181 IDDIQVLSYPCDKSPHFLRLGDEVEVNAQNATFQCIATGRDAVHNKMLQRRNGEDI 240

QY 241 QTKNINHRRAASFLQEWTKTDQLYRCVTSERGSVSNPAQLIVREPPRPPIAPPOLL 300  
 DB 241 QTKNINHRRAASFLQEWTKTDQLYRCVTSERGSVSNPAQLIVREPPRPPIAPPOLL 300

QY 301 GVGPTYLLIQLNANSIIGDGPPIILKEVEYRMTSGSWTETHAVNAPTYKMLHLDPDTEYI 360  
 DB 301 GVGPTYLLIQLNANSIIGDGPPIILKEVEYRMTSGSWTETHAVNAPTYKMLHLDPDTEYI 360

QY 361 RVLTRPGEGETGLPGPLITRTKCAEPMRTPTKTKIAEIQARRIAVDWESLGYNITRCH 420  
 DB 361 RVLTRPGEGETGLPGPLITRTKCAEPMRTPTKTKIAEIQARRIAVDWESLGYNITRCH 420

QY 421 TPNVTICVHYFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESET 480  
 DB 421 TPNVTICVHYFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESET 480

QY 481 IIQTDDEVPVPVKSLOGTSPENKI FLNWKPELPNGIITQYEVSYSSIRSFDPAPVA 540  
 DB 481 IIQTDDEVPVPVKSLOGTSPENKI FLNWKPELPNGIITQYEVSYSSIRSFDPAPVA 540

QY 541 GPPQTVSNLWNSTHRVFVHLHPGTTYYQFFIRASTVKGFGPATAINVTNISAPSLPDYEG 600  
 DB 541 GPPQTVSNLWNSTHRVFVHLHPGTTYYQFFIRASTVKGFGPATAINVTNISAPSLPDYEG 600

QY 601 VDASLNETHATITVLLRPAQAKGAPISAYQIIVVEQLHPHRYKREAGAMECTQVPVYQNA 660  
 DB 601 VDASLNETHATITVLLRPAQAKGAPISAYQIIVVEQLHPHRYKREAGAMECTQVPVYQNA 660

QY 661 LSGGAPYFAAELPGLNPEPAPFTVGNRTYKGFNPNPLAPRKGYNIYFOAMSSVEKET 720  
 DB 661 LSGGAPYFAAELPGLNPEPAPFTVGNRTYKGFNPNPLAPRKGYNIYFOAMSSVEKET 720

QY 721 KTQCVRIATKAAATEBEPEVDPAPQTDVRVKIAGISAGILVFILLLLVIVIVKSKLA 780  
 DB 721 KTQCVRIATKAAATEBEPEVDPAPQTDVRVKIAGISAGILVFILLLLVIVIVKSKLA 780

QY 781 KKRKDMGNTRQEMTHVNMNDRSYADQSTLHAEDPLSLTFMDQNFSPRLPNDPLVPTA 840  
 DB 781 KKRKDMGNTRQEMTHVNMNDRSYADQSTLHAEDPLSLTFMDQNFSPRLPNDPLVPTA 840

QY 841 VLDEHNSATAESSRLLDVPRYLCEGTESPYQGLHPAIRVADLLQHLNLMKTSYSGPK 900  
 DB 841 VLDEHNSATAESSRLLDVPRYLCEGTESPYQGLHPAIRVADLLQHLNLMKTSYSGPK 900

QY 901 EYESFFEQQSASWDVAKKQNRKNRYGNIITAYDHSRVILQPVEDDPSSDYINANYIDI 960  
 DB 901 EYESFFEQQSASWDVAKKQNRKNRYGNIITAYDHSRVILQPVEDDPSSDYINANYIDI 960

QY 961 WLVRDGYORPSHYTATQGPVHETVYDFWRVWYQSQSACIVMVTNLVEGRVKCYWPD 1020  
 DB 961 WLVRDGYORPSHYTATQGPVHETVYDFWRVWYQSQSACIVMVTNLVEGRVKCYWPD 1020

QY 1021 TEVTGDFKVTCTVEMEPLAEYVVRFTTLERRGYNIREVKQPHFTGWPDPHGVPYHATGLLS 1080  
 DB 1021 TEVTGDFKVTCTVEMEPLAEYVVRFTTLERRGYNIREVKQPHFTGWPDPHGVPYHATGLLS 1080

QY 1081 FIRVKLSNPPSAGPIVVHCSAGAGRTGCIYIVIMLMDABREGVVDIYNCVKALRSRI 1140  
 DB 1081 FIRVKLSNPPSAGPIVVHCSAGAGRTGCIYIVIMLMDABREGVVDIYNCVKALRSRI 1140

QY 1141 NMVQTEQYIFIHDAIILEACLGCGETAIPVCEFKAAAFDMIRIDQSTNSSHLKDEFOTLNS 1200  
 DB 1141 NMVQTEQYIFIHDAIILEACLGCGETAIPVCEFKAAAFDMIRIDQSTNSSHLKDEFOTLNS 1200

QY 1201 VTPRLQAEDECSIACLPRNHDKNRDMMLPPDRCLPFLITIDGESNYINAALMDSYRPA 1260  
 DB 1201 VTPRLQAEDECSIACLPRNHDKNRDMMLPPDRCLPFLITIDGESNYINAALMDSYRPA 1260

QY 1261 AFIVTQVPLPNTVKDFWRLVYDYGCTSIWMLNEVDLSQGCPOYWPPEGMLRYGPQVECM 1320  
 DB 1261 AFIVTQVPLPNTVKDFWRLVYDYGCTSIWMLNEVDLSQGCPOYWPPEGMLRYGPQVECM 1320

QY 1321 SCSNDCDVINRI FRICNLTRPOEGYLMVQOQYILGWASHREVPGSKRSFLKLIQVEKWO 1380  
 DB 1321 SCSNDCDVINRI FRICNLTRPOEGYLMVQOQYILGWASHREVPGSKRSFLKLIQVEKWO 1380

QY 1381 ECEGEGRITIIHCLNGGSGMFCAGIIVVEMVKRQNVVDVFAVKTLRNSKPNMVEAP 1440  
 DB 1381 ECEGEGRITIIHCLNGGSGMFCAGIIVVEMVKRQNVVDVFAVKTLRNSKPNMVEAP 1440

QY 1441 EQYRFCYDVALEYLESS 1457  
 DB 1441 EQYRFCYDVALEYLESS 1457

RESULT 2  
 AAR63633  
 ID AAR63633 standard; protein; 1457 AA.

XX AAR63633;  
 AC AAR63633;  
 XX 21-OCT-2004 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 08-JUN-1995 (first entry)  
 XX  
 DE Murine receptor-type protein tyrosine phosphatase precursor protein.  
 XX Receptor-type protein tyrosine phosphatase protein; cellular signal;  
 KW RPTase-kappa; enzyme.  
 XX Mus musculus.  
 OS Unidentified.

XX Key Location/Qualifiers  
 FH Peptide 1..25  
 FT /label= signal  
 FT Region 33..189  
 FT /label= A5 surface protein homology  
 FT Domain 733..774  
 FT /label= Transmembrane  
 FT Domain 926..1158  
 FT /label= PTPase I  
 FT Domain 1218..1455  
 FT /label= PTPase II  
 XX WO9424161-A1.  
 PN  
 XX 27-OCT-1994.  
 PD  
 XX 20-APR-1994; 94WO-US004377.  
 PF

XX 21-APR-1993; 93US-00049384.  
 PR 01-JUL-1993; 93US-00087244.  
 XX (UNY-) UNIV NEW YORK MEDICAL CENT.  
 PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX Schlessinger J, Sap JM, Ullrich A, Vogel W, Fuchs M;  
 PI WPI; 1994-341769/42.  
 XX N-PSDB; AAO72914.  
 DR Mammalian receptor-type protein tyrosine phosphatase-kappa (RPTP-k)  
 XX protein and DNA - useful to identify cpds. which bind to RPTP-k and  
 PT modulate enzymatic activity. Also inhibition of type II RPTP homo:phili  
 PT binding (Engl).  
 XX Claim 2; Fig 1; 144pp; English.  
 PS The novel receptor-type protein tyrosine phosphatase protein or  
 XX Glycoprotein is termed RPTP kappa (also known as Rptase-kappa). The first  
 CC approx. 170AAs of RPTP kappa show similarity (26% overall identity) to a  
 CC region in the Xenopus cell surface protein A5 with features of Ig-like  
 CC domains. There are four putative fibronectin type III-like repeats  
 CC (residues 286-681). The tandem repeat of two Fipase homologues is typical  
 CC for most RPTPases. A feature of RPTP kappa is the extended distance  
 CC between its transmembrane domain and the start of the first phosphatase  
 CC homology domain. The RPTP kappa cDNA sequence comprises a 5' UTR of 1072  
 CC bps and a 3' UTR of 388 bps. The translational initiation codon is  
 CC identified by a std. environment for initiation of translation (Kozak)  
 CC and by the existence of an upstream in-frame stop codon, and is followed  
 CC by a hydrophobic region that may serve as a signal peptide. (Updated on  
 CC 25-MAR-2003 to correct PN field.)  
 CC Revised record issued on 21-OCT-2004 : Correction to feature table key  
 XX Sequence 1457 AA;

Query Match 99.4%; Score 7762; DB 2; Length 1457;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1449; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MDVAAALPAFVALWLLYPPLGSLAQFSAGCTFDDGFGACDYHQDLYDDPFEWVHVS 60  
 DB 1 MDVAAALPAFVALWLLYPPLGSLAQFSAGCTFDDGFGACDYHQDLYDDPFEWVHVS 60

QY 61 AQSPHYLPPEWPGSYMVVDSSNHDGCEKARLQPTMKENDTHCIDPSYLLYSQKGLNPG 120  
 DB 61 AQSPHYLPPEWPGSYMVVDSSNHDGCEKARLQPTMKENDTHCIDPSYLLYSQKGLNPG 120

QY 121 TLMILVRVNGKPLANPIWNTGTGRDMLRAELAVSTFWNEQVIFEAEVSGRSGYIA 180  
 DB 121 TLMILVRVNGKPLANPIWNTGTGRDMLRAELAVSTFWNEQVIFEAEVSGRSGYIA 180

QY 181 IDIQVLSYPCDKSPHFLRGDVEVNAQONATFCIATGRDAVHNKMLQRRNGEDIPVA 240  
 DB 181 IDIQVLSYPCDKSPHFLRGDVEVNAQONATFCIATGRDAVHNKMLQRRNGEDIPVA 240

QY 241 OTKNINHRRFAASFRLEQVTKTDQDLYRCVYTSQSRGSGVSNFAQLIVREPPRIAPQLL 300  
 DB 241 OTKNINHRRFAASFRLEQVTKTDQDLYRCVYTSQSRGSGVSNFAQLIVREPPRIAPQLL 300

QY 301 GVGFTYLLIQLNANSIIGDGPILIKVEYRMTSGSWTETHAVNAPTLYKLWHLDPDTEYI 360  
 DB 301 GVGFTYLLIQLNANSIIGDGPILIKVEYRMTSGSWTETHAVNAPTLYKLWHLDPDTEYI 360

QY 361 RVLLTRPEGGTGLPGPPLITRTKCAEPMRTPTKLKIAEQARRIADWESLGYNITRCH 420  
 DB 361 RVLLTRPEGGTGLPGPPLITRTKCAEPMRTPTKLKIAEQARRIADWESLGYNITRCH 420

QY 421 TFWNTICYHFRGHNESRACLDMDPKAPOHVNVNHLPPYTNVSLKMLITNPEGRKSEET 480  
 DB 421 TFWNTICYHFRGHNESRACLDMDPKAPOHVNVNHLPPYTNVSLKMLITNPEGRKSEET 480

QY 481 IIQTDEDPGVPVKSLQGSTFENKIFLNWKEPLEPENGIIITQYEVSVSSIRSFDPVPVA 540  
 DB 481 IIQTDEDPGVPVKSLQGSTFENKIFLNWKEPLEPENGIIITQYEVSVSSIRSFDPVPVA 540

QY 541 GPPQTYSNLWNSTHRVFMHLHPCGTYQFFIRASTVKGFGPATAINVTNTISAPSLPYEG 600  
 DB 541 GPPQTYSNLWNSTHRVFMHLHPCGTYQFFIRASTVKGFGPATAINVTNTISAPSLPYEE 600

QY 601 VDASLNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQNA 660  
 DB 601 VDASLNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQNA 660

QY 661 LSGGAPYFAAELPPGNLPEPAPFTVGDNRTYGFNPPPLAPRKGNIIYFOAMSSVKEKET 720  
 DB 661 LSGGAPYFAAELPPGNLPEPAPFTVGDNRTYGFNPPPLAPRKGNIIYFOAMSSVKEKET 720

QY 721 KTCQVRIATKAAATEPEVTPDPAKQTDVRVKIAGISAGILVFLILLVIVIVKSKLA 780  
 DB 721 KTCQVRIATKAAATEPEVTPDPAKQTDVRVKIAGISAGILVFLILLVIVIVKSKLA 780

QY 781 KKPKDANGTRQSWTHMVNAMDYSADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPTA 840  
 DB 781 KKPKDANGTRQSWTHMVNAMDYSADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPTA 840

QY 841 VLDENHSATAESSRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHLINLMKTSDSYGFK 900  
 DB 841 VLDENHSATAESSRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHLINLMKTSDSYGFK 900

QY 901 EYESFEQGSASNDVAKDONRAKRYGNIIDYHSRVILQVEDDPSSDIYANVIDI 960  
 DB 901 EYESFEQGSASNDVAKDONRAKRYGNIIDYHSRVILQVEDDPSSDIYANVIDI 960

QY 961 WLVRDGYQRPESHVIAIQGPVHETVDFWRMWQEQSACIWMVTNLVEVGRVKYKWPDD 1020  
 DB 961 WLVRDGYQRPESHVIAIQGPVHETVDFWRMWQEQSACIWMVTNLVEVGRVKYKWPDD 1020

QY 1021 TEVYGFVKTCVEMSEPLAEYVVRTFTLRRGYNEIREVKQFHTGPDHGVPHATGLLS 1080  
 DB 1021 TEVYGFVKTCVEMSEPLAEYVVRTFTLRRGYNEIREVKQFHTGPDHGVPHATGLLS 1080

QY 1081 FIRRKLNSPPSAGPIVWHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRI 1140  
 DB 1081 FIRRKLNSPPSAGPIVWHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRI 1140

QY 1141 NMVQTEEQYIFHDAILEACLCGETAIPVCEFKAAVFDIMIRIDQSTNSSHLKDEFOFLNS 1200  
 DB 1141 NMVQTEEQYIFHDAILEACLCGETAIPVCEFKAAVFDIMIRIDQSTNSSHLKDEFOFLNS 1200

QY 1201 VTPRLQAECDCSIACLPRNHDKNRFDMLPPDRCLPFLITIDGESSNYINAALMDSYRQPA 1260  
 DB 1201 VTPRLQAECDCSIACLPRNHDKNRFDMLPPDRCLPFLITIDGESSNYINAALMDSYRQPA 1260

QY 1261 AFITVQYPLPNTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCPOQYWPBEGMLRYGPIQVECM 1320  
 DB 1261 AFITVQYPLPNTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCPOQYWPBEGMLRYGPIQVECM 1320

QY 1321 SCSDMCDVNRIFRIENLTPQEGYLMVQOQFOYLGWASHREVPGSKRSFLKLILQVEKQW 1380  
 DB 1321 SCSDMCDVNRIFRIENLTPQEGYLMVQOQFOYLGWASHREVPGSKRSFLKLILQVEKQW 1380

QY 1381 EECBEGEGRTIIHCLNGGSGRGMFCFCAIGIVEMVXGQNVVDVFAVKTLSKNSKNMVEAP 1440  
 DB 1381 EECBEGEGRTIIHCLNGGSGRGMFCFCAIGIVEMVXGQNVVDVFAVKTLSKNSKNMVEAP 1440

QY 1441 EQYRFCYDVALEYLESS 1457  
 DB 1441 EHYRFCYDLPDLEYLESS 1457

RESULT 3  
 AAR63632  
 ID AAR63632 standard; protein; 1439 AA.



Db 1062 SFIRVKLSPPSAGPIVHCSAGAGTGCYIVIDMLDAERGVDYIYNCVKALRSR 1121  
Qy 1140 INMQTEEQIFIHDAILEACLCGETAIPVCEPKAAAFDMIRIDSQTNSSHLKDEFQTLN 1199  
Db 1122 INMQTEEQIFIHDAILEACLCGETAIPVCEPKAAAFDMIRIDSQTNSSHLKDEFQTLN 1181  
Qy 1200 SVTPRLQAECSIACLPRNHDKNRFDMLPPDRCLPLITIDGSSNYINAALMDSYRQP 1259  
Db 1182 SVTPRLQAECSIACLPRNHDKNRFDMLPPDRCLPLITIDGSSNYINAALMDSYRQP 1241  
Qy 1260 AAFIVTOYPLPNTVKDFWRLVYDYGCTSIWMLNEVDLSQCPQYWPBEGMLRYGPIQVEK 1319  
Db 1242 AAFIVTOYPLPNTVKDFWRLVYDYGCTSIWMLNEVDLSQCPQYWPBEGMLRYGPIQVEK 1301  
Qy 1320 MSCMDCDVINRIFRICNLTRPQEGYLMVQOFOYLGWASHREVPGSKRSFLKILQVEKW 1379  
Db 1302 MSCMDCDVINRIFRICNLTRPQEGYLMVQOFOYLGWASHREVPGSKRSFLKILQVEKW 1361  
Qy 1380 QECCEGEGRTIICHLNGGGRSGMFCAGIIVEMVKRQNVVDVFAVKTILRNSKPNMVEA 1439  
Db 1362 QECCEGEGRTIICHLNGGGRSGMFCAGIIVEMVKRQNVVDVFAVKTILRNSKPNMVEA 1421  
Qy 1440 PEQYRFCYDVALEYLESS 1457  
Db 1422 PEQYRFCYDVALEYLESS 1439

RESULT 4  
ADJ68478  
ID ADJ68478 standard; protein; 1439 AA.  
XX ADJ68478;  
AC  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human heat mitochondrial protein as a therapeutic target SeqID284.  
XX  
KW mitochondrial; human; screening assay; diabetes mellitus;  
KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
KW osteopathic; ophthalmological; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN W02003087768-A2.  
XX  
XX 23-OCT-2003.  
XX  
XX 04-APR-2003; 2003WO-US010870.  
XX  
XX 12-APR-2002; 2002US-0372843P.  
XX 17-JUN-2002; 2002US-0389987P.  
XX 20-SEP-2002; 2002US-0412418P.  
XX  
XX (MITO-) MITOKOR.  
XX PA (BUCK-) BUCK INST AGE RES.  
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;  
XX Warnock DE;  
XX WPI; 2003-845369/78.  
XX  
XX Identifying a mitochondrial target for drug screening assays and for  
XX treating diseases associated with altered mitochondrial function,  
XX comprises detecting a modified polypeptide in a sample and correlating  
XX with the disease.  
XX  
XX Claim 1; SEQ ID NO 284; 180pp; English.  
XX  
XX

CC This invention relates to novel mitochondrial targets that can be used  
CC for therapeutic intervention in treating a disease associated with  
CC altered mitochondrial function. Specifically, it refers to a method for  
CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, nootropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytostatic activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.  
XX  
SQ Sequence 1439 AA;  
  
Query Match 97.1%; Score 7592; DB 7; Length 1439;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 1420; Conservative 13; Mismatches 5; Indels 20; Gaps 4;  
  
Qy 1 MD-VAAALPAFVALWLLYEPWLLGSLGQFSAGGCTFDDGPGACDYHQDLYDDFEWVHV 59  
Db 1 MDTTAAALPAFVALLLSPWLLGSAQGFAGGCTFDDGPGACDYHQDLYDDFEWVHV 60  
  
Qy 60 SAQEPHYLPPEMQGSSYMWVDSNNHDPGEKARLQPTMKENDTHCIDFSYLLYSQKGLNP 119  
Db 61 SAQEPHYLPPEMQGSSYMWVDSNNHDPGEKARLQPTMKENDTHCIDFSYLLYSQKGLNP 120  
  
Qy 120 GTNLILVRNKGPLANPINNVGTGTGRDMLRAELAVSSFWPNEYQVIFEAESGGRSGYI 179  
Db 121 GTNLILVRNKGPLANPINNVGTGTGRDMLRAELAVSSFWPNEYQVIFEAESGGRSGYI 180  
  
Qy 180 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONAFQCIATGRDAVHNLKWLQRRNGEDIPV 239  
Db 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONAFQCIATGRDAVHNLKWLQRRNGEDIPV 240  
  
Qy 240 AQTKNINHRFAASFRLOEVTKTQDQILYRCVTSERGSVSNFAQLIVRPPRIAPPOL 299  
Db 241 AQTKNINHRFAASFRLOEVTKTQDQILYRCVTSERGSVSNFAQLIVRPPRIAPPOL 300  
  
Qy 300 LGVGPTVLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPTYKLUHLDPDTEYE 359  
Db 301 LGVGPTVLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPTYKLUHLDPDTEYE 360  
  
Qy 360 IRVLLTRPGEGGTGLPGPLITITKCAEPNRTKTLKIAEIQARRIADVDESIGYNTTRC 419  
Db 361 IRVLLTRPGEGGTGLPGPLITITKCAEPNRTKTLKIAEIQARRIADVDESIGYNTTRC 420  
  
Qy 420 HTFNVTICVHYFRGHNESRADCLMDPKAPQHVHNLPPYTNVSLKMLTNPEGRKESEE 479  
Db 421 HTFNVTICVHYFRGHNESKADCLMDPKAPQHVHNLPPYTNVSLKMLTNPEGRKESEE 480  
  
Qy 480 TTIQTDEDVGPVPVKSLOQTSFENKIFLNWKEPFPNGIITQVEYSYSSIRSFDPAPVP 539  
Db 481 TTIQTDEDVGPVPVKSLOQTSFENKIFLNWKEPFPNGIITQVEYSYSSIRSFDPAPVP 540  
  
Qy 540 AGPPQTVSNLWNSHTHVFMHLHFGTYTQFFIRASTVKGFGPATAINVTNISAPSLDYE 599  
Db 541 AGPPQTVSNLWNSHTHVFMHLHFGTYTQFFIRASTVKGFGPATAINVTNISAPSLDYE 600  
  
Qy 600 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQN 659  
Db 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQN 660  
  
Qy 660 ALSGAGPYFAAELPPGNLPEPAPFTVGDNRITYKGFWMNPPLAPRKGYNIYFQAMSSVEKE 719  
Db 661 AMSGAGPYFAAELPPGNLPEPAPFTVGDNRITYKGFWMNPPLAPRKGYNIYFQAMSSVEKE 720  
  
Qy 720 TKTCQVRIATKAAATBEPEVIPPAPKOTDRVKIAGISAGILVFILLLLVIVIKKSKL 779  
Db 721 TKTCQVRIATK-AATBEPEVIPPAPKOTDRVKIAGISAGILVFILLLLVIVIKKSKL 779

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QY 780 AKKRKDMGNTROEMTHMVNADRSYADOSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPT 839
Db 780 AKKRKDMGNTROEMTHMVNADRSYADOSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPT 831
QY 840 AVLDEHNSATAESSRLLDVPRYLCGTESPYQTQLHPAIRVAOILQHINLMKTSDSYGF 899
Db 832 ----ENHNSATAESSRLLDVPRYLCGTESPYQTQLHPAIRVAOILQHINLMKTSDSYGF 887
QY 900 KEEYESFEGQSASWDVAKQONRAKRYGNIAYDHSRVLQPVEDDPSSDIYINANVID 959
Db 888 KEEYESFEGQSASWDVAKQONRAKRYGNIAYDHSRVLQPVEDDPSSDIYINANVID 946
QY 960 IWLVDGYORSHYIATGPHVETVYDFRWVWQEOSACIWMVTNLVEGVKCYKWPD 1019
Db 947 -----DGYPORSHYIATGPHVETVYDFRWVWQEOSACIWMVTNLVEGVKCYKWPD 1001
QY 1020 DTEVYGFDFKVCVENEPLAEYVVRTFTLLRRGYNEIREVKQFHFPGWPDHGVPHATGLL 1079
Db 1002 DTEVYGFDFKVCVENEPLAEYVVRTFTLLRRGYNEIREVKQFHFPGWPDHGVPHATGLL 1061
QY 1080 SFIRVKLSNPPSAGPIVHCSAGAGRTGCVIIVIMLDMAREGVVDIYNCVKALRSRR 1139
Db 1062 SFIRVKLSNPPSAGPIVHCSAGAGRTGCVIIVIMLDMAREGVVDIYNCVKALRSRR 1121
QY 1140 INMVQTESQYIFIHDAILEACLCGETAIPVCEFKAAAYEDMIRIDISQTNSSHLKDBFQTLN 1199
Db 1122 INMVQTESQYIFIHDAILEACLCGETAIPVCEFKAAAYEDMIRIDISQTNSSHLKDBFQTLN 1181
QY 1200 SVTPRLQAECDSCIAPRNDKRNRFMDMLPPDRCLPFLITIDGESSNINAAALMDSYRQP 1259
Db 1182 SVTPRLQAECDSCIAPRNDKRNRFMDMLPPDRCLPFLITIDGESSNINAAALMDSYRQP 1241
QY 1260 AAFIVTQYPLNVTXDFWRLVYDYGCTSIIVMLNEVDLSQGCPCQYWPBEGMLRYGPIQVEC 1319
Db 1242 AAFIVTQYPLNVTXDFWRLVYDYGCTSIIVMLNEVDLSQGCPCQYWPBEGMLRYGPIQVEC 1301
QY 1320 MSCSMDCDVINRIFRICNLTRPQEGYLMVQOQYLGWASHREVPQSKSFLLILOVEKW 1379
Db 1302 MSCSMDCDVINRIFRICNLTRPQEGYLMVQOQYLGWASHREVPQSKSFLLILOVEKW 1361
QY 1380 QBECEGEGRTIIHCLNGGSGMFCALGIVVMYKRONVVDVHAVKTLRNSKPNMVEA 1439
Db 1362 QBECEGEGRTIIHCLNGGSGMFCALGIVVMYKRONVVDVHAVKTLRNSKPNMVEA 1421
QY 1440 PEQYRFDVDALEYLESS 1457
Db 1422 PEQYRFDVDALEYLESS 1439
```

## RESULT 5

```
AAAY29591
ID AAAY29591 standard; protein; 1440 AA.
```

AC AAAY29591;

XX AAAY29591;

DT 14-OCT-1999 (first entry)

DE Human protein phosphatase k.

XX Human; protein phosphatase k; HPTPK.

XX Homo sapiens.

XX KR98026246-A.

XX 15-JUL-1998.

XX 08-OCT-1996; 96KR-00044614.

XX 08-OCT-1996; 96KR-00044614.

XX (KOAD ) KOREA ADV INST SCI &amp; TECHNOLOGY.

```
XX Hah HJ, Kil MC, Yang Y, Byun GH;
XX WPI; 1999-335582/28.
DR N-ESDB; AAZ08539.
XX Human protein phosphatase, base sequence thereof and amino acid sequence
PT thereof.
XX Disclosure; Fig 1a-d; 14pp; Korean.
XX The present sequence represents human protein phosphatase k (HPTPK)
XX Sequence 1440 AA;
QY 1 MD-VAAALPAFVALMLLYPWLGLSALGQFSAGGCTFDDGPGACDYHQDLYDDPEWHV 59
Db 1 MDTTAAAVPAFVALLLSPLGLSAGQGSAGGCTFDDGPGACDYHQDLYDDPEWHV 60
QY 60 SAQEPHYLPPEMPOGSMYVVDSSNHDPEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 119
Db 61 SAQEPHYLPPEMPOGSMYVVDSSNHDPEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 120
QY 120 GTLNLVRVNGKPLANPINWVTGTRDMLRAELAVSTFWPNEYQVIFPEAEVSGRSGYI 179
Db 121 GTLNLVRVNGKPLANPINWVTGTRDMLRAELAVSTFWPNEYQVIFPEAEVSGRSGYI 180
QY 180 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFCIATGTRDAVHNKMLQRRNGEDIPV 239
Db 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFCIATGTRDAVHNKMLQRRNGEDIPV 240
QY 240 AQTKNINHRRAAASFRLOEVTKTDQDLYRCVTSQERSGSVNFAQLIVREPPRPIAPQL 299
Db 241 AQTKNINHRRAAASFRLOEVTKTDQDLYRCVTSQERSGSVNFAQLIVREPPRPIAPQL 300
QY 300 LGVGTYLLIQLNANSIIGDGPILKEVEYMTSGSWTETHAVNAPTLYKWLHLDPTDEYE 359
Db 301 LGVGTYLLIQLNANSIIGDGPILKEVEYMTSGSWTETHAVNAPTLYKWLHLDPTDEYE 360
QY 360 IRVLLTRPGEGETGLPGPPLITRTKCAEPMTPTKLTAEIOARRIADVMSLGNITRC 419
Db 361 IRVLLTRPGEGETGLPGPPLITRTKCAEPMTPTKLTAEIOARRIADVMSLGNITRC 420
QY 420 HTFNVTICYHYFRGHNESRADCLDMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEE 479
Db 421 HSFNVTICYHYFRGHNESKADCLDMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEE 480
QY 480 TIIQTDDEVPGVPVKSLQGTSPENKIPLNWKPELPNGIITQYEVSVSSIRSFDPAPVP 539
Db 481 TIIQTDDEVPGVPVKSLQGTSPENKIPLNWKPELPNGIITQYEVSVSSIRSFDPAPVP 540
QY 540 AGPPQTVSNLWNSTHRVFHLHPGTYYOFFTRASTVKGFGPATAINVTNINSAPSLDYE 599
Db 541 AGPPQTVSNLWNSTHRVFHLHPGTYYOFFTRASTVKGFGPATAINVTNINSAPSLDYE 600
QY 600 GVDASLNETATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQN 659
Db 601 GVDASLNETATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQN 660
QY 660 ALSGAGPYFAAELPPGNLPEPAPFTVGDNRNRYKGFWMNPPPLAPRGYNYIYFOAMSVEKE 719
Db 661 AMSGAGPYFACTPPGNLPEPAPFTVGDNRNRYKGFWMNPPPLAPRGYNYIYFOAMSVEKE 720
QY 720 TKTCVRIATKAAATEEPEVDPKAKOTDRVVVKGISAGILVFTLLLVIVIVKSKL 779
Db 721 TKTCVRIATKAAATEEPEVDPKAKOTDRVVVKGISAGILVFTLLLVIVIVKSKL 780
QY 780 AKKRKDMGNTROEMTHMVNADRSYADOSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPT 839
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Db 781 AKRKDAMGNTRQEMTHWVAMDRSYADQSTLHAEDPLSITFMDOHNFSPRY----- 832
Qy 840 AVLDENHSATAESRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHINLMKTSDSYGF 899
Db 833 ---ENHSATAESRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHINLMKTSDSYGF 888
Qy 900 KEYESFFEGQSADWAKKQDNRAKRYGNIITAYDHSRVLQPVEDPSSDYINANYID 959
Db 889 KEYESFFEGQSADWAKKQDNRAKRYGNIITAYDHSRVLQPVEDPSSDYINANYI- 947
Qy 960 IWLRYDGYQRPShYIATQGPVHETVDFWVRWQESACIWMVNLVVGVRVKCYKWPD 1019
Db 948 ----DGYQRPShYIATQGPVHETVDFWVRWQESACIWMVNLVVGVRVKCYKWPD 1002
Qy 1020 DTEVYDGFKVTCEMEPLASYVVRFTFLRRGYNEIREVKQHFHTGMPDHGVPVHATGLL 1079
Db 1003 DTEVYDGFKVTCEMEPLASYVVRFTFLRRGYNEIREVKQHFHTGMPDHGVPVHATGLL 1062
Qy 1080 SFTRRVKLSNPPSAGPIVHCHSAGAGRTGCIYVIDIMLMAEREGVVDIYNCVKALBSRR 1139
Db 1063 SFTRRVKLSNPPSAGPIVHCHSAGAGRTGCIYVIDIMLMAEREGVVDIYNCVKALBSRR 1122
Qy 1140 INNVQTEEQYIFTHDAILEACLCGETAIPVCEPKAAAFDMIRIDSQTNSSHLKDEPOTLN 1199
Db 1123 INNVQTEEQYIFTHDAILEACLCGETAIPVCEPKAAAFDMIRIDSQTNSSHLKDEPOTLN 1182
Qy 1200 SVTPRLQAECDSCIACLRNHDKNRPMMLPPDRCLPELITIDGESSNYINAALMDSYRQP 1259
Db 1183 SVTPRLQAECDSCIACLRNHDKNRPMMLPPDRCLPELITIDGESSNYINAALMDSYRQP 1242
Qy 1260 AAFIVTQYPLPNTVKDFWRLVYDYGCTSIYVNLNEVDLSQCPQYWPBEGMLRYGPTQVE 1319
Db 1243 AAFIVTQYPLPNTVKDFWRLVYDYGCTSIYVNLNEVDLSQCPQYWPBEGMLRYGPTQVE 1302
Qy 1320 MSCMCDVNLNFRICNLNTRPOEGLMWQOFOYLGWASHREVPGSKRSFLKLILOVEKW 1379
Db 1303 MSCMCDVNLNFRICNLNTRPOEGLMWQOFOYLGWASHREVPGSKRSFLKLILOVEKW 1362
Qy 1380 QEBCEBEGRTIIHCLNGGGRSGMFCAGIIVEMVKRQNVVDVVFHAVKTLRNSKPNMVEA 1439
Db 1363 QEBCEBEGRTIIHCLNGGGRSGMFCAGIIVEMVKRQNVVDVVFHAVKTLRNSKPNMVEA 1422
Qy 1440 PEQYRFDYVALEYLESS 1457
Db 1423 PEQYRFDYVALEYLESS 1440

RESULT 6
AD123886
ID AD123886 standard; protein; 1440 AA.
XX AC AD123886;
XX AC AD123886;
XX AC AD123886;
DT 22-APR-2004 (first entry)
XX DE Human PTPRK protein SEQ ID NO:4.
XX KW antisense oligonucleotide; human;
XX KW protein tyrosine phosphatase receptor type K; PTPRK; cytostatic;
XX KW antiinflammatory; antidiabetic; antisense gene therapy; diabetes;
XX KW inflammation; hyperproliferative disorder; cancer; chromosome 6.
XX OS Homo sapiens.
XX PN WO2004005312-A1.
XX PD 15-JAN-2004.
XX PF 27-JUN-2003; 2003WO-US016237.
XX PR 03-JUL-2002; 2002US-00189429.
XX PA (ISIS-) ISIS PHARM INC.
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XX PI Cowser LM, Freier SM;
XX DR WPI; 2004-083493/08.
XX DR N-PSDB; ADI23748.
XX PT New antisense oligonucleotide, having a sequence targeted to a nucleic
XX PT acid encoding PTPRK, useful for preparing a composition for treating
XX PT diabetes, inflammation or hyperproliferative disorder, e.g., cancer.
XX PS Example 13; SEQ ID NO 4; 150pp; English.
XX PS The present invention describes an antisense oligonucleotide (I), having
XX CC a sequence comprising 8-80 base pairs, targeted to a nucleic acid
XX CC encoding protein tyrosine phosphatase receptor type K (PTPRK), that
XX CC specifically hybridizes with the nucleic acid encoding PTPRK and inhibits
XX CC expression of PTPRK. Also described: (1) a composition comprising the
XX CC compound and a carrier or diluent; (2) a method of inhibiting the
XX CC expression of PTPRK in cells or tissues; (3) a method of treating an
XX CC animal having or suspected of having a disease or condition associated
XX CC with PTPRK; and (4) a method for screening for an antisense compound. (I)
XX CC has cytostatic, antiinflammatory and antidiabetic activities, and can be
XX CC used in antisense gene therapy. The antisense oligonucleotide (I) can be
XX CC used for preparing a composition for treating diabetes, inflammation or
XX CC hyperproliferative disorder, e.g., cancer. The present sequence
XX CC represents human PTPRK, which is used in an example from the present
XX CC invention. The human PTPRK gene is located on chromosome 6, more
XX CC specifically to 6q22.2-23.1.
XX SQ Sequence 1440 AA;
```

```
Query Match 96.9%; Score 7567.5; DB 8; Length 1440;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 1414; Conservative 16; Mismatches 9; Indels 19; Gaps 3;
Qy 1 MD-VAALPAFVALWLLYEPWLLGSALGQFSAGGCTFDDGPGACDYHQDLYDDFEWVHV 59
Db 1 MDTAAAAVPFVALLLLSPWLLGSAQGFAGGCTFDDGPGACDYHQDLYDDFEWVHV 60
Qy 60 SAQEPHYLPPEMPPQGSVMYVDSNHPDGEKARLQPLTKMENDTHCIDFSYLLYSQKGLNP 119
Db 61 SAQEPHYLPPEMPPQGSVMYVDSNHPDGEKARLQPLTKMENDTHCIDFSYLLYSQKGLNP 120
Qy 120 GTNLNLRVNVKGPLANPIWNVGTGTRDMLRSLAVSTFWPNEYQVIFAEVSGRSGYI 179
Db 121 GTNLNLRVNVKGPLANPIWNVGTGTRDMLRSLAVSTFWPNEYQVIFAEVSGRSGYI 180
Qy 180 AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATFQCIATGORDAVHNNKMLQRRNGEDIPV 239
Db 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATFQCIATGORDAVHNNKMLQRRNGEDIPV 240
Qy 240 AQTKNINHRRFAASFRLOEVTQDQLYRCVTSERGSVSNFAQLIVREPPRPIAPPQL 299
Db 241 AQTKNINHRRFAASFRLOEVTQDQLYRCVTSERGSVSNFAQLIVREPPRPIAPPQL 300
Qy 300 LGVGPYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLWHLDPDTEYE 359
Db 301 LGVGPYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLWHLDPDTEYE 360
Qy 360 IRVLLTRPGEVGLPGPPLITTKCAEPMRTKTLKIAIRIADVDHESLYGNTTRC 419
Db 361 IRVLLTRPGEVGLPGPPLITTKCAEPMRTKTLKIAIRIADVDHESLYGNTTRC 420
Qy 420 HTFNVTICVHYFRGHNESRADCLMDPKAPQHVVNHLPPYTNVSLKMLNPEGRKESEE 479
Db 421 HSNFTVICVHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLNPEGRKESEE 480
Qy 480 TTIQTDEDVGPVPVKSLOQTSFENKIFLNWKEPLEPNGIITQYEVSYSIRSFPDPAVPV 539
Db 481 TTIQTDEDVGPVPVKSLOQTSFENKIFLNWKEPLEPNGIITQYEVSYSIRSFPDPAVPV 540
Qy 540 AGPPQTVSNLWNSHTHVFHMLHGPVTYQFFIRASTVKGFGPAPATINVTWISAPSLPDYE 599
```

Db 541 AGPQTQVNLNNSTHVHMLHPGTTGYQFFIRASTVKGFGPATAINVTNNTISAPTLDPYE 600  
Qy 600 GVDASLNATATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKRBAGAMECYQVPVYQN 659  
Db 601 GVDASLNATATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKRBAGAMECYQVPVYQN 660  
Qy 660 ALSGGAPYFAELPFGNLPPAPFTVGDNRITKGFWMNPPLAPRGYNIYFQAMSSVEKE 719  
Db 661 AMSGGAPYFAELPFGNLPPAPFTVGDNRITKGFWMNPPLAPRGYNIYFQAMTSVEKE 720  
Qy 720 TKTCQVRIATKAAATEEPEVIPPDAKQDRVVKIAGISAGILVFLILLVIVIVKSKL 779  
Db 721 TKTCQVRIATKAAATEEPEVIPPDAKQDRVVKIAGISAGILVFLILLVIVIVKSKL 780  
Qy 780 AKKRKDMGNTROEMTHVMNMDRSYADQSTLHAEDPLSLTFMDQHNFSPLPNDPLVPT 839  
Db 781 AKKRKDMGNTROEMTHVMNMDRSYADQSTLHAEDPLSLTFMDQHNFSPLPNDPLVPT 832  
Qy 840 AVLDEHNSATAESSELLDVPRLCEGTSPYOTGOLHPAIRVADLLOHINLMKTSDSYGF 899  
Db 841 AVLDEHNSATAESSELLDVPRLCEGTSPYOTGOLHPAIRVADLLOHINLMKTSDSYGF 888  
Qy 900 KEEYESFEGQASMDVAKDONRAKNRYGNIIDYHSRVILQPVEDDPSDDYINANYID 959  
Db 901 KEEYESFEGQASMDVAKDONRAKNRYGNIIDYHSRVILQPVEDDPSDDYINANYID 947  
Qy 960 IWLXBDGQRPQSHYIATQPVHETVYDFRVMVWQESACIIVMTNVLVEGRVKCYKYPWD 1019  
Db 961 IWLXBDGQRPQSHYIATQPVHETVYDFRVMVWQESACIIVMTNVLVEGRVKCYKYPWD 1002  
Qy 1020 DTEVYGDQKVTQVMEPLAEVYVTRFTLERRGYNEIREVKQPHFTGWPDPVPHATGLL 1079  
Db 1021 DTEVYGDQKVTQVMEPLAEVYVTRFTLERRGYNEIREVKQPHFTGWPDPVPHATGLL 1062  
Qy 1080 SFIRRVKLSNPSSAGPIVHCSAGAGRTGCIYVIDIMLDMAREGVDIYNVCVLRSSR 1139  
Db 1081 SFIRRVKLSNPSSAGPIVHCSAGAGRTGCIYVIDIMLDMAREGVDIYNVCVLRSSR 1122  
Qy 1140 INNVQTEQYIFIHDAILEACLCGETAIPVCBFKAAYFDMIRIDQTNSSHLKDBFQTLN 1199  
Db 1141 INNVQTEQYIFIHDAILEACLCGETAIPVCBFKAAYFDMIRIDQTNSSHLKDBFQTLN 1182  
Qy 1200 SVTPRLQAEDECSIACLPRNHDKNRMFLPPDRCLPELITIDGESSNYINAAALMDSYRQ 1259  
Db 1201 SVTPRLQAEDECSIACLPRNHDKNRMFLPPDRCLPELITIDGESSNYINAAALMDSYRQ 1242  
Qy 1260 AAFIVTQYPLNTVDFWRLVYDYGCTSIIVMLNEVDLSQGCPCQYWPBEGMLRYGPIQVE 1319  
Db 1261 AAFIVTQYPLNTVDFWRLVYDYGCTSIIVMLNEVDLSQGCPCQYWPBEGMLRYGPIQVE 1302  
Qy 1320 MSCMDCDVINRIFRICNLTRPOEGLYLVQOYQYILGWASHREVPGSKSFLKLIQVEKW 1379  
Db 1321 MSCMDCDVINRIFRICNLTRPOEGLYLVQOYQYILGWASHREVPGSKSFLKLIQVEKW 1362  
Qy 1380 QBECEGEGRTIICHLNGGREGMFCAGIIVVMVKRQNVVDVFAVKTLRNKKPMVEA 1439  
Db 1381 QBECEGEGRTIICHLNGGREGMFCAGIIVVMVKRQNVVDVFAVKTLRNKKPMVEA 1422  
Qy 1440 PEQYRFDVDALEYLESS 1457  
Db 1441 PEQYRFDVDALEYLESS 1440

## RESULT 7

ID AAR63631  
XX AAR63631 standard; protein; 1407 AA.

AC AAR63631;

XX 21-OCT-2004 (revised)

DT 25-MAR-2003 (revised)

DT 08-JUN-1995 (first entry)

DE Murine receptor-type protein tyrosine phosphatase protein (RPTP-kappa).  
XX Receptor-type protein tyrosine phosphatase protein; cellular signal;  
KW RPTPase-kappa; enzyme.  
XX Mus musculus.  
OS Unidentified.  
FH Key Location/Qualifiers  
FT Peptide 1..25  
FT /label= signal  
FT Region 210..270  
FT /label= Ig-like repeat  
FT Domain 703..724  
FT /label= Transmembrane  
FT Domain 877..1108  
FT /label= PTPase 1  
FT Domain 1168..1404  
FT /label= PTPase 2  
XX WO9424161-A1.  
PN 27-OCT-1994.  
XX 20-APR-1994; 94WO-US004377.  
XX 21-APR-1993; 93US-00049384.  
PR 01-JUL-1993; 93US-00087244.  
XX (UYNV-) UNIV NEW YORK MEDICAL CENT.  
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
XX Schlessinger J, Sap JM, Ullrich A, Vogel W, Fuchs M;  
PI WPI; 1994-341769/42.  
XX Mammalian receptor-type protein tyrosine phosphatase-kappa (RPTP-k)  
PT protein and DNA - useful to identify cpds. which bind to RPTP-k and  
PT modulate enzymatic activity. Also inhibition of type II RPTP homo:phili  
XX binding (Eng).  
PS Claim 2; Fig 3; 144pp; English.  
XX NB: It appears that one line, comprising 50AAs is missing from Figure 3  
CC (cf AAR63631). The novel receptor-type protein tyrosine phosphatase  
CC protein or glycoprotein is termed RPTP kappa (also known as RPTase-  
CC kappa). The first approx. 170AAs of RPTP kappa show similarity (26%  
CC overall identity) to a region in the Xenopus cell surface protein A5 with  
CC features of Ig-like domains. There are four putative fibronectin type III  
CC -like repeats (residues 296-681). The tandem repeat of two PTPase  
CC homologues is typical for most RPTases. A feature of RPTP kappa is the  
CC extended distance between its transmembrane domain and the start of the  
CC first phosphatase homology domain. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
CC Revised record issued on 21-OCT-2004 : Correction to feature table key  
XX Sequence 1407 AA;

Query Match 94.9%; Score 7412; DB 2; Length 1407;  
Best Local Similarity 95.6%; Pred No. 0;  
Matches 1393; Conservative 5; Mismatches 9; Indels 50; Gaps 1;  
Qy 1 MDVAAAALPAFVALWLLYPWLLGSLALQGFAGGCTFDDGPGACDYHQDLYDDFEWVHVS 60  
Db 1 MDVAAAALPAFVALWLLYPWLLGSLALQGFAGGCTFDDGPGACDYHQDLYDDFEWVHVS 60  
Qy 61 AQEPHYLPPEMPQGSYMYVDSNNHDPGEKARLQLPMTKENDTHCIDFSYLLYSQKLNPG 120  
Db 61 AQEPHYLPPEMPQGSYMYVDSNNHDPGEKARLQLPMTKENDTHCIDFSYLLYSQKLNPG 120  
Qy 121 TLNILRVNKGPLANPIWNVTGTRDMLRAELAVSTFWPNEYQVIFAEVSGSGSYIA 180  
Db 121 TLNILRVNKGPLANPIWNVTGTRDMLRAELAVSTFWPNEYQVIFAEVSGSGSYIA 180

Db 121 TLNLLVRVNGKPLANFIWNTGTFGRDWLRABELAVSTFWNEVQVIFEAESVSGRSGYIA 180  
Qy 181 IDDIQVLSYPCDKSPHFLRLGDEVNAGQATQCIATGRDAVHNKMLQRRNGEDIPVA 240  
Db 181 IDDIQVLSYPCDKSPHFLRLGDEVNAGQATQCIATGRDAVHNKMLQRRNGEDIPVA 240  
Qy 241 QTKNIHRRFAASFRLOEVTKTODLYRCVTSQERSGVSNFAQLIVREPPRIAPQLL 300  
Db 241 QTKNIHRRFAASFRLOEVTKTODLYRCVTSQERSGVSNFAQLIVREPPRIAPQLL 300  
Qy 301 GVGPVTLLIOLNANSIGDGPILKEVEYRMTSGSWTETHAVNAPTVKMLHLPDTEYEI 360  
Db 301 GVGPVTLLIOLNANSIGDGPILKEVEYRMTSGSWTETHAVNAPTVKMLHLPDTEYEI 360  
Qy 361 RVLLTRPGEGTGLPGPPLITRTKCAEPMTPTKTKIAETQARRIAVDMESLGNITRCH 420  
Db 361 RVLLTRPGEGTGLPGPPLITRTKCAEPMTPTKTKIAETQARRIAVDMESLGNITRCH 420  
Qy 421 TFNVITCYHYFRGHNSRADCLDMDPKAPQHVNHLPPYTNVSLKMLITNPGKSEET 480  
Db 421 TFNVITCYHYFRGHNSRADCLDMDPKAPQ----- 450  
Qy 481 IIQTDEDPGVPVKSLQGTSPENKIFLNKKEPLEPNGIITQYEVSVSSIRSFDPAPVA 540  
Db 451 -----SPEHKIFLHWKSEPLEPNGIITQYEVSVSSIRSFDPAPVA 490  
Qy 541 GPPQTVSNLWNSHHVFMHLHPTGTYQFFIRASTVKGFGPATAINVTNISAPSLPDYEG 600  
Db 491 GPPQTVSNLWNSHHVFMHLHPTGTYQFFIRASTVKGFGPATAINVTNISAPSLPDYEG 550  
Qy 601 VDASLNETATITVLLRPAQAKAPISAYQIVVEQLHPHRTKREAGMECYQVPTVYQNA 660  
Db 551 VDASLNETATITVLLRPAQAKAPISAYQIVVEQLHPHRTKREAGMECYQVPTVYQNA 610  
Qy 661 LSGGAPYFAAEPLPGNLPAPPTVGDNRTYKGFNPPPLAPRGYNIYFOAMSSVEKET 720  
Db 611 LSGGAPYFAAEPLPGNLPAPPTVGDNRTYKGFNPPPLAPRGYNIYFOAMSSVEKET 670  
Qy 721 KTCQVRIATKAAATEBEVIPPDAKQTDVVKIAGISAGILVFILLVIVIVVKSKLA 780  
Db 671 KTCQVRIATKAAATEBEVIPPDAKQTDVVKIAGISAGILVFILLVIVIVVKSKLA 730  
Qy 781 KKKDAMGNTRQEMTHVMNANDRSYADQSLTHAEDPLSLTFMDQHNFSRPLPNDPLVPTA 840  
Db 731 KKKDAMGNTRQEMTHVMNANDRSYADQSLTHAEDPLSLTFMDQHNFSRPLPNDPLVPTA 790  
Qy 841 VLDENHSATAESRLDVPRLCEGTESPYQTQLHPAIRVADLLOHINLMKTSDSYGFK 900  
Db 791 VLDENHSATAESRLDVPRLCEGTESPYQTQLHPAIRVADLLOHINLMKTSDSYGFK 850  
Qy 901 EYESPFEGOSASVDVAKKQONRAKNRYGNI IAYDHSRVILQPVDDPSSDIYNANVYDI 960  
Db 851 EYESPFEGOSASVDVAKKQONRAKNRYGNI IAYDHSRVILQPVDDPSSDIYNANVYDI 910  
Qy 961 WLVRDGYQRPESHYIATQGPVHETVYDFWRMWQEQSACIWMVTLNVEVGRVKCYKWPDD 1020  
Db 911 WLVRDGYQRPESHYIATQGPVHETVYDFWRMWQEQSACIWMVTLNVEVGRVKCYKWPDD 970  
Qy 1021 TEYVGFVKTCVMEPLAEVYVFTFLRRGYNEIREVKQFHTGPDHGPVPHATGLLS 1080  
Db 971 TEYVGFVKTCVMEPLAEVYVFTFLRRGYNEIREVKQFHTGPDHGPVPHATGLLS 1030  
Qy 1081 FIRRVLKSNPPSAGPIVHCSAGAGRTGCVIVIDIMDMAEREGVVDIYNVCVKAISRRI 1140  
Db 1031 FIRRVLKSNPPSAGPIVHCSAGAGRTGCVIVIDIMDMAEREGVVDIYNVCVKAISRRI 1090  
Qy 1141 NMVQTEEQYIFIHDAILEACLGETAIPVCEPKAAVFDIMRIDSQTNSSHLKDEFQTLNS 1200  
Db 1091 NMVQTEEQYIFIHDAILEACLGETAIPVCEPKAAVFDIMRIDSQTNSSHLKDEFQTLNS 1150  
Qy 1201 VTPRLOAEDCSIACLPRNHDKNFMMDLPPDRCLPLFITIDGSSSNYINAAALMDSTRQPA 1260  
Db 1151 VTPRLOAEDCSIACLPRNHDKNFMMDLPPDRCLPLFITIDGSSSNYINAAALMDSTRQPA 1210

Qy 1261 APITVQYPLPNTVKDFWRLVYDYGCTSI VMLNEVDLSQGPCQYWPBEGMLRYGPIQVECM 1320  
Db 1211 APITVQYPLPNTVKDFWRLVYDYGCTSI VMLNEVDLSQGPCQYWPBEGMLRYGPIQVECM 1270  
Qy 1321 SCSCMDCDVNIRFRI CNLTPQEGYLMVQOFOYLGWASHREVPGSKRSFLKLILQVEKWQ 1380  
Db 1271 SCSCMDCDVNIRFRI CNLTPQEGYLMVQOFOYLGWASHREVPGSKRSFLKLILQVEKWQ 1330  
Qy 1381 ECEEGEGRTIIHCLNGGSGRMFCAGI GIVEMVKRQNVVDVVFHAVKTLRNSKPNMVEAP 1440  
Db 1331 ECEEGEGRTIIHCLNGGSGRMFCAGI GIVEMVKRQNVVDVVFHAVKTLRNSKPNMVEAP 1390  
Qy 1441 EQYRFCYDVALEYLESS 1457  
Db 1391 EQYRFCYDVALEYLESS 1407

RESULT 8  
AAM79159  
ID AAM79159 standard; protein; 1452 AA.  
XX AC AAM79159;  
XX AC AAM79159;  
XX DT 06-NOV-2001 (first entry)  
XX Human protein SEQ ID NO 1821.  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
XX tissue growth factor; immunomodulatory; cancer; leukaemia;  
XX nervous system disorder; arthritis; inflammation.  
XX Homo sapiens.  
XX WO200157190-A2.  
XX 09-AUG-2001.  
XX 05-FEB-2001; 2001WO-US004098.  
XX 03-FEB-2000; 2000US-00496914.  
XX 27-APR-2000; 2000US-00560875.  
XX 19-JUL-2000; 2000US-00598075.  
XX 01-SEP-2000; 2000US-00620325.  
XX 15-SEP-2000; 2000US-00654936.  
XX 20-OCT-2000; 2000US-00663561.  
XX 30-NOV-2000; 2000US-00693325.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;  
XX Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
XX WPI: 2001-476283/51.  
XX N-PSDB; AAK52292.  
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful  
XX in diagnosis and gene therapy.  
XX Claim 20, Page 4196-4199; 6221pp; English.  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to  
XX cytokine, cell proliferation or cell differentiation or which may induce  
XX production of other cytokines in other cell populations. The  
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or  
XX peptide therapy. The polypeptides have various cytokine-like activities,  
XX e.g. stem cell growth factor activity, haematopoiesis regulating  
XX activity, tissue growth factor activity, immunomodulatory activity and  
XX activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
CC (AAK52582) and 3666 (AAH0020) are omitted as the relevant pages from the  
CC sequence listing were missing at the time of publication  
XX  
SQ Sequence 1452 AA;

Query Match	61.8%;	Score	4823.5;	DB 4;	Length	1452;			
Best Local Similarity	61.5%;	Pred. No. 0;							
Matches	892;	Conservative	210;	Mismatches	320;	Indels	29;	Gaps	9;
QY	22	LLGSALGFGSAGGCTGDDGPGACDHYDLDYDFEWHVHVSQAEPHYLPPEMPOGSMVYVDS	81						
DB	14	LLLTAAGTFSGGCLFDEPYSTCGYSQSEGDDFNWEQVNTLTKPTSDPWPMSGFMLVNA	73						
QY	82	SNHDGPEKARLQLPTMKENDTHCIDFSYLLYSQKGLNPGTILNLRVKNKGPLANPWNVT	141						
DB	74	SGRPEGORALLLPOLKENDTHCIDFHYFVSSKSNPPGLLNIVYKVNNGPLGNPNWIS	133						
QY	142	GFTGDMWLAELAVSTFWPNEVQVIFAEVSGRSYVIAIDDIQVLSYPCDKSPHFLRLG	201						
DB	134	GDPTWNAEALATSTFWPNFYQVIFEV-ITSGHQYLAIDEVKLGHPCHCTRTPHFLRIQ	192						
QY	202	DVEVNAGQATFOCIATCRDAVHKNLWLRNGEDIIPVAQTKNINHRFAAASFRLQEVTK	261						
DB	193	NVEVNAGQATFOCSAIGRTVAGDRMLQGDVDRAPLKEIKVTSRRFIASFNVVNTK	252						
QY	262	TDQDLRYCVTQSERGSGVSNFAQLVREPPRPTAPPQLLGVGPTYLLIQLNANSIIGDP	321						
DB	253	RDAGKYRCWIRTEGGVGISNFAELVWKEPPVAPPQLASVGATYLIQLNANSINGDP	312						
QY	322	ITLKEVEYRMTSGSWETHANVAPYKJLWHLDPDTEYEIRVLLTRPGEGGTGLPGPLIT	381						
DB	313	IVAREVEYCTAGSNDQPVDSYSYKIGHLDPDTEYEISVLLTRPGEGGTGSPGALRT	372						
QY	382	RTKCAEPMRTPKTLKIAEIQARRIADWESLGYNTIRCHTFNVTCIYHYFRGHNSRAD-	440						
DB	373	RTKCADPMRGPKLEVEVKSRQITIRWEPFGVNVTRCHSYNLTVHYCYQVGQEQVRE	432						
QY	441	-CLDMDPKAPQHVNVHLPYTNVSLKMLINPEGRKSEETIITOTDEDVPGVPVKSLQG	499						
DB	433	VSWDTENSHPQITITNLSPYTNVSVKILMNPGRKESQELIVQTDDELPGAVPTESIQG	492						
QY	500	TSFENKIFLNWKEPLENGIITQYEVSYSSIRSPDPAPVAGPPQTVSNLWNSTHVRVNH	559						
DB	493	STFEKKIFLOWREPTQTYGVITLYEITYKAVSSFDPEIDLNSQGRVSKLGNETHFLPFG	552						
QY	560	LHPGTTYOFFIRASTVKGFGPATINVTNISAPSLPDYEGVDASINETATTITVLLRPA	619						
DB	553	LYPGTTYSTIRASTAKGFGPATNOFTTKISAPSPMAYE-LSTPLNQTDNTIVVLKPA	611						
QY	620	QAKGAPISAYQIVRQLPHRTKREAGAMECYQVPVTVQNALGGGAPYFAAELPPGNLP	679						
DB	612	HSRGAPSVYQIVVEERPRRTKTEILKCYVPVFIHFQNASLINSQYFAAEFFPADSLQ	671						
QY	680	EPAPTVGDNRTYKGFWNPPILAPRGYNYIYQAMSSVEKTKTCQVRIATKAAATEEPEV	739						
DB	672	AAQPTIGDNKTYGYNWTPLLPYKSYRYIYFQAASRANGETKIDCVQVATKGAATPKP--	729						
QY	740	IPDPAKQTRVVKIAGISAILVILLVIVIVVKSKLAKRKDAMGNTRQEMTMVN	799						
DB	730	VPEPEQTDHTVKIAGVINGIILLFVILFGLVVLWKKRKLAKRKETMSTRQEMTMVN	789						
QY	800	AMDRSYADQSTLHAEDPLSLTFMDQHNFSRPLNDP-----LVPTAVL-DENH	846						
DB	790	SMDKSYAEQGTNCDE--AFSPMDTHNLNRSVSSPSSTMTKNTLTSTSVPSNYPDETH	846						
QY	847	SATASSRLLDVPRY-LCEGTESPYQTQLHPAIRVADILLQHINLMKTSYSGPKEEYES	905						
DB	847	TWASDTSSLVQSHTYKKREPADVPYQTQLHPAIRVADILLQHTQMKCAGYGFKEEYES	906						
QY	906	FFEQSASWDAKQDNRAKNRYGNIAYDHSRVILQPVDEDDPSDYINANYIDIWLYRD	965						

DB	907	FFEQSAPWDSAKKDNRMKNRYGNIAYDHSRVLRLQTIEGDITNSDYINGNYI-----D	960
QY	966	GYQRPISHYIATQGPVHTVVDVFWVMVQESACIWMVNTLVGVRVKCYKWPDDTEYVG	1025
DB	961	GYHRPNHYIATQGPVHTVVDVFWVMVQESACIWMVNTLVGVRVKCYKWPDDTEYVG	1020
QY	1026	DFKVTCEVMEPLAEBYVVRFTFLBRRGYNEIREVQKQFHTGWPDPGVPHATGLLSFIRRV	1085
DB	1021	DIKVTLETETALLAEBYVIRTAVERKRGVHEIREIQFHTGWPDPGVPHATGLLGFRQV	1080
QY	1086	KLNSPPSAGPTIVHCSAGAGRTGCIYIVIDIMLMAEREGVVDIYNCVKALRSRRINMYOT	1145
DB	1081	KSKSPPSAGPLVHCSAGAGRTGCFIVIDIMLMAEREGVVDIYNCVRELSSRRINMYOT	1140
QY	1146	BEQVIFHDAILEACLGCTAI PVCEPKAAYFDMIRIDSQTNSSHLDKDEFOTLNSVTPRL	1205
DB	1141	BEQVIFHDAILEACLGCTSVSPASQVRSLYDMNKLDPQTNSSQIKEEPFTLNMVTPRL	1200
QY	1206	QAEPCSIACLPNRHDKNRFMDMLPPDRCLPPLITIDGESSNYINAAALMDSYRQPAAFIVT	1265
DB	1201	RVEDCSALLPRNHEKRCMDILPPDRCLPPLITIDGESSNYINAAALMDSYRQPAFIVT	1260
QY	1266	QYPLNTVKDFWRLVYDYGCTSIYMLNEVDLSQCGPQYWPBEGMLRYGPIQVECMCSMD	1325
DB	1261	QHPLNTVKDFWRLVYDCHTSVVMNLNDVDPALCPQYWPBEGVHRHGPIQVEFPVSADLE	1320
QY	1326	CDVNRIFRINLTPQEGYLMVOQFQYLGWASHREVPKSGKSLKLILQVEKQWEECEE	1385
DB	1321	EDIIISRIYRIYNAARPDQGYRMVQFQFLGWPMTYRDPVSKRSFLKLIRQVDRKQEEYNG	1380
QY	1386	GEGRTHICLNGGSGRMFCAIGIVEMVKRQNVVDVFAVKTILNRSKPNMVEAPEQYRF	1445
DB	1381	GEGRTHICLNGGSGRTFCAISIVCEMLRQRTVDVFAVKTILNRSKPNMVDLDDQYKF	1440
QY	1446	CYDVALEYLES 1456	
DB	1441	CYEVALEYINS 1451	
RESULT 9			
ID	ABR58629	standard; protein; 1452 AA.	
XX	ABR58629;		
AC	ABR58629;		
XX	09-JUL-2003 (first entry)		
DT	Human cancer related protein SEQ ID NO:286.		
XX	Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;		
XX	heart disease; atherosclerosis; endometriosis.		
OS	Homo sapiens.		
XX	WO2003025138-A2.		
PN	27-MAR-2003.		
PD	17-SEP-2002; 2002WO-US029560.		
XX	17-SEP-2001; 2001US-0323469P.		
XX	20-SEP-2001; 2001US-0323887P.		
PR	13-NOV-2001; 2001US-0350666P.		
PR	08-FEB-2002; 2002US-0355145P.		
PR	08-FEB-2002; 2002US-0355257P.		
PR	12-APR-2002; 2002US-0372246P.		
XX	(EOSB-) EOS BIOTECHNOLOGY INC.		
PA	Afar D, Aziz N, Gish KC, Havezi PA, Mack DH, Wilson KE;		
PI	Zlotnik A;		
XX	WPI; 2003-354600/33.		



KW protein tyrosine phosphatase receptor type mu; PTPRM; cytosolic;  
 KW antidiabetic; gene therapy; expression pattern;  
 KW hyperproliferative disorder; cancer; metabolic disorder; diabetes;  
 KW infection; inflammation; tumour formation; human.  
 XX  
 OS Homo sapiens.  
 OS Unidentified.  
 XX  
 PN US2004014699-A1.  
 XX  
 XX 22-JAN-2004.  
 XX  
 XX 18-JUL-2002; 2002US-00200293.  
 XX  
 XX 18-JUL-2002; 2002US-00200293.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 XX Cowsert LM, Dobie KW;  
 XX  
 DR WPI; 2004-121596/12.  
 DR N-PSDB; ADI80645.  
 XX  
 PT New antisense compound targeted to a nucleic acid molecule encoding  
 PT protein tyrosine phosphatase receptor type mu, useful for treating cancer  
 PT or diabetes or modulating expression of protein tyrosine phosphatase  
 PT receptor type mu.  
 XX  
 XX Example 13; Page 33-38; 56pp; English.  
 XX  
 CC This invention relates to a novel compound with an oligonucleotide 8-80  
 CC nucleotides in length targeted to a nucleic acid molecule encoding  
 CC protein tyrosine phosphatase receptor type mu (PTPRM) which specifically  
 CC hybridises with the nucleic acid molecule encoding PTPRM and inhibits the  
 CC expression of PTPRM or specifically hybridises with at least 8-nucleotide  
 CC portion of a preferred target region on a nucleic acid molecule encoding  
 CC PTPRM. The invention may be useful for the production of compositions  
 CC with a cytostatic or antidiabetic activity. In addition, the disclosed  
 CC sequences may be useful for gene therapy. The compound, particularly the  
 CC antisense oligonucleotide is useful in modulating the function of nucleic  
 CC acid molecules encoding PTPRM. The antisense compound can also be used as  
 CC research tools and diagnostics. It can also be used as tools in  
 CC differential and/or combinatorial analyses to elucidate expression  
 CC patterns of a portion or the entire complement of genes expressed within  
 CC cells and tissues. The compound can also be used for treating diseases or  
 CC conditions associated with PTPRM, preferably hyperproliferative disorder,  
 CC for example cancer or metabolic disorders, for example diabetes. The  
 CC compound can also be used as prophylaxis, for example to prevent or delay  
 CC infection, inflammation or tumour formation. The present sequence is that  
 CC of the human protein tyrosine phosphatase receptor type mu (PTPRM) which  
 CC is related to the invention.  
 XX  
 SQ Sequence 1452 AA;

Query Match 61.6%; Score 4812.5; DB 8; Length 1452;  
 Best Local Similarity 61.4%; Pred. No. 0;  
 Matches 891; Conservative 209; Mismatches 322; Indels 29; Gaps 9;

QY 22 LIGSALGQFSAGCCTFDDGPGACDYHDLDDFEVWHVYSAQEPHYLPPEMPOGSMYVDS 81  
 DB 14 LLLTAGETFSGGCLFDEPYSTCGYSQSEGDDFNVEQVNTLTPTSDPWPMSGSLMUNA 73  
 QY 82 SNHDFGEKARLQPTMKENDTHCIDFSLYLLYSQKGLNPGLNVLVRNKGKPLANPINWY 141  
 DB 74 SGRPEGORAHLLLPOLKENDTHCIDPHYFVSKSNPPGLLVVKNVNGPLGNPINWIS 133  
 QY 142 GTFGDNLRAELAVSTFWNEVQVIFEAESVSGRGYTAIDDIQVLSYPCDKSPHFLRLG 201  
 DB 134 GDFPTWNAELAISTFWNFYQVIFEV-ITSGHQGYLAIDKVKVLGHFCTPTPHFLRIQ 192  
 QY 202 DVEVNAQGNATFOCATGDAVHKNLQRRNGEDIPVAQTKNINHRFAASFRLOEVTK 261  
 DB 193 NVEVNAQGFATFQCSAIGTAVAGDRLMLQIGIDVRDAPLKEIKVTSRRFIASFNVNITK 252

QY 262 TDQDLYECVTSQSBGVSNFQAQLIVREPPRIAPOLLGVGPTVLLIQLNANSIIGDGP 321  
 DB 253 RDAGKYECMIRTEGGVGISNVAELVKEPPVPIAPPOLASVGATYLMQLNANSIINGDGP 312  
 QY 322 IILKEVEYRMTSGSWTETHAVNAPTYKLWHLDPDTEYEIRVLLTRPGEGGTGLPGPLIT 381  
 DB 313 IVAREVEYCTASGSWDRQPDVSTSYKIGHLDPDTEYEISVLLTRPGEGGTGSGPALRT 372  
 QY 382 RTKCAEPMRTPKTLKIAEIQARRIADVWESLGYNITRCHTENVITCYHYFQHESRAD- 440  
 DB 373 RTKCADPMRGPRKLEVVVEVKSQITIRWEPGYNVTRCHSYNLTAVHYCYQVGGQEQVREE 432  
 QY 441 -CLDMDPKAQHVNVNHLPPYTNVSLKMLLTNPEGRKSEETIIOTDEDPGVPVKSLQG 499  
 DB 433 VSWDTENSHFQHTITNLSPTYTNVSKLILMPEGRKESQELIVQTDPLGAVPTESIQG 492  
 QY 500 TSPENKIFLWKEPLENGIITQVEVSSIRSDDPAVPVAGPPQTYSNLWNSTHHVPMH 559  
 DB 493 STFEKIFLOWREPTQYGVITLYEITYKAVSSFDPEIDLNSQSGRVSKLGNETHFLPFG 552  
 QY 560 LHPGTTYQFFIRASTVKGFGPATAINVTNISAPSLPDYEGVDASLNETAITITVLLRPA 619  
 DB 553 LYPGTTYFTIRASTAGFGPPATNQFTTKISAFSMPAYE-LETPLAQNDTNTVTMLKPA 611  
 QY 620 QAKGAPISAOIVVEQLHPHRTKREAGMECYQVPTYQNALSGGAPYFAELPPGNLP 679  
 DB 612 HSRGAPSVYQIVVEBERPRRTKTTILKCYPIIHFQNASLLNSQYFFAAEFADSLQ 671  
 QY 680 BPAPFTVDNRTYKGFWNPLAPRKGYNIYFOAMSSVEKETKTCVRLATKAAATEEPEV 739  
 DB 672 AAQPTTIGDNKTYNGYNTPLPYKSVRIYFOAASRANGETKIDCVQVATKGAATPKP-- 729  
 QY 740 IPDPAKQTRVVKIAGISAGILVIFILLVIVIVKSKLAKKRKADMGNTQBMTHWVN 799  
 DB 730 VPEPEKQTDHTVKIAGVIAGILLFVIFLVVLMKKRKLAKRKETMSSTRQBMTHWVN 789  
 QY 800 ANDRSYADQSTLHAEDPLSLTFPMQHNPSPLNDP-----LVPTAVL-DENH 846  
 DB 790 SMDKSYAEQGTNCDE---AFSMDTHNLNGHSVSPSFTMTKTNTLSTSVNSYYPDETH 846  
 QY 847 SATAESRLLDVPY-LCEGTESPVTGOLHPALRVADLLQHLINLMKTSDSYGFKEYES 905  
 DB 847 TMSDTSLSLVOSHYYKREPADVPIYQGLHPALRVADLLQHLITQMKCABGYGFKEYES 906  
 QY 906 FFEGQSASWDVAKDQNRKRYGNI IAYDSHRVILQPVEDDPPSSDYINANYIDILWYRD 965  
 DB 907 FFEGQSAPWDSAKKDNRMKNRYGNI IAYDSHRVRLQTIEGDTNSDYINGNYI-----D 960  
 QY 966 GYQRPISHYIATQGPVHETVYDFWRMWOESACIWMVTNLVEGVRKCYKWPDDTEVYG 1025  
 DB 961 GYHRPNHYIATQGPMEQTIYDFWRMWHENTASIIIMVTNLVEGVRKCYKWPDDTEIYK 1020  
 QY 1026 DFKYTCVEMEPLAEYVVRFTFLRRGYNEIREVKQFHTGWPDPHGVYPYHATGLLSFIRRV 1085  
 DB 1021 DIKVTLETLEAEVIRTPAVEKRGVHEIREIRQFHTGWPDPHGVYPYHATGLLGFVRQV 1080  
 QY 1086 KLSPPSAGPIVWHCSAGAGRTGCYIVIDIMLDAEREGVVDIYNCVKALSRRRINMVQT 1145  
 DB 1081 KSKSPSAGPLVHCHSAGAGRTGCFIVIDIMLDAEREGVVDIYNCVKALSRRRINMVQT 1140  
 QY 1146 BEQYFIHDAILEACLCGETAIPVCEFKAAAFDMIRIDISQTNSSHLKDEFOQLNSVTPL 1205  
 DB 1141 BEQYFIHDAILEACLCGETSPASQVRSYLDYDMNKLDPTQTNSSQIKBEFRTLNMTPL 1200  
 QY 1206 QAEDCSIACLPRNHDKNRMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAFVIT 1265  
 DB 1201 RVDCSIALPRNHEKNRMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAFVIT 1260  
 QY 1266 QYPLPNTVKDFWRLVYDCTSI VMLNEVDLSQGCQPYWPBEGMLRYGP IQVECMSCSD 1325  
 DB 1261 QHPLPNTVKDFWRLVLDVHCTSVVMLNDVDAQLCFQYWPENGVRHHRGPIQVEFVSADLE 1320

Qy 1326 CDVNRIFRNLTRPQGYLMVQOQFQYLGHASHREVPVSGSRSPKLILOVEKWECEEE 1385  
 Db 1321 EDIISRIIRFYNAARPDQGYRMVQOQFQFLGPMYRDTFVSKRSFLKLIQVQDKWQEEYNG 1380  
 Qy 1386 GEGRTIHLNGGSGMFCAGIGVWEMVKRONVVDVFAVKTLRNKPNNVFAPEQVRF 1445  
 Db 1381 GEGTVVHCLNGGSGRTFCAISIVCEMLRHQRIVDFHAVKTLRNKPNVVDLDDQKP 1440  
 Qy 1446 CYDVALEYLES 1456  
 Db 1441 CYEVALEYLNS 1451

## RESULT 11

ADJ68277  
 ID ADJ68277 standard; protein; 1452 AA.

XX AC ADJ68277;

XX DT 06-MAY-2004 (first entry)

XX DE Human heat mitochondrial protein as a therapeutic target SeqID83.  
 XX KW mitochondrial; human; screening assay; diabetes mellitus;  
 XX KW Huntington's disease; osteoarthritis;  
 KW Leber's hereditary optic neuropathy; LHON;  
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
 KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;  
 KW osteopathic; ophthalmological; cytostatic.

XX OS Homo sapiens.

XX PN WO2003087768-A2.

XX PD 23-OCT-2003.

XX PR 04-APR-2002; 2003WO-US010870.

XX PR 12-APR-2002; 2002US-0372843P.

XX PR 17-JUN-2002; 2002US-0389987P.

XX PR 20-SEP-2002; 2002US-0412418P.

XX PA (MITO-) MITOKOR.

XX PA (BUCK-) BUCK INST AGE RES.

XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

XX PI Warnock DE;

XX XX WPI; 2003-845369/78.

XX PT Identifying a mitochondrial target for drug screening assays and for  
 PT treating diseases associated with altered mitochondrial function,  
 PT comprises detecting a modified polypeptide in a sample and correlating  
 PT with the disease.

XX Claim 1; SEQ ID NO 83; 180pp; English.

XX CC This invention relates to novel mitochondrial targets that can be used  
 CC for therapeutic intervention in treating a disease associated with  
 CC altered mitochondrial function. Specifically, it refers to a method for  
 CC identifying proteins of the human heart mitochondrial proteome that are  
 CC useful for drug screening assays, as well as therapeutic targets. The  
 CC present invention describes a method for identifying such proteins that  
 CC can be used in the treatment of various diseases associated with altered  
 CC mitochondrial function including diabetes mellitus, Huntington's disease,  
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
 CC compositions have neuroprotective, nontropic, antidiabetic,  
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
 CC cytostatic activities. This polypeptide sequence is a human heart  
 CC mitochondrial protein of the invention.

XX SQ Sequence 1452 AA;

Query Match 61.3%; Score 4789.5; DB 7; Length 1452;  
 Best Local Similarity 61.1%; Pred. No. 0;  
 Matches 887; Conservative 211; Mismatches 324; Indels 29; Gaps 9;

Qy 22 LLGSAIGQFSAGGCTFDGPGACDYHQDLVDDFEFHVHSAQEPHYLPPEMQSGYMWVDS 81

Db 14 LLTAAGETFSGGCLFDEPYSTCGYSQSEGDENWEQVNTLTPTSDPMPWPGSLMLVNA 73

Qy 82 SNHDPGEKARLQLPWKENDTHCIDFSYLLYSQKGLNPCTNLILVRNKGPLANPNVVT 141

Db 74 SGRPEGORAHLLLPQKENDTHCIDFHYFVSSKSNPPGLLVVVKVNGPLGNPINIS 133

Qy 142 GFTGRWLRAELAVSTFWPNEYOVIFEAEVSGRSGYIAIDDIQVLSYPCDKSPHFRLRG 201

Db 134 GDTPTWNRALAIISTFWPNFYQVIFEV-ITSGHQGYLAIDVKKVLGHCPCTRTPHFLRIQ 192

Qy 202 DVEVNAQNATFOCIATGRDAVHNKWLQRNGEDIPVAQTKNINHRFFAASFRLEQVTK 261

Db 193 NVEVNAQFATFOCSAIGRTVAGDRLWLQGDVDRDAPLKEIKVTSSRRFIASFNVVTTK 252

Qy 262 TDQDLRCVTSQSRGSGVSNPQALIVREPPRPTAPPOLLGVGPTYLLIQLNANSIIGDP 321

Db 253 RDAGKYRCMIRTEGGVGSINYAEVLVKEPVPPIAPPQLASVGATYLIQLNANSINGDP 312

Qy 322 IILKEVYRMTSGSWTETHAVNAPTYKLWHLDDPTEYIEIRVLLTRPGEGGTGLPGPLIT 381

Db 313 IVAREVEYCTASGSWDRQPDVSTSYKIGHLDDPTEYISVLLTRPGEGGTGSGPALRT 372

Qy 382 RTKCAEPMRTPKTKIAEIQARRIADVDSLGYNITRCHTNVITCYHYFRGHNESRAD- 440

Db 373 RTKCADPMRGPRKLEVVVEVKSQITIRWEPFGVNTVTRCHSYNLVHYCYQVGGQVREE 432

Qy 441 -CLDMDPKAPQHVNHLPPTNVLSKMLINTPGRKESEETITQTDDEVPQVVKSLQ 499

Db 433 VSWDTESSHPOHTITNLSPYTNVSKVILNMPGKESQELIVQTDDELPGAVPTESIQ 492

Qy 500 TSFENKIFLNWKEPBPNGIITOVEVSYSSIRSDPAVPVAGPPQTVSNLWNSHHVFMH 559

Db 493 STFEKIFLOWREPTQYGVITLYEITYKAVSFPDEIDLSNQSGRVSKLGNETHFFFG 552

Qy 560 LHFQTTYQFFIRASTVKGFGPATAINVTTNISAPSPDYEGVDASLNATETITVLLRPA 619

Db 553 LYPGTTYFTIRASTAKGFGPPATNQFTTKISAPMPAYE-LETPLNQTDNTVTVMLKPA 611

Qy 620 QAKGAPISAYQIVVEQLHPHRTKREAGMECYQVPTYQNALSGGAPYFAAEPLPGNLP 679

Db 612 HSRGAPVSVYQIVVEEERPRRTKTTBILKCYVPVIFHFNASLLNSQYFAAEFPADSLQ 671

Qy 680 EPAPFTVGDNRITYKGFWMNPPLAPRKGYNIYFOAMSSVEKETQCVRIATKAATESPEV 739

Db 672 AAQFTTIGDNKTYNGVWNTPLLYKSYRIYQAASTRANGETKIDCVQVATKGAATPKP-- 729

Qy 740 IPDPKQTDNRVWKIAGISAGILVFILLLLVIIVTKSKLAKKKRDKAMGNTRQSMTHVN 799

Db 730 VPPEKQTDHTVKIAGIAGILLFVIFLGVLMKKRKLAKKKEKETSQSMTRQEMTVVN 789

Qy 800 AMDRSVADQSTLHAEDPLSLTFMDQHNFSRPLNDP-----LVPTAVL-DENH 846

Db 790 SMDKSYAEQGTNCDE--AFSMDTNLNGRSVSSPSSFTMTKNTLTSTVSPNSYYPDETH 846

Qy 847 SATAESRLLDVRY-LCEGTESPYQTQGLHPAIRVADLLOHNLNMTSUSYGFKEYES 905

Db 847 TMASDTSSLSQSHYTKKREPADVPYQTQGLHPAIRVADLLOHITQMKCAGYGFKEYES 906

Qy 906 FFGQSGASWDVAKDQNRKKNYGNITAYDHSRVILQPVDDPSDDYINANYIDILYRD 965

Db 907 FFGQSGAPWDSAKDENMKNRVGNIIAYDHSRVRLQTIISGDTNSDINGNYI-----D 960

Qy 966 GYORPSHYIATQGFVHETVYDFWRVMWQEOSACIVMVNVLVGRVVKCYKTPDDTEYIG 1025

Db 961 GYHRENHYIATQPMQETIYDFWRVMWHENTASIIIMVNLNVEVGRVKCKYWPDDTEIYK 1020  
 Qy 1026 DKVTCVEMEPLEAVYVFTFLERRGYNEIREVKQFHETGPDHGVPHATGLLSFIRRV 1085  
 Db 1021 DIKVTLEIETELAEYVIRTEFAVEKRGVHEIREIQFHFTGMPDHPGVPHATGLLGFVRQV 1080  
 Qy 1086 KLSNPPSAGPIVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNCVKALRSRRINMVQT 1145  
 Db 1081 KSKSPSAGPLVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNCVRELRSRRINMVQT 1140  
 Qy 1146 BEQYFIHDAILEACLCGETAIPVCEFAKAYFDMIRIDSQTNSSHLKDEFOQLNSVTPRL 1205  
 Db 1141 BEQYFIHDAILEACLCGDTSPASQVRSYLDNMKLDLPQTNSSQIKKEEFRTLNMTPTL 1200  
 Qy 1206 QAEDCSIACLRHNKXNFMMLPPDRCLPFLITIDGESSNYINAAIMDSYRQPAAFIVT 1265  
 Db 1201 RVEDCSIALPRNHEKRCMDILPPDRCLPFLITIDGESSNYINAAIMDSYRQPSAFIVT 1260  
 Qy 1266 OYPLPNTVKDFWRLVVDYGCYSIVMLNEVDSOGCPQYWPBEGMLRYGPIOVCEMCSMD 1325  
 Db 1261 QHPLPNTVKDFWRLVLDVHCTISVVMNLNDVDPALCPQYWPENGVRHHPGPIQVEFVSADLE 1320  
 Qy 1326 CDVINRIFRICNLTRPQEGYLMVOQFYLGWASHREVPCKSRFLKLILQVEKMOECEE 1385  
 Db 1321 EDIISKIPRIYNAARPDQHRMVQQFQFLGWPMDYRDTVPKRSALLIRQVDKQOEYNG 1380  
 Qy 1386 GEGRTIICLNGGSGMFCALGIVVEMVKRQNVVDVFAVKTILNSKPNMVEAPEQYRF 1445  
 Db 1381 GEGRTVWHLNGGSGSGTFCALISIVCEMLRHQRTVDVFAVKTILRNKPNMVDLDDQYKF 1440  
 Qy 1446 CYDVALEYLES 1456  
 Db 1441 CYEVALEYLNS 1451  
 RESULT 12  
 AAM80143  
 ID AAM80143 standard; protein; 1455 AA.  
 XX  
 AC AAM80143;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human protein SEQ ID NO 3789.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorder; arthritis; inflammation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157190-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US004098.  
 XX  
 PR 03-FEB-2000; 2000US-00496914.  
 PR 27-APR-2000; 2000US-00560875.  
 PR 20-JUN-2000; 2000US-00598075.  
 PR 19-JUL-2000; 2000US-00620325.  
 PR 01-SEP-2000; 2000US-00654936.  
 PR 15-SEP-2000; 2000US-00663561.  
 PR 20-OCT-2000; 2000US-00693325.  
 PR 30-NOV-2000; 2000US-00728422.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;  
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
 XX

DR WPI; 2001-476283/51.  
 DR N-ESDB; AAK53276.  
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful  
 PT in diagnosis and gene therapy.  
 XX Claim 20; Page 437-438; 6221pp; English.  
 PS The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAM78323-AAW80302) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the  
 CC sequence listing were missing at the time of publication  
 XX  
 SQ Sequence 1455 AA;  
 Query Match 61.2%; Score 4783; DB 4; Length 1455;  
 Best Local Similarity 61.0%; Pred. No. 0;  
 Matches 887; Conservative 210; Mismatches 326; Indels 30; Gaps 10;  
 Qy 22 LLGSAAGQFSAGGCTFDDPGACDYHQDLYDDFEWVHVSAQEPHYLPPEMFGSGYMYVDS 81  
 Db 14 LLTAAGETFGGCLFDEPYSTCGYSQSBGDDFNWEQVNTLTKTSDPMPGSGFMLVNA 73  
 Qy 82 SNHDPGEKARLQLPMTKENDTHCIDFSYLLYSQKGLNPGTILNLYRVNKGPLANINWVT 141  
 Db 74 SGRPEGORAHLLLPQKENDTHCIDFHYFVSKSNPEGLLNYYVKNVNGPLGNPINWIS 133  
 Qy 142 GFTGRDLRAELAVSTFWPNEYQVIFEAEEVGGSGGYIAIDDIOVLSPCKSPHFLRLG 201  
 Db 134 GDFRTWNRAELASTFWPNFYQVIFEV-ITSGHGHYLAIDEVKVLGHPCFTRTPHFLRIQ 192  
 Qy 202 DVEYNAGQATFQCIATGRDAVHNKMLQRRNGEDIPVAOTKNINHRHFAASFRLOEVTK 261  
 Db 193 NVEYNAGQATFQCSAIGRTVAGDRLWLQGDVDRDAPLKEIKVTSSRRFIASFNVNVTTK 252  
 Qy 262 TDQLYRCVTOSESGSVSNFAQLIVREPPPIAPPOLLGVGPTVLLQLNANSIIGDGP 321  
 Db 253 RDAGKYRMIIRTEGGVGISYAEVLVKEPPVPIAPPQLASVGATYLTQLNANSINGDGP 312  
 Qy 322 IILKEVEYRMTSGSWTETHAVNAPTYKLWHLDPDTEYEIRVLLTRPGGGTGLPGPPLIT 381  
 Db 313 IVAREVEYCTAGSGWNRDQFVDSYKIGHLDPDTEYEISVLLTRPGGGTSGPGALRT 372  
 Qy 382 RTKCAEPMRTPTKLIABIQARRIADVWESLGYNITRCHTFNVITCYHYFRGHNSRAD- 440  
 Db 373 RTKCADPMRGPRKLEVEVKSQITIRWEPTGYNVTRCHSYNLTVHYCYVGGQGVAREE 432  
 Qy 441 -CLDMDPKAPQHVNNHLPPTYNVSLKMLITNPEGRKESEETIIOTDEDVPGVPVKSQ 499  
 Db 433 VSWDTENSHPQHTITNLSPYTNVSVKYLIMNPEGRKESQELIVQTDLPAGVPTESIQ 492  
 Qy 500 TSFENKIFLNWKEPLEPNGIITQYEVSYSSIRSDPAPVPVAGPPQTVNLNNSHVFHFMH 559  
 Db 493 STFEKIFLOWREPTQTVGVTLYEITYKAVSSFPEDIDLSNQSRVSKLGNETHFLPFG 552  
 Qy 560 LHPGTTYOFFIRASTVKGFGPATAINVTNISAPSLPDYEGVDASINETATITVLLRPA 619  
 Db 553 LYPGITYSFTIRASTAKGFGPPATNQFTTKISAPSPAYE-LETPLNQTDNTVTVMKFA 611  
 Qy 620 QAKGAPISAYQIVVQSLPHPHRTKREAGAMECYQVPTVYQNALSGGAPYFAELPQNL 679  
 Db 612 HSRGAPVSVYQIVVEEERPRRTKTKTEILKCYVPVIFHFNQNASLNSYFFAAEFADSLQ 671  
 Qy 680 EPAPFTVGDNRTYKGFWMNPPLAPRGYNIYFQAMSSVEKETKTQCVRATKAAATEEPREV 739

Db 672 AAQFTTGDNKTNGYNTWTELLPYKSYRIYFQAASRANGETKIDCVQVATKGAATPKP-- 729  
Qy 740 IPOPAKQTDVVKIAGISAGILVIFILLVIVIVVVKSKLAKKRKDAMGNTROBMTHVN 799  
Db 730 VPPEKQTDHTVIAGIAGILVIFILVVLVVKKKLAKKKEKETSQTRQEDLDWIG 789  
Qy 800 AMD--RSYAOQSTLHABDPLSLTFMDOHNFSPRLPNDP-----LVPTAVL-DE 844  
Db 790 ELNGPRSYAEGTKLATRAFS--FMDTHNLNGRSVSPSSFTMTKTNTLSTSVNYSYPDE 847  
Qy 845 NHGATAESSLLDVPXY-LCEGTESPYQTGLHPAIRVADLLQHLINIMKTSDSGFKEEY 903  
Db 848 THMASITSSLVQSHTYKKEPADVPYQTGLHPAIRVADLLQHTQMKCAEGYGFKEEY 907  
Qy 904 ESFPEGQASMDVAKQDNRAKRYGNIAYDSRSVILQVDEDDPSDDYINANYIDWLWY 963  
Db 908 ESFPEGQAPWDSAKDENMKRYGNIAYDSRSVRLQTEGDTNSDYINGVY----- 962  
Qy 964 RDGVRPSHYATQGPVHETVYDFWRMVWQEQSACIVMTNLVEVGRVKYKVPDDTEV 1023  
Db 963 -DGYHRPNHYIATQGPQETIYDFWRMVWHENTASIIWMTNLVEVGRVKCKYKVPDDTEI 1021  
Qy 1024 YGFEKTCVSEMEPLAEVYVTFETLEREGYNEIREVKQFHETGPDHGVPHYATGLLSFIR 1083  
Db 1022 YKDIKVTLIETELAEYVIRTFVEKRGVHEIREIQFHTGPDHGVPHYATGLLGFRV 1081  
Qy 1084 RVKLSNPSPSAGPIVWHCSAGAGRTGCVIVIDIMLMAEREGVVDIYNCVKALRSRRINMV 1143  
Db 1082 QVKSPPSAGPLVWHCSAGAGRTGCVIVIDIMLMAEREGVVDIYNCVRELRSRRVNMV 1141  
Qy 1144 QTEQYIFIHDAILEACLCEGTETALPVCEFKAAYPDMIRIDSQNSSHLKDEPOTLNSVTP 1203  
Db 1142 QTEQYVFIHDAILEACLCEGTETVPASQVRSLYYDMNKLDPQTNSSQIKEEPRTLNMTVP 1201  
Qy 1204 RLQAECSIACLRNDKRFMDLPDRCLPLITITIDGESSNYINAALMDSYRQPAFI 1263  
Db 1202 TLRVEDCSIALPRNHEKRCMDLTPDRCLPLITITIDGESSNYINAALMDSYKQPSAFI 1261  
Qy 1264 VTQVPLNTVKDFWRLVYDYGCTSIVMNLNEVDLSQGCPOYWPBEGMLRYGPIOVCEMCS 1323  
Db 1262 VTQHPLENTVKDFWRLVLDYHCTSVMLNDVDPAQLCPQWPENGVRHGPQVFEVSAD 1321  
Qy 1324 MDCDVINRIFRICNLTRPOEGYLMVQOQOYLGMASHREVPFGSKRSFLKLILQVEKMOEC 1383  
Db 1322 LEEDIIISRIYNAARPDQGRVMVQOQOFLGMPMYRDTVPVSKSFLKLIRQVDKMOEY 1381  
Qy 1384 BEGEGRIIHLNGGSGHMFCAIGIUVEMVKQNVVDVFAVKTLSNKPNNVBAEQY 1443  
Db 1382 NGEGRTVHVHCLNGGSGSGTFCAISIVCEMLRHQRTVDVFAVKTLSNKPNNVVDLDQY 1441  
Qy 1444 RFCYDVALEYLES 1456  
Db 1442 KFCYEVALEYLNS 1454

RESULT 13  
ADB79775  
ID ADB79775 standard; protein; 1436 AA.  
XX AC ADB79775;  
XX AC ADB79775;  
DT DT 04-DEC-2003 (first entry)  
DE DE Rat putative receptor tyrosine phosphatase, SEQ ID 15.  
XX KW Analgesic; pain; streptozocin-induced diabetes; rat.  
XX OS Rattus norvegicus.  
XX PN EPI279744-A2.  
XX PD 29-JAN-2003.

XX 26-JUL-2002; 2002EP-00255249.  
XX 27-JUL-2001; 2001GB-00018354.  
PR 07-FEB-2002; 2002GB-00002910.  
XX (WARN ) WARNER LAMBERT CO.  
XX Brookesbank RA, Dixon AK, Lee K, Pinnock RD;  
XX WPI; 2003-395407/38.  
XX N-PSDB; ADB79775.  
DR DR Use of isolated gene sequences and encoded polypeptides that are  
PT upregulated in the spinal cord in response to streptozocin-induced  
PT diabetes for screening compounds for the treatment of pain, or for  
PT diagnosing pain.  
XX PS Claim 1; Page 59-64; 334pp; English.  
XX The present invention relates to nucleotide sequences which are useful in  
CC the screening of compounds for the treatment of pain, or for the  
CC diagnosis of pain. The nucleotide sequences are up-regulated in the  
CC spinal cord in response to streptozocin-induced diabetes. The present  
CC sequence was used to illustrate the invention.  
XX SQ Sequence 1436 AA;  
Query Match 58.8%; Score 4591; DB 7; Length 1436;  
Best Local Similarity 59.9%; Pred. No. 0;  
Matches 859; Conservative 210; Mismatches 330; Indels 36; Gaps 12;  
Qy 32 AGGCTTDDGPG---ACDYHQDLYDDFEWVHVSAQEPHYLPEPMPQGSYMVVDSNNHPGE 88  
Db 24 AAGCTTEASDPVPCFESQAQYDDFQWEQVRIHPGTRTPEDLPHGAYLWVNASQHTPGQ 83  
Qy 89 KARLQPTMKENDTHCIDFSYLLYSOKGLNPGTILNLRVNGKPLANDPINNVGTORDW 148  
Db 84 RAHIIQTLLSENDTHCQFSYFLYSRDGHSPGLGVYVRVNGGPGLSAVNMVMTGSHGRQW 143  
Qy 149 LRALAVSWFMPNEYOVIFEAESVSGRSYVIAADDIQLVSPCDKSPHFLRLGDEVNAG 208  
Db 144 HQALAVSTWPMNEFQVLPALISPHKGYIGLDDILLFSYPCAKAPHFRLGDEVNAG 203  
Qy 209 QNATFOCIATGRDAVHNKMLWQRNGEDI PVAOTKMINHRRFAASFLQSVTKTDQLYR 268  
Db 204 QNASFQCMAGRAAEAEHFLOQSGVLYPAAGVRHLSHRFLATPLASVGRSEQDLYR 263  
Qy 269 CVTQSERGSGVSNFAOLIVREPPRIAPOLLGVGPTYLLIQLNANSIIGDGPILKEVE 328  
Db 264 CVSQAPRGAGVSNFAELIVKEPPTIAPOLLRAGPTYLLIQLNTNSIIGDGPVIRKEIE 323  
Qy 329 YRMTSGSWTETHAVNAPTYKLVHLDPDTEYEIVLALTRPGCGGTGLPGPLITRTKCAEP 388  
Db 324 YRMARGEVAEVHAVNLQTYKLVHLDPDTEYEIVLALTRPGCGGTGLPGPLISRTKCAEP 383  
Qy 389 MRTPKTLKIAEIOARRIADWESIGYNTIRCHTFNVTICYHYFRG--HNESRADCLDMDP 446  
Db 384 TRAPKGLAFIAEIOARQLTQWEPLGYNVTRCHTYAVSLCYRYTLGGSHNTIRECVKWER 443  
Qy 447 KAPQHVNVNHLPPYTNVSLKMLTNPEGRKESEETIIQTDEDPVGPVVKSLQGTSTFNKI 506  
Db 444 GASRYTIKNLLPPRNTHVRLILTNPEGRKEGKVTQTDEDPVGGIAAESLTPTLEDMI 503  
Qy 507 FLNWKPELPENGLITQYEVSYSSIRSFDPAVPVAGPQTVSNLWNSHTHVFMHLHPCTTY 566  
Db 504 FLKWEFPQEPENGLITQYEVSYQSISSDPAVNPVGPRTTISKLRTNYHYFVSNLHPCTTY 563  
Qy 567 QFFIRASTVKGFGFATAINVTNISAPSLPDYRGVDASLNENETATTITVLLRPAQAKAPI 626  
Db 564 LFSVRARTSKFGQAALTEITTNISAPSP-DYADMPSPGSESENTIIVLRPAQGRAPI 622  
Qy 627 SAYQIVVEQLHPHRTKREAGAMECYQVPVVTYQNALSGGAPYFAAEPLPGNLPAPPTV 686

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Db 623 SVYQVVVEERPRRLRRPGAQDCFSVPLTFETALARGLVHYFGAELAASSILLEAMPTV 682
Qy 687 GDNRYKGFNWPPLAPRGYNIIYFOAMSVEKETTKQCVRIATKAAATEEVEVDPDAKQ 746
Db 683 GDNQYRGFNWPLRPLKAYLIIYFOAASHLKGELTCLIRIARKAKESKRPL-EVSQR 741
Qy 747 TDRVVKIAGISA-GILVFLLLVVIVAVIKSKLAKKBDANGNTRQEWTHVMVAMDRSY 805
Db 742 SEEMGLIIGICAGGLAVILLGALIIIVIRKGPVNMWK-ATVNYRQEKTHMMSAVDRSF 800
Qy 806 ADQSTLHAEDPLSLTFMDQHFNPRPLPNDPLVPTAVLDENHSATAESRL-L-DVPRYLCE 864
Db 801 TDQSTLQEDERLGLSMDAPGVSPR-----GDQRSGVTEASSLGGSPRRPCG 849
Qy 865 GTESPYQTQLHPAIRVADLLOHINLMKTSOSYGFKEEYEFEGQSASVDVAKKQNR 924
Db 850 RKGSYPHTGQLHPARVADLLOHINQMKTAEYGFKEEYEFEG----WDATKKDKLK 905
Qy 925 KNRVNIITAYDHSRVILOVEDDPSDDYINANIIDILYRDGYQRPQSHYIATQGPVHTV 984
Db 906 GGRQPVSAIDRHVHKLHPLADPADYISANI-----DGYHRSNFIATQGPKEMI 959
Qy 985 YDFRMVWQEQSACIVMVTNLVEGRVKCYKYPDDTVEYGDFTKVTCEMPLAEYVVRT 1044
Db 960 YDFRMVWQEQSACIVMTKLVEGRVKCSRWPEDSMDYGDIKITLVKTETLAEYVVRT 1019
Qy 1045 FTLERRGYNREIVKQFHTGPHDGHGVPYHATGLLSFIRRVKLSNPPSAGPIVHCSAGA 1104
Db 1020 FALERGGYSARHEVRQFHTAMPERGVPYHATGLLAFIRRVKASTPPDAGPIVHCSAGT 1079
Qy 1105 GRTGCVIIVIDMLDMAEREGVVDIYNCKVALBSRINNVQTEEOVIFTHDAILEACLGE 1164
Db 1080 GRTGCVIIVDVMLDMAECEGVVDIYNCKVTLCSRRVNIQTEEOVIFTHDAILEACLGE 1139
Qy 1165 TAIPVCEFAAAYFDMIRIDSOTNSHLKDEFOTLNSVTPRLQAEBCSIACLPNRNHDKNRF 1224
Db 1140 TTPVNEFATYREMRIDPQNSQLREEFQTLNSVTPPLDVECSIALLPNRNHDKNRS 1199
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Qy 1402 GMFCAIGIVEMVKRQNVVDVFAVKTILRNSKNMVEAPEQYRVCYDVALEYLES 1456
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## RESULT 14

AA25768

ID AA25768 standard; protein; 1499 AA.

XX AC

XX AA25768;

XX DT 16-OCT-2001 (first entry)

XX DE Human protein sequence SEQ ID NO:1283.

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
genetic disease; haematopoietic disorder; platelet disorder; asthma;  
thrombocytopenia; osteoporosis; severe combined immunodeficiency;  
allergic rhinitis; diabetes; multiple sclerosis; depression;  
Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
neurological disorder.

XX Homo sapiens.

OS WO200153455-A2.

XX 26-JUL-2001.

XX 22-DEC-2000; 2000WO-US035017.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI, 2001-457603/49.

XX N-FSDB; AAH99709.

Isolated human polynucleotides encoding polypeptides, useful for the  
treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

XX Claim 20; Page 267; 1217pp; English.

AAH99166 to AAH99904 encode the human proteins given in AA25225 to  
AA25963. The proteins can have activities based on the tissues and cells  
they are expressed in, such as: antiinflammatory; antirheumatic;  
antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;  
central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
cardiovascular; antianemic; antiaggregant; haemostatic; vulnerary;  
antitumor; osteopathic; dermatological; antiallergic; antiasthmatic;  
antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
encoding them can be used in gene therapy, antisense therapy and vaccine  
production. The proteins and polynucleotides are useful for screening for  
agonists or antagonists of a protein and for the treatment and diagnosis  
of disorders associated with the activity of a protein e.g. inflammation,  
rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
infections, autoimmunity, genetic diseases, haematopoietic disorders,  
anaemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers,  
osteoporosis, severe combined immunodeficiency, eczema, allergic  
rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
Alzheimer's disease, Parkinson's disease, neurodegenerative and  
neurological disorders

XX Sequence 1499 AA;

XX Query Match 58.6%; Score 4577; DB 4; Length 1499;

XX Best Local Similarity 59.6%; Pred. No. 0;

XX Matches 862; Conservative 206; Mismatches 331; Indels 48; Gaps 14;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:44:18 ; Search time 133.324 Seconds  
(without alignments)  
3777.694 Million cell updates/sec

Title: US-09-887-669-1  
Perfect score: 7809  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7809	100.0	1457	9 US-09-887-669-1	Sequence 1, Appli
2	7582	97.1	1439	16 US-10-408-765A-284	Sequence 284, App
3	7571	97.0	1439	9 US-09-887-669-2	Sequence 2, Appli
4	4843.5	62.0	1452	9 US-09-887-669-8	Sequence 8, Appli
5	4789.5	61.3	1452	16 US-10-408-765A-83	Sequence 83, Appl
6	4591	58.8	1436	14 US-10-205-219-15	Sequence 15, Appl
7	4577	58.6	1499	15 US-10-296-115-1283	Sequence 1283, Ap
8	4552	58.3	1444	15 US-10-058-270A-98	Sequence 98, Appl
9	4542.5	58.2	1463	14 US-10-176-847-22	Sequence 22, Appl
10	4542.5	58.2	1463	14 US-10-205-823-343	Sequence 343, App
11	4359	55.8	1442	16 US-10-408-765A-805	Sequence 805, App
12	4325	55.4	1430	13 US-10-087-993-34	Sequence 34, Appl
13	2471.5	31.6	623	15 US-10-296-115-1190	Sequence 1190, Ap

14	2216	28.4	815	15	US-10-296-115-1390	Sequence 1390, Ap
15	1526	19.5	1502	9	US-09-808-602-54	Sequence 54, Appl
16	1526	19.5	1502	10	US-09-800-198-44	Sequence 44, Appl
17	1494.5	19.1	1948	9	US-09-808-602-55	Sequence 55, Appl
18	1494.5	19.1	1948	10	US-09-800-198-45	Sequence 45, Appl
19	1492.5	19.1	1897	17	US-10-482-029-52	Sequence 52, Appl
20	1488.5	19.0	1907	15	US-10-291-265-250	Sequence 250, App
21	1482.5	19.0	1912	17	US-10-772-636-64	Sequence 64, Appl
22	1476	18.9	1495	15	US-10-258-666-12	Sequence 12, Appl
23	1441	18.5	2037	15	US-10-087-684-39	Sequence 39, Appl
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25	1438	18.4	2029	15	US-10-087-684-38	Sequence 38, Appl
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28	1337	17.1	1585	15	US-10-369-493-5570	Sequence 5570, Ap
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30	1170.5	15.0	793	17	US-10-777-144-3	Sequence 3, Appli
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33	1155	14.8	802	17	US-10-777-144-1	Sequence 1, Appli
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37	1137	14.6	659	15	US-10-366-547-65	Sequence 65, Appl
38	1137	14.6	774	13	US-10-087-192-1017	Sequence 1017, Ap
39	1127.5	14.4	700	15	US-10-366-547-63	Sequence 63, Appl
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44	1097	14.0	305	9	US-09-788-626-9	Sequence 9, Appli
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ALIGNMENTS

RESULT 1

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; Sequence 1, Application US/09887669  
; Publication No. US20020082397A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLESSINGER, JOSEPH  
; APPLICANT: SAP, JAN M.  
; APPLICANT: ULLRICH, AXEL  
; APPLICANT: VOGEL, WOLFGANG  
; APPLICANT: FUCHS, MIRIAM  
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA  
; FILE REFERENCE: 038602/1246  
; CURRENT APPLICATION NUMBER: US/09/887,669  
; CURRENT FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: 09/234,883  
; PRIOR FILING DATE: 1999-01-21  
; PRIOR APPLICATION NUMBER: 08/087,244  
; PRIOR FILING DATE: 1993-07-01  
; PRIOR APPLICATION NUMBER: 08/049,384  
; PRIOR FILING DATE: 1993-04-21  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1457  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-887-669-1

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; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
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Qy 1020 DTEVYGDVKVTCVMEPLAEYVVRFTFLRRGYNEIREVKQFHTGWPDRHGVPHATGLL 1079
Db 1002 DTEVYGDVKVTCVMEPLAEYVVRFTFLRRGYNEIREVKQFHTGWPDRHGVPHATGLL 1061
Qy 1080 SFIRRVKLSNPPSAGPIVHVCSSAGATGCVIVIDIMLDAEREGVVDIYCNVKALRSR 1139
Db 1062 SFIRRVKLSNPPSAGPIVHVCSSAGATGCVIVIDIMLDAEREGVVDIYCNVKALRSR 1121
Qy 1140 INMVQTEBQIFIHDAILEACLCGETAIPVCEFKAAAFDMIRIDSQTNSSHLKDEFOFLN 1199
Db 1122 INMVQTEBQIFIHDAILEACLCGETAIPVCEFKAAAFDMIRIDSQTNSSHLKDEFOFLN 1181
Qy 1200 SVTPRLQAEBCSIACLPRNHDKNRFDMLPPDRCLPFLITIDGSSNYINAAIMDSYRQP 1259
Db 1182 SVTPRLQAEBCSIACLPRNHDKNRFDMLPPDRCLPFLITIDGSSNYINAAIMDSYRQP 1241
Qy 1260 AAFITVQYPLNTVKDFWRLVYDYGCTSIUMLNEVDLSQCGPQYWPPEGMLRYGPIQVEK 1319
Db 1242 AAFITVQYPLNTVKDFWRLVYDYGCTSIUMLNEVDLSQCGPQYWPPEGMLRYGPIQVEK 1301
Qy 1320 MSCSMDCDVNIRIFRICNLTRPQEGYLMVQOFOYLGWASHREVPGRSKFLKILQVEKW 1379
Db 1302 MSCSMDCDVNIRIFRICNLTRPQEGYLMVQOFOYLGWASHREVPGRSKFLKILQVEKW 1361
Qy 1380 QEECEGEGRTHICLNGGGRSGMFCAGIIVEMVKRQNVVDVPHAVKTLRNSKPNMVEA 1439
```

```
Db 1362 QEECEGEGRTHICLNGGGRSGMFCAGIIVEMVKRQNVVDVPHAVKTLRNSKPNMVEA 1421
Qy 1440 PEQYRFCYDVALEYLESS 1457
Db 1422 PEQYRFCYDVALEYLESS 1439
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## RESULT 3

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US-09-887-669-2
; Sequence 2, Application US/09887669
; Publication No. US20020082397A1
; GENERAL INFORMATION:
; APPLICANT: SCHLESSINGER, JOSEPH
; APPLICANT: SAP, JAN M.
; APPLICANT: ULLRICH, AXEL
; APPLICANT: VOGEL, WOLFGANG
; APPLICANT: FUCHS, MIRIAM
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
; FILE REFERENCE: 038602/1246
; CURRENT APPLICATION NUMBER: US/09/887,669
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/234,883
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 08/087,244
; PRIOR FILING DATE: 1993-07-01
; PRIOR APPLICATION NUMBER: 08/049,384
; PRIOR FILING DATE: 1993-04-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-669-2
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## Query Match

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Best Local Similarity 97.0%; Score 7571; DB 9; Length 1439;
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;
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Qy 1 MD-VAAALPAFVALMLLYPWPILLGSALGQFSAGGCTFDDGPGACDYHQDLYDDFEWVHV 59
Db 1 MDTTAAALPAFVALLLLSPWLLGSAGQFSAGGCTFDDGPGACDYHQDLYDDFEWVHV 60
Qy 60 SAQEPHYLPPEMPEGQSVWVVDSSNHPGEGAKRLQPTMKENDTHCIDFSYLLSQKGLNP 119
Db 61 SAQEPHYLPPEMPEGQSVWVVDSSDHPGEGAKRLQPTMKENDTHCIDFSYLLSQKGLNP 120
Qy 120 GTNLILVRNKGPLANPIMNVGTGTRDWLRABELAVSTFWPNEYQVIFEAESGGRSGYI 179
Db 121 GTNLILVRNKGPLANPIMNVGTGTRDWLRABELAVSTFWPNEYQVIFEAESGGRSGYI 180
Qy 180 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFOCIATGRDAVHNKLMLORRNGEDIPV 239
Db 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFOCIATGRDAVHNKLMLORRNGEDIPV 240
Qy 240 AQTKNINHRFAASFRLOEVTKTDQDLRYCVTOSERGSVSNFAQLIVRPPPIAPPOL 299
Db 241 AQTKNINHRFAASFRLOEVTKTDQDLRYCVTOSERGSVSNFAQLIVRPPPIAPPOL 300
Qy 300 LGVPTVLLIQLNANSIIGDGPPIILKEVEYMTSGSWTETHAVNAPTYKLMHLDPDTEYE 359
Db 301 LGVPTVLLIQLNANSIIGDGPPIILKEVEYMTSGSWTETHAVNAPTYKLMHLDPDTEYE 360
Qy 360 IRVLLTRPGEGETGLPGPPLITRICKAEPMTPTKTLKIAEQARRIADVMSLGYNITRC 419
Db 361 IRVLLTRPGEGETGLPGPPLITRICKAEPMTPTKTLKIAEQARRIADVMSLGYNITRC 420
Qy 420 HTFNVTICYHYFRGHNSRADCLMDPKAPQHVVNHLPPYTNVSLKMLTNPEGRKESEE 479
Db 421 HTFNVTICYHYFRGHNSKADCLMDPKAPQHVVNHLPPYTNVSLKMLTNPEGRKESEE 480
Qy 480 TIIOTDEDVGPVVKSIQGTFSFNKJFLANKPELNGIITQYEVSSIRSIRSDPAVPV 539
```

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Db 481 TIIQTDVDPGVPVKSLQTSFENKIFLNKKEPLDPNGIITQYEISYSSIRSDPAVPV 540
Qy 540 AGPPTQVNLNTHHVMHLPHTGYOFFFTRASTVKFGFPATAINVTNTISASRLDPE 599
Db 541 AGPPTQVNLNTHHVMHLPHTGYOFFFTRASTVKFGFPATAINVTNTISAPTLDPYE 600
Qy 600 GVDASLNSTATITVLLRPAQAKGAPISAYQIVVQELPHPHETKREAGAMECVQVPVTYQN 659
Db 601 GVDASLNSTATITVLLRPAQAKGAPISAYQIVVQELPHPHETKREAGAMECVQVPVTYQN 660
Qy 660 ALSGAPYFAELPPGNLPPAPPTVGDNRITKGFNPPPLAPRKGYNIFYQAMSSVBEKE 719
Db 661 AMSGAPYFAELPPGNLPPAPPTVGDNRITKGFNPPPLAPRKGYNIFYQAMSSVBEKE 720
Qy 720 TKTCQVRIATKAAATEBEVIPPDAKQTRDVVKIAGISAGILVFILLLLVIVIKKSKL 779
Db 721 TKTCQVRIATK-AATEBEVIPPDAKQTRDVVKIAGISAGILVFILLLLVIVIKKSKL 779
Qy 780 AKKRDKAMGNTRQEMTHMVMANDRSYADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPT 839
Db 780 AKKRDKAMGNTRQEMTHMVMANDRSYADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPT 839
Qy 840 AVLDSHSAATESRLLDVPRYLCGETSPYQTQGLHPAIRVADLLQHNLMKTSDSYGF 899
Db 842 ----ENHSATAESSRLLDVPRYLCGETSPYQTQGLHPAIRVADLLQHNLMKTSDSYGF 887
Qy 900 KEEYESFEGQSASWDVAKKQONRAKNRYGNIAYDHSRVLQPVEDDPSDDYINANYID 959
Db 888 KEEYESFEGQSASWDVAKKQONRAKNRYGNIAYDHSRVLQPVEDDPSDDYINANYI- 946
Qy 960 IWLRYDGYQRSHYIATQGPVHETVYDFWRVMVQEOSACIWMVNTLVGVKCYKYPD 1019
Db 947 ----DGYQRSHYIATQGPVHETVYDFWRVMVQEOSACIWMVNTLVGVKCYKYPD 1001
Qy 1020 DTEVYDGFQVTCVMEPLAEYVVRTFTLRRGYNEIREVKQFHTGWDGHPVPHATGLL 1079
Db 1002 DTEVYDGFQVTCVMEPLAEYVVRTFTLRRGYNEIREVKQFHTGWDGHPVPHATGLL 1061
Qy 1080 SFIRRVKLSNPPSAGPIVVHCSAGAGRTGCVIIVDIMLDMAREGVVDIYNCVKALRSRR 1139
Db 1062 SFIRRVKLSNPPSAGPIVVHCSAGAGRTGCVIIVDIMLDMAREGVVDIYNCVKALRSRR 1121
Qy 1140 INMWQTEQYFIHDAILEACLCGETAIPVCEFKAAAYFDMIRIDQTSNSSLKQDFQTLN 1199
Db 1122 INMWQTEQYFIHDAILEACLCGETAIPVCEFKAAAYFDMIRIDQTSNSSLKQDFQTLN 1181
Qy 1200 SVTPRLQAECDSCIACLRNHDKNRPMWMLPPDRCLPFLITIDGESSNTYINAAALMDSYROP 1259
Db 1182 SVTPRLQAECDSCIACLRNHDKNRPMWMLPPDRCLPFLITIDGESSNTYINAAALMDSYROP 1241
Qy 1260 AAFIVTQVPLPNTVKDFWRLVYDGYCTSIIVMLNEVDLSQGCQFYWPBEGMLRYGPIQVEC 1319
Db 1242 AAFIVTQVPLPNTVKDFWRLVYDGYCTSIIVMLNEVDLSQGCQFYWPBEGMLRYGPIQVEC 1301
Qy 1320 MSCSMDCDVINRIFRICNLTRPOEGLVMVQOQYILGWASHREVPGSKSFLLILOVEKW 1379
Db 1302 MSCSMDCDVINRIFRICNLTRPOEGLVMVQOQYILGWASHREVPGSKSFLLILOVEKW 1361
Qy 1380 QBECEGEGRTIIHCLNGGSGMFCAGIIVVEMVKRQNVVDVFAVKTLRNSKKNMVEA 1439
Db 1362 QBECEGEGRTIIHCLNGGSGMFCAGIIVVEMVKRQNVVDVFAVKTLRNSKKNMVEA 1421
Qy 1440 PEQYRFCYDVALEYLESS 1457
Db 1422 PEQYRFCYDVALEYLESS 1439
```

## RESULT 4

US-09-887-669-8

; Sequence 8, Application US/09887669

; Publication No. US20020082397A1

; GENERAL INFORMATION:

```
; APPLICANT: SCHLESSINGER, JOSEPH
; APPLICANT: SAP, JAN M.
; APPLICANT: ULLRICH, AXEL
; APPLICANT: VOGEL, WOLFGANG
; APPLICANT: FUCHS, MIRIAM
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
; FILE REFERENCE: 038602/1246
; CURRENT APPLICATION NUMBER: US/09/887,669
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/234,883
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 08/087,244
; PRIOR FILING DATE: 1993-07-01
; PRIOR APPLICATION NUMBER: 08/049,384
; PRIOR FILING DATE: 1993-04-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-669-8
```

```
Query Match 62.0%; Score 4843.5; DB 9; Length 1452;
Best Local Similarity 61.9%; Pred. No. 0;
Matches 898; Conservative 206; Mismatches 318; Indels 29; Gaps 9;

Qy 22 LLGSAQCQFSAAGCTTDDGACDYHQDLYDDFWVHVSAOEHPHYLPMPGSGSMVYVDS 81
Db 14 LLTAAGETTSGGCLFDEPYSTCGYSQSEGDDFNWEQVNTLTKTPTSDPMPSPGSLMLVNA 73
Qy 82 SNHDPGEKARLQPTMKENDTHCIDFSVLLYSQKGLNPGLTILVRVKNKGLANPIWNT 141
Db 74 SGRPEGORAHLLLPOLKENDTHCIDFHYFVSSKSNPPGLLVVYKVNNGPLGNPINWIS 133
Qy 142 GFTGRDLRLARLAVSTFWPNEYQVIFAEVSGRSGYIAIDDIQVLSYPCDKSPHFLRLG 201
Db 134 GDPTRTWNRALALSTFWPNFYQVIFEV-ITSGHQGLAIDEVKVLGHPCRTTTHFLRIQ 192
Qy 202 DVEVNAQONATFOCIATGRDAVHNKMLQORNGBDIPVAOTKNIHRRFAASRLQEVTK 261
Db 193 NVEVNAQOFATFQCISAIGRTVAGDRLWLQIGIDVRDAPLKEIKVTSSRRFIASFNVVNTTK 252
Qy 262 TDQDLRYCVTQSGRSGVSNFAQLIVRPPPIAPPQLLGVPYVLLIQLNANSIIGDGP 321
Db 253 RDAGKYRMTIRTEGGVGISNYAELVWKEPPVPIAPPQLASVGATVYLTQLNANSINGDGP 312
Qy 322 IILKEVEYRMTSGSWTETHAVNAPYKLVHLLDPDTEYRIRVLLTRPGEGGTGLPGPLIT 381
Db 313 IVAREVEYCTASGSWNRQPVDSYSYKIGHLLDPDTEYRISVLLTRPGEGGTGSPGALRT 372
Qy 382 RTKCAEPMRTPTKLIKIAIOARRJAVDWESIGYINIRCHTFNVTICYHYFRGHNESRAD- 440
Db 373 RTKCADPMRGPRKLEVEVVKSRQITIRWEPFGYVNVTRCHSYNLTVHYCYVGGQGVREE 432
Qy 441 -CLDMDPKAPOHVNVNHLPPYTNVSLKMLTTPGKESFEETIOTDEVDVGPVPVKSQ 499
Db 433 VSWDTENSHPOHTITNLSPYTNVSKLILMMPGKESQELTVQTDQDLPAGVPTESIQ 492
Qy 500 TSFENKIFLNKKEPLEPNIGIITQYEVSYSSIRSDPAVPVAGPPQTVSNLWNSTHHVFMH 559
Db 493 STFEKIFLOWREPTQYTGVTLYEITYKAVSSDPDEIDLNSQSRVSKLGNETHFLPFG 552
Qy 560 LHPGTYTOFFIRASTVKFGFPATAINVTNTISAPSLPDYEGVDASLNSTATITVLLRPA 619
Db 553 LYPGTYSTFIRASTAKGFGPPATNQFTTKISAFSPMPAYE-LETPLNQTNDNTVTVMKPA 611
Qy 620 QAKGAPISAYQIVVQELPHPHETKREAGAMECVQVPVTYONALSGGAPYRAELPPGNLP 679
Db 612 QSRGAPSVYQIVVVEEERPRTKTTEILKCYVPPIHFQNASLLNSQYIFAAEFADSLQ 671
Qy 680 EPAPFTVGDNRITYKGFWMNPPLAPRKGYNIFYQAMSSVVEKETKTCQVRIATKAAATEBEV 739
```

Db 672 AAQPTTGDKNTYNGYNTPLPYKSYRIYFQAASRANGETKIDCVQATKGAATPKP-- 729  
Qy 740 IPDPAKQTRVVKIAGISAGILVIFILLVIVIVVKSKLAKKRDAMGNTRQEMTHVN 799  
Db 730 VPEPEKQTDHTVKIAGIAGILVIFILLVIVIVVKSKLAKKRDAMGNTRQEMTHVN 789  
Qy 800 AMDSYADQSTLHAEDPLSLTMDQHNFSPLPNDP-----LYPTAVL-DENH 846  
Db 790 SMDKSYAEOGTNCDE--AFSMDTHNLGRSVSSPSTFMTKNTLSTSPNSYYPDETH 846  
Qy 847 SATAESRLLDVPRY-LCEGTESPYQTGOLHPAIRVADLLQHLINLMKTSYGFKEYES 905  
Db 847 TMASDTSLSVQSHYTKREPADVPYQTGOLHPAIRVADLLQHLITOMKCAGYGFEYES 906  
Qy 906 FFEQOSASWDVAKQONRAKNRYGIIAYDHSRVILQVEDDPSDDYINAYIDIMLYRD 965  
Db 907 FFEQOSASWDVAKQONRAKNRYGIIAYDHSRVILQVEDDPSDDYINAYIDIMLYRD 960  
Qy 966 GYQRPISHYATQGPVHETVDFRWVWQESACIWMVNLVEGVRVKCYKWPDDTEVYG 1025  
Db 961 GYRPNHYIATQGPVHETVDFRWVWQESACIWMVNLVEGVRVKCYKWPDDTEVYG 1020  
Qy 1026 DFKVTCVEMEPLEAYVYRTTLERRGYNEIREVKQFHTGWDHGVPHYATGLLSFIRRV 1085  
Db 1021 DIKVTLETETELLAEYVIRTAVERKGIIEIREKQFHTGWDHGVPHYATGLLSFIRRV 1080  
Qy 1086 KLSNPPSAGIIVVHCSAGAGRTGCIYVIDIMLMAEREGVVVDIYNCVKALRSRRINNVQT 1145  
Db 1081 KKSPPSAGIIVVHCSAGAGRTGCIYVIDIMLMAEREGVVVDIYNCVKALRSRRINNVQT 1140  
Qy 1146 EQYIFIHDAILEACLCGETAIPVCEPKAAYFDMIRIDSQTSNHLKDFQTLNSVTPRL 1205  
Db 1141 EQYVFTHDAILEACLCGETAIPVCEPKAAYFDMIRIDSQTSNHLKDFQTLNSVTPRL 1200  
Qy 1206 QAEDCSFACIIPRHNKRNKRWMDLPPDRCLPLITIDGESNYINAAALMDSYROPAPFIVT 1265  
Db 1201 RVSDCSFACIIPRHNKRNKRWMDLPPDRCLPLITIDGESNYINAAALMDSYROPAPFIVT 1260  
Qy 1266 QYPLPNTVKDFWRLVLDYDGTCTSIYMLNEVDLSQCPQYWPPEEGMLRGPYQVECMSCMD 1325  
Db 1261 QHPLPNTVKDFWRLVLDYDGTCTSIYMLNEVDLSQCPQYWPPEEGMLRGPYQVECMSCMD 1320  
Qy 1326 CDVINRIFRNLTRPOEGLVMOQFQYLGWASHREVPGRSKRFLKLILOVEKQWCEBEE 1385  
Db 1321 EDIISRIFRINAAARPQDGYRMVQFQFLGWPMTYRDFVSKRFLKLIROVDKQWCEYNG 1380  
Qy 1386 GEGRTIHLCLNGGSGRGMPCAGIIVVEMKRONVVDVFAVKTLSKKNMVEAPEQYRF 1445  
Db 1381 GEGRTIHLCLNGGSGRGMPCAGIIVVEMKRONVVDVFAVKTLSKKNMVEAPEQYRF 1440  
Qy 1446 CYDVALEYLES 1456  
Db 1441 CYEVALEYLNS 1451

## RESULT 5

US-10-408-765A-83  
; Sequence 83, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408, 765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 83

; LENGTH: 1452

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-408-765A-83

Query Match 61.3%; Score 4789.5; DB 16; Length 1452;

Best Local Similarity 61.1%; Pred. No. 0;

Matches 887; Conservative 211; Mismatches 324; Indels 29; Gaps 9;

Qy 22 LLGSALGQPSAGACTPDDGPGACDYHQDLVDDPEWHVHSAQEPHYLPPEMQSGYMWVDS 81  
Db 14 LLTAAGETESGCLFDEPYSTCGYQSQEGDDNWEQVNTLTKTPTSDPMPWPSGLMLVNA 73  
Qy 82 SNHDPGEKARLQLPWKENDTHCIDFSLYLLYQKGLNPGTLNLRVKNKGPLANPIWVNT 141  
Db 74 SGPEQORAHLLPOLKENDTHCIDFHYFVSSKSNPPGLLVYVKNNGPLGNPINNIS 133  
Qy 142 GFTGRDMLRAELAVSTFWPNEYQVIFEAESVGGSGRYAIDDIQVLSYPCDKGPHFLRLG 201  
Db 134 GPTRTWNRRAELAISTFWPNFYQVIFEV-ITSGHQGYLAIDEVKVLGHPCTRTPHFLRIQ 192  
Qy 202 DVEYNAGONATFOCIATGRDAVKNLWQRNGEDIPVAQTKNINHRPRAASFLRQVTK 261  
Db 193 NVEVNAQOFATFQCSAIGRTVAGDRLWLGQIDVRDAPLKEIKVTSSRRFIASFNVNTTK 252  
Qy 262 TDQDLVRCVTOSESGSVSNFAOLIVREPPRTAPPOLGCVGPTLYLLIQLNANSIIGDGP 321  
Db 253 RDAGKTRCMIRTEGGVIGISNIAELVWKEPPVPVAPPOLASVGATYLLIQLNANSINGDGP 312  
Qy 322 ILLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYEIRVLLTRPGEGETGLPGPPLIT 381  
Db 313 IVAREVEYCTASGSWMDRQPDVSTSYKIGHLDPDTEYEIRVLLTRPGEGETGLPGPALRT 372  
Qy 382 RTKCAEPMRTPKLTABEQARIAVDWESLGNITRCHTFNTVITCYHTRFGHESRAD- 440  
Db 373 RTKCADPMRGPRLKEVVEVKSQITIRWEPFGYVNVTRCHSYNLTVHYCYVGQGOEYREE 432  
Qy 441 -CLDMPKAPQHVNLHPVYTVNLSKMLNPNRKESEBETIQTDDSDVPGVPVKSLOG 499  
Db 433 VSWDTEHPQHTITNLSPYTNVSKLILNPNRKESEBETIQTDDSDVPGVPVKSLOG 492  
Qy 500 TSPENKIFLWKEPLPENGIIQYEVSYSSIRSFDPVAVPVPVQVTSNLSNTHYFMH 559  
Db 493 STEEBKIFLWKEPPTQYVITLYEITYKAVSSFDPEIDLSNQSGRVSKLGNETHPLFFG 552  
Qy 560 LHPGTTYQPIRATVKGPGAPATAVNTTINISAPSLPDYEGVDASLNETHATTTVLLRPA 619  
Db 553 LYPGTTYSEFTRASTAKGPGPATNQFTTKISAPMPAYE-LETPLNQTDNTVTVMKPA 611  
Qy 620 QAKGAPISAVQIVVEQLPHRTRKAGAMBCYQVPTYQNALSGGAPYFAAELPPGNLP 679  
Db 612 HSRGAPVSVYQIVVEEERPRRTKTTTEILKCYVPIPHFQNASLNSQYFAAFPPADSLQ 671  
Qy 680 EPAPFTVGNRTYKGFNPNPLAPRKGYNIYFOAMSSVEKETKTCQVRIATKAAATEPEV 739  
Db 672 AAQPTTGDKNTYNGYNTPLPYKSYRIYFQAASRANGETKIDCVQATKGAATPKP-- 729  
Qy 740 IPDPAKQTRVVKIAGISAGILVIFILLVIVIVVKSKLAKKRDAMGNTRQEMTHVN 799  
Db 730 VPEPEKQTDHTVKIAGIAGILVIFILLVIVIVVKSKLAKKRDAMGNTRQEMTHVN 789  
Qy 800 AMDSYADQSTLHAEDPLSLTMDQHNFSPLPNDP-----LYPTAVL-DENH 846  
Db 790 SMDKSYAEOGTNCDE--AFSMDTHNLGRSVSSPSTFMTKNTLSTSPNSYYPDETH 846  
Qy 847 SATAESRLLDVPRY-LCEGTESPYQTGOLHPAIRVADLLQHLINLMKTSYGFKEYES 905  
Db 847 TMASDTSLSVQSHYTKREPADVPYQTGOLHPAIRVADLLQHLITOMKCAGYGFEYES 906  
Qy 906 FFEQOSASWDVAKQONRAKNRYGIIAYDHSRVILQVEDDPSDDYINAYIDIMLYRD 965

Db 907 FPEGASPDWAKDENRKNRYGNI IAYDHSRVLRTQIEGDTNSDYINGNYI-----D 960  
Qy 966 GYORSHYIATQGPVHETVYDFWRWVWQESACIWMVNLVEVGRVKYKWPDDTEVYG 1025  
Db 961 GYHRENHYIATQGPVHETVYDFWRWVWQESACIWMVNLVEVGRVKYKWPDDTEVYG 1020  
Qy 1026 DPKVTVCEMEPLAEVYVTFELTEREGYNEIREVKGPHFTGPHDGHGVPVYHATGLLSFIRRV 1085  
Db 1021 DIKVTIELLELLAEVYVTFELTEREGYNEIREVKGPHFTGPHDGHGVPVYHATGLLSFIRRV 1080  
Qy 1086 KLSNPPSAGPIVHVSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRINMVQT 1145  
Db 1081 KSKSPSAGPLVHVSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRINMVQT 1140  
Qy 1146 BEQYFIHDAILEACLCGETAIPVCEFKAAVPMIRIDISQTNSSHLKDEPOTLNSVTPRL 1205  
Db 1141 BEQYFIHDAILEACLCGETSVFASQVRSYYDMNKLDPQTNSSQIKBEFRTLNMTPTL 1200  
Qy 1206 QAEDCSIACLPRNHDKNRPMMLPPDRCLPFLITIDGSSNYINAALMDSYRQPAAFIVT 1265  
Db 1201 RVEDCSIACLPRNHDKNRPMMLPPDRCLPFLITIDGSSNYINAALMDSYRQPAAFIVT 1260  
Qy 1266 QYPLENTVKDFWRLVYDYGCTSIYMLNEVDLSQCGPQYWPBEGMLRYGPIQVECMSCSMD 1325  
Db 1261 QHPLNTVKDFWRLVLDYHCTSVMLNDVDPALCPQYWPENGVRHGHGPIQVEFVSADLE 1320  
Qy 1326 CDVINRIFRNCNLTPOQGYLMVQOXYLGNASHREVPGSKRSFLKLILOVEKMOECEE 1385  
Db 1321 EDIISRIFRYNAARPDQHRMVQOFLGWPMDYRDTVPKRSALLIRQVDKMOEYNG 1380  
Qy 1386 GEGRTIICLANGGSGMFCAGIYVWVKRQNVVDVHAKVTLNSKNVVEAPEOYRF 1445  
Db 1381 GEGRTVWCLNGGSGSGTFCALISVCEMLRHQRTVDVHAKVTLNRNKNMVDLDDQYKF 1440  
Qy 1446 CYDVALEYLES 1456  
Db 1441 CYEVALEYLNS 1451

## RESULT 6

US-10-205-219-15  
; Sequence 15, Application US/10205219  
; Publication No. US20030138803A1  
; GENERAL INFORMATION:  
; APPLICANT: Warner-Lambert Company  
; APPLICANT: Lee, Kevin  
; APPLICANT: Dixon, Alistair  
; APPLICANT: Brooksbank, Robert  
; APPLICANT: Pincock, Robert  
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain  
; FILE REFERENCE: WL-A-018200  
; CURRENT APPLICATION NUMBER: US/10/205,219  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: GB 0118354.0  
; PRIOR FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 1436  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Receptor protein tyrosine phosphatase-lambda  
US-10-205-219-15

Query Match 58.8%; Score 4591; DB 14; Length 1436;  
Best Local Similarity 59.9%; Pred. No. 0;  
Matches 859; Conservative 210; Mismatches 330; Indels 36; Gaps 12;  
Qy 32 AGGCTFDDGFG---ACDHYQDLYDDFVWVHSAQEPHYLPPEMPOGSSYMWVDSNHPGE 88  
Db 24 AAGCTFEASDFVWPCFESQAYDDFQWEQVRIHPQTRTFEDLPHGAYLMVNASQHTPGQ 83

Qy 89 KARLQLPTMKENDTHCIDFSYLLYSOKGLNPGTLLNLRVNVKGPLANPIVNVVGTGTGRDW 148  
Db 84 RAHIIFOTLSENDTHCQFSYFLSRDGHSPGLTGVYRVNGGPLEGSAWMTTSGHGRQW 143  
Qy 149 LRAELAVSTFWPNEQYQVIFAEVSGGRSGYTAIDDIQVLSYPCDKSPHFLRLGDEVEVNA 208  
Db 144 HQAELAVSTFWPNEQVLFALISPDHKGVIIGLDDILLFSYPCAKAPHSRLGDEVEVNA 203  
Qy 209 QNATFOCIATGRDAVHKLWLRNGREDIPVAQTKNINHRPFAASFRLOETKTKDODLYR 268  
Db 204 QNASFOCWAAGRAAEAEHFFLQROSGVLVPAAGVHRHISHRRFLATFPLASVGRSEQDLYR 263  
Qy 269 CVTOSERGSGVSNFAQLIVREPPIAPPOLLGVGPTVLLIQLNANSIIGDGPILKEVE 328  
Db 264 CVSQAPRGAGVSNFAELIVKEPPIAPPOLLRAGPTVLLIQLNANSIIGDGPVIRKEIE 323  
Qy 329 YRMTSGSWTETHAVNAPTYKWLHLDPDTEYBIRVLLTRPGEGETGLPGPPLITRTKCAEP 388  
Db 324 YRMARGPWAEEVHVNLTQYKWLHLDPDTEYBISVLLTRPGGGTGRPGPPLISRTKCAEP 383  
Qy 389 MRPKTKIABIQARRIADWESLGYNITRCHTFNVTICYHYFRG--HNSRADCLMDP 446  
Db 384 TRAPKGLAFABIQARQLTQWEPLGYNVTRCHTYAVSLCYRYTLGGSHQNTIRECVKMER 443  
Qy 447 KAPOHVNVHLLPPYTNVSLKMLLTNPEGRKSEETIIOTDEDVPGVPVVKSLQGSTFENKI 506  
Db 444 GASRYTIKNLLPPFNHVRLLTNPEGRKEGKVTFTQDEDVPGIAAESLTFPLEDNI 503  
Qy 507 FLNWKPLENPGIITQYEVSYSSIRSPDPAVPVAGPQTVSNLWNSTHVVHMLHPGTTY 566  
Db 504 FLKWEEOEPNGLITQYEVSYQSISSPDPAVNVPGPRTISKLRNETVHVSFNLHPGTTY 563  
Qy 567 QPFRASTVKGFGPATAVNTTINISAPSLPYEGVDASLNETATITVLLRPAQAKGAPI 626  
Db 564 LFSVRASTKSGQAAALTEITNISAPSF-DYADMPSPLGSESENTITVLLRPAQGRGAPI 622  
Qy 627 SAYQIVVEQLPHRTKREAGAMECVQVPVTVYONALSGGAPYVFAELPPGNLPEPAPTV 686  
Db 623 SVYQVVEEERPRRLRREPQACQCFVPLTFTETALRGLVHFGNELAASLEAMPFTV 682  
Qy 687 GDNRTYKGFNPPPLAPRGYNIYFQAMSSVEKETKTCVRIATKAAATEEPEVDPDAKQ 746  
Db 683 GDNQTYRGFWNPPLEPRKAYLIYFQAASHLKGTELNCIRIARAKAACKESKRPL-EVSQR 741  
Qy 747 TDRVVKIAGISA-GILVIFILLVIVIVKSKLAKKKDANGTRQENTHWNWMDRSY 805  
Db 742 SEEMGLILGICAGGLAVLILLGAIIVIRKGPVNMTK-ATVANYRQKTHMMSAVDRSF 800  
Qy 806 ADQSTLHAEDPLSLTFMDORNFSPRLPNDPLVPTAVLDENHSATAESSRLL-DVPRYLCE 864  
Db 801 TDQSTLQSDERLGLSFMADPGYSR-----GDQSGGVTEASLSLGGSPRRPG 849  
Qy 865 GTESPYQTGQLHPAIRVADLLQHINLMKTSYSGFKEEYESFFEGQSASWDVAKKDQNR 924  
Db 850 RKGSYPYHTGQLHPAVRVADLLQHINQMKTASGYFKQYEVESFFEG---WDATKKKDKLK 905  
Qy 925 KRYGNIAYDHSRVILQPDVEDDSSDIYNNYIDILWYRDGYQRPSPHYIATQGPVHETV 984  
Db 906 GGRQEPVSAYDRHHVKLHPMLADPDADYISANYI-----DGYHRSNFIATQGPKEPI 959  
Qy 985 YDFWRWVWQESACIWMVNLVEVGRVKYKWPDDTEVYGDVFKVTCVEMPELAVYVVRT 1044  
Db 960 YDFWRWVWQESACIWMITKLVEVGRVKCSYWPEDSDNYGDIKITLVKTETLAVYVVRT 1019  
Qy 1045 FTLERRGYNEIREVKQFHFTGWPDHGVPHYATGLLSFIRRVKLSNPPSAGPIVHVSAG 1104  
Db 1020 FALERGGYSARHEVRQFHFTAWPEHGVPHYATGLLAFIRRVKASTPPDAGPIVHCSACT 1079  
Qy 1105 GRTGCIYVIDMLDMAEREGVVDIYNCVKALRSRRINNVQTEEQYIFHDAILEACLCGE 1164  
Db 1080 GRTGCIYVIDMLDMAECEGVVDIYNCVKTLCSRRVNMVQTEEQYIFHDAILEACLCGE 1139  
Qy 1165 TAI PVCEPKAAVFDIMIRIDSQTNSHLKDEFTLNSVTPRLQAEDCSIACLPRNHDKNRF 1224

Db 1140 TTPVNEFRATYREIMRIDPOSNSQREEFQTLNSVTPPLDVEBESIALLPNRDKRS 1199  
Qy 1225 MDMLPPDRCLPFLITIDGESSNYINAALMDSYRQPAAFIVTQYPLPNTVKDFWRLVVDYG 1284  
Db 1200 MDVLPDRCLPFLISSDGPNNYINAALTSYTSRAAFIVTLHLPLQSTTPDFWRLVVDYG 1259  
Qy 1285 CTSIWMLENEVDLSQ---CPQYWPBEGMLRYGPTQVCMSCMDCDVINRIFRINLTRP 1341  
Db 1260 CTSIWMNLQNSAWPCLQYWPBEGMLRYGPTQVCMSCMDCDVINRIFRINLTRP 1319  
Qy 1342 QEGYLMVQOFOYLCWASHREVPKRSFLKILQVEKWOBCBEGRTIIHCLNGGGRS 1401  
Db 1320 QEGHLLVRHQFLRWSAYRTPDSRKAFHLHLAEDVKWQ--AESGDGRTVVHCLNGGGRS 1377  
Qy 1402 GMFCAIGVVMKRONQVVDVFAVKTLRNSKPNMVEAPEQRYFCYDVALEYLES 1456  
Db 1378 GTFCACATVLEMIRCHSLVDVFFAAKTLRNYKPNMVTMDQYHFCYDVALEYLEA 1432

RESULT 7  
US-10-296-115-1283  
; Sequence 1283, Application US/10296115  
; Publication No. US20040053248A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq Inc  
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 784PCT  
; CURRENT APPLICATION NUMBER: US/10/296,115  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 1478  
; SEQ ID NO 1283  
; LENGTH: 1499  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-296-115-1283

Query Match 58.68; Score 4577; DB 15; Length 1499;  
Best Local Similarity 59.68; Pred. No. 0;  
Matches 862; Conservative 206; Mismatches 331; Indels 48; Gaps 14;

Qy 34 GCTFDDGPG--ACDYHQDLYDDPEWVHVSQAQEPHYLPPEMPOGSSYMWVDSNNHDPGEKA 90  
Db 71 GCTFEESDPAVPEYCSQAQYDDFQWEQVRIHPGTRAPADLPHGSLYLMVNTSQAPQRA 130  
Qy 91 RLQLPTMKENDTHCIDFSYLLYSQKGLNPGTLNILVRNKGPLANPIWNVTGTGRDWLR 150  
Db 131 HVIFQSLSENDTHCVQPSYFLYSRDGHSPTGLGVYVRVNGGPLGSAVWMTGSHGRQWHQ 190  
Qy 151 AELAVSTFWNEQVIFEAEEVSGRSYIAIDDIQVLSYPCDKSPHPLRLGDVEVNAQON 210  
Db 191 AELAVSTFWNEQVIFEAEEVSGRSYIAIDDIQVLSYPCDKSPHPLRLGDVEVNAQON 250  
Qy 211 ATFOCIATGDVAHNLKWLORNGEDIPVAOTKNIHRRFAASPLRLOEVTKDODLYRCV 270  
Db 251 ASFCMAAGRAAEAEFLRQSGALVPAAGVRHISHRRFLATPPLAAVSRABODLYRCV 310  
Qy 271 TQSERGSGVS--NFAQLIVRPPRPPIAPPQLLGVGPTYLLLIQLNANSIIGDGPILKEVEY 329  
Db 311 SQAPRGRTSLNFAEFWKEPPTPIAPPQLLAGRTYLLIQLNTNSIIGDGPVIRKEIEY 370  
Qy 330 RMTSGSWTEHAVNAPYKULWHLDPDTEYEIRVLLTRPBGGGTGLPGPPLITRTKCAEPM 389  
Db 371 RMARGPWAEEVHVSQYKYLWHLDPDTEYEIRVLLTRPBGGGTGLPGPPLISRTKCAEPM 430  
Qy 390 RTPKTKIAEQABRIADVDESGLNITRCHTENVITCYHYFRG--HNESRADCLMDPK 447  
Db 431 RAPKGLAFABIQARQLQWEPLGYNVTRCHTYTSLVCYHYTLGSSHNQITRECVKTEQG 490

Qy 448 APOHVVNHLPPYNTVNSLKMILTNPEGRKESEETIIQTDDEDPGVPVPVKSLOGTSFENKIF 507  
Db 491 VSRVTMKNLLPYRNHVRLVLTNPEGRKEGKEVTFQTDDEDPGVPVIAAESLTFTPLEDMIF 550  
Qy 508 LNKKEPLEPNGIITQVEVSYSSRSFDPAPVAGPPTQVSNLWNSTHHVFMLHPGTYYQ 567  
Db 551 LKWEPEQEPNGLITQVEISYQSISSDPANVPGRRTISKLNETTHVSNLHPGTYYL 610  
Qy 568 FFIRASTVKGFGPATANVTNINISAPSLDPYEGVDASLNETATTITVLLRPAQAKGAPIS 627  
Db 611 FSVRARTKGFGQAALTEITTNISAPSF-DYADWPSPLGESENITITVLLRPAQGRGAPIS 669  
Qy 628 AYQIVVEQLH-PRHTKREAGAMECYQVPTVYQNALSCGAPYFAAEPLPGNLPPEAPFTV 686  
Db 670 VYQVIVBEEQSGRRLRREBPGQDCFPVPLTFEAALARGLDVDFGAEALASLPEAMPFTV 729  
Qy 687 GDNRTYKGFNPPPLAPRKGYNIYFOAMSSVEKETKTCOVRIATKAAATEBPEVDPDAKQ 746  
Db 730 GDNKTRGFNPPPLEPKAYLIYFOAASHUKGETRLNCIRIARKAAKESKRPL-EVSQR 788  
Qy 747 TDRVVKIAGISA-GILVFIILLVVIIVVKSK-----LAKRKKDAMGNTRQ 792  
Db 789 SEEWGLILGICAGGLAVLILLGAIIVIRKGRDHVAYSYPKPVNMTK----ATVNRQ 844  
Qy 793 EMTHMVNMDRSYADQSTLHAEDPLSLTFMDQHNFSPLPNDPLVPTAVLDENHSATAES 852  
Db 845 EKTHMSAVDRSFTDQSTLQEDERLGLSFMDTGYSTR-----GDQRSGGVTEA 893  
Qy 853 SRL--DVPRVLCBGTSPYOTGOLHPAIRVADILLOHINLMKTSDSYGFKEEYESFFRGQS 911  
Db 894 SSLGSGSPRRPCRGKSPYHTGQLHPAVRVADLLQHINQMKTAGYGFKEYESFFRG-- 951  
Qy 912 ASWDVAKKQONRAKNRYGNIAYDHSRVILQPVDEDDPSSDIYINANYIDILYLRDGYORPS 971  
Db 952 --NDATKKDKVKSGRQEPMPAYDRHRVKLHPMLGDPNADYINANYIDIRINREGYHSN 1009  
Qy 972 HYIATQGPVHETVYDFWRMWVQSQSACIVMTNLVEVGRVKCYKWPDDTEVYGDPKVC 1031  
Db 1010 HFATQGPKEVYDFWRMWVQHECSSIVMITKLVEVGRVKCSRYWPDESDTYGDIKML 1069  
Qy 1032 VEMEPLAEYVVRFTLERRGYNEIREVKOFHFGWPDHGVYPYHATGLLSRIRVKLSNPP 1091  
Db 1070 VKTETLAAYVVRTPALERRGYRSARHEVRQPHFTAWPEHGVYPYHATGLLAFIRRVKASTPP 1129  
Qy 1092 SAGPIVHCSAGAGRTGCIYIVIMLDMABREGVVDIYNCVKALRSRRINNVOETEEQVIF 1151  
Db 1130 DAGPIVHCSAGTRGTCYIVLDMLDMAECGVDIYNCVKLCSRVNMVQTEEQVIF 1189  
Qy 1152 IHDAILEACLCGETAIPVCEKAAAYFDMIRIDSQTNSSHLKDFQTLNSVTPRLQABDCS 1211  
Db 1190 IHDAILEACLCGETTIPVSEFKATYKEMIRIDPQSNSSQLREEFQTLNSVTPPLDVECS 1249  
Qy 1212 IACLPRNHDKRPMMLPPDRCLPPLITIDGESSNYINAALMDSYRQPAAFIVTQYPLN 1271  
Db 1250 IALLPRNRDKRSMVLPDRCLPFLISTDGSNNYINAALTDSYTSRAAFIVTLHPLOS 1309  
Qy 1272 TVKDFWRLVVDYDCTSIWMLENEVDLSQ---CPQYWPBEGMLRYGPTQVCMSCMDCV 1328  
Db 1310 TTPDFWRLVVDYDCTSIWMNLQNSAWPCLQYWPBEGMLRYGPTQVCMSCMDCV 1369  
Qy 1329 INRIFRINLTRPQEGYLMVQOFOYLCWASHREVPKRSFLKILQVEKWOBCBEGRTIIHCLNGGGRS 1388  
Db 1370 VARVFRVQNTISRLQEGHLLVRHQFLRWSAYRTPDSRKAFHLHLAEDVKWQ--AESGDG 1427  
Qy 1389 RTIHCINGGGRSGMFCAGIIVVMKRONQVVDVFAVKTLRNSKPNMVEAPEQRYFCYD 1448  
Db 1428 RTIHCINGGGRSGTFCACATVLEMIRCHNLVDVFFAAKTLRNYKPNMVTMDQYHFCYD 1487  
Qy 1449 VALEYLE 1455  
Db 1488 VALEYLE 1494



; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST  
; FILE REFERENCE: MRI-039  
; CURRENT APPLICATION NUMBER: US/10/176.847  
; CURRENT FILING DATE: 2002-06-21  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 1463  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-176-847-22

Query Match 58.2%; Score 4542.5; DB 14; Length 1463;  
Best Local Similarity 56.7%; Pred. No. 0;  
Matches 843; Conservative 242; Mismatches 341; Indels 61; Gaps 11;  
3 VAAALPAFVALWLLYLPWLLGSLGQPSAGGCTFDGPGACDHYQDL-YDDREWHVSA 61  
4 LAALALLLRLQL-----PPLPGARASAPGCGCFDEHNSCGYSVALGTNGFTWEQINT 59  
62 QEPHYLPPEPQGSVMVVDSSNHDPEGEKARLQLPTMKENDTHCIDFSYLLYSQKGLNPGT 121  
60 TEKPMLOQAVPTGSGFMVNVSSGRASGQKAHLLPLTLEKENDTHCIDFHYFSSRRDRSPGA 119  
122 LNILVRVKNGLANPINWVTGTRDMLRAELAVSTFWPNEYQVIFEAESVGGSGGYIAI 181  
120 LNVYKVGNGPQGNPNVNVSVVTEGWVKAELAISTFWPHFYQVIFESVSLKHPGYIAV 179  
182 DDLOVLSYPCDKSPHFLRGDVEVNAONATFOCIATGRDAVHNKMLQRNGEDI PVAQ 241  
180 DEVRVLAHPCKRPHFLRLQNVNVGNQATFOCIAGGKWSQHDKWLQOQWNGRDTALMV 239  
242 TKINHRFRFAASFLRLQVKTQDLYRCVTSQSERGSGVSNFAQLIVREPPRPIAPPOLLG 301  
240 TRVNHRRFATVSADTAQRSVSKYKVCVIRSDGSGSVNVAELIVKEPTPIAPPELLA 299  
302 VGPTYLILQIANSIIGDGPILKEVEYRTSGSWTETHAVNAPYTKLMLDPTDEYAIR 361  
300 VGATYLWIKFNANSIIGDGPILKEVEYRTTGTWAEITHVDSBNYKMLDPTDEYAIR 359  
362 VLLTRPGEGETGLPGPLITRTKCAEPMPRTKILKIAEIOARRTAVDWESLGNITRCHT 421  
360 VLLTRPGEGETGPGAPLITRTKCAEPVQNVNVEIVDIRAQTLQWEPFPGVAVTRCHS 419  
422 FNTVICHYFRGHNESRADCLMDPKAPQVWVHLPYTNVLSKMLITNPEGRKESEETI 481  
420 YNLTVQYQV--FNQOQYEAEEVLOTSSHTLRLGRPFMTIRLLLSNPEGRMESELV 477  
482 IQTDEDVPGVPVKSLQGSTFENKIFLNWKEPLEPNGIITQYEVSYSSIRSFDPAVPVAG 541  
478 VQTEEDVPGAVPLESIQGGPFEEKIYQWKPNETNGVITLYEINYKAVGSLDPSADLSS 537  
542 PPQTVSNLWNSHTHVFMHLHPGTYQYFIRASTVKGFGPDATAINTVNTNISAPSLPDYEGV 601  
538 QRGKVFPLRNETHHLFVGLYPTGTYSTTIKASTAKGFGPPVTTRIAIKISAPSMPEYD-T 596  
602 DASLNATATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKBRAGAMECYQVPPVYONAL 661  
597 DPLNETDTTITVMLKPAQGRGAPSVYQIVVKEERLOKRRRAADIIECFSPVPSYRNAS 656  
662 SGGAPYYFAAELPGLNLPAPFTVGNRTYKGFWNPPLAPRKGYNIYFOAMSSVEKETK 721  
657 SLDSLHYFAAELKPNALPVQPTVGNKTYNGWNPPLPSLKSYSIYFOALSXANGETK 716  
722 TQCVRIATKA-----AATEPEVIPPQAKOTDRVVKIAGISAGILV 762  
717 INCVRLATKAPMGSAQVTPGTPLCLLTAGASTQNSNTV-EPEKQVDNTVMKAGVIAGLLM 775  
763 FILLILLVIVIVKK-----SKLAKKEDANGTRQEMTHVNMABRSYADOS 809  
776 FIILLGMLTIKRRRNAYSYSYVLSQKRLAKKQKQTSQGAQREMGMPVSA-DKPTTKLS 834

Qy 810 TLHABDPLSLTFMDQHNFSRPLPNDPLVPTFAVLDENHSATAESSRLLDVPRYLCEGTESP 869  
Db 835 ASRNDGCFSSSQDVNGFTDGSRGELSOPLTI-QTH-----PYRTCDPVEMS 881  
Qy 870 YQTQLHPAJRVADLLQHINLMKTSDSYGPKKEEYEFEGOSASWDVAKKDONAKRYG 929  
Db 882 YPRDQFOLAJRVADLLQHITQMKGGQYGFKEEYEALEPEGQTASWDKADENRNKRYG 941  
Qy 930 NIAYDHSRVILQPVEDDPSDIYANANYIDWLRYDGYQRPESHYIATQGPVHETVYDFWR 989  
Db 942 NIISYDHSRVLLVLVDGDPHSDIYANANYI-----DCYHRPRHYIATQGPMEQTVKDFWR 995  
Qy 990 MVWQESACIWMVNTLVNVEGRVKCYKYPDDETVYGFKTCVEMPELAEVWTFPLER 1049  
Db 996 MIWQENSASIVMVTNLNVEGRVKCYRYWPDDETVYGDIKVTLIETPELAEYVIRFTVQK 1055  
Qy 1050 RGYNEIRVEKQFTGMPDHGVPYHATGLLSFTIRRVKLSNPPSPAGPIVWVHCSAGARTGC 1109  
Db 1056 KGHEIRRELRLHFTSWPDHGVPCYATGLLGFVQVFLAPPEAGPIVWVHCSAGARTGC 1115  
Qy 1110 YIVIDMLDMAEREGVVDIYNCVKALRSRRINMVQTEEQYIFIHDAILEACLCGETAIPV 1169  
Db 1116 FIALDTMLDMAENEGVVDIFNCVRELRQAQVNLVQTEEQYVFDALILEACLCGNTAIPV 1175  
Qy 1170 CEFKAAFYDMIRIDSQNTSSHLKDEFTQTLNSVTPLQAECDSCIACLRPNHDKNRFMDMLP 1229  
Db 1176 CEFRLSYNISRDPQNTSSQIKDEFTQTLNIVTPRVPEDCSIGLLPRNHDKNRSMVDLP 1235  
Qy 1230 PDRCLPLIITIDGESSNYINAAWMDSYROPAAFTVTOYPLPNTVKDFWLVYDYGCTSIIV 1289  
Db 1236 LDRCLPLISVDGESSNYINAAWMDSHKQPAFVVTVOHPLENTVADFWLVDFVNCSSV 1295  
Qy 1290 MLNEVDLSQCCPOVWPEEGMLRYGPIQVECMSCMCDVINRIFRICNLRPQSGYLMVQ 1349  
Db 1296 MLNEMDTAQFCMQWPEKTSCTGCGPIQVEFVSADIDEDIHFRICNLMARPODGYRIVQ 1355  
Qy 1350 QFQYLVGASHREVPVSGKRSFLKILQVKEQWCEBCEGERTIHLCLNGGSGRMFCFCAIGI 1409  
Db 1356 HLQYIGWPAYRDTPPSKRSLLKVVRLKQWQEQYDQREGRTVVHCLNGGSGRTFCAICS 1415  
Qy 1410 VVEMVKRQNVVDVFAVKTLLRNKSPKNVPEAPEQYRCFYDVALEVLVS 1456  
Db 1416 VCEMIQQNIIDVFHIVKTLRNKSNMNETLEQYKFFVYVALEYLSS 1462

RESULT 10  
US-10-205-823-343  
; Sequence 343, Application US/10205823  
; Publication No. US20030108963A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Gannavarapu, Manjula  
; APPLICANT: Gorbacheva, Bella  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Wonsay, Angela M.  
; APPLICANT: Glatz, Karen  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Anderson, Dustin  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; THERAPY OF PROSTATE CANCER  
; FILE REFERENCE: MRI-044  
; CURRENT APPLICATION NUMBER: US/10/205,823  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 60/307,982  
; PRIOR FILING DATE: 2001-07-25  
; PRIOR APPLICATION NUMBER: 60/314,356  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/325,020  
; PRIOR FILING DATE: 2001-09-25



QY 34 GCTFDDGPG---ACDYHODLYDDPEWVHVSAQEBHYLPPPEMPOGSMYVVDSSNHDGPEKA 90  
 Db 33 GCTFEEDGPAVPCFYSQAQYDDQFMDPGS-----PADLPFGSYLWNTVSHPAQORA 85  
 QY 91 RLQLPWTWKENDTHCIDFSYLLYSOKGLNPGTFLNLRVNGKPLANPTWVVTGFTGRDMLR 150  
 Db 86 HVIFQSLSENTHCVQFYSFLYSRDGHSPGTLGVYVAVNGPGLGSAVWNTVGHSGROWHQ 145  
 QY 151 AELAVSTFWPNEYQVIFPEAEVSGRSGYIAIDDIQVLSYPCDKSPHFLRLGDEVEVNAQON 210  
 Db 146 AELAVSTFWPNEYQVIFPEALISPDRCYMGMLDDICILSYPCAKAPHSRLGDEVEVNAQON 205  
 QY 211 ATQCTATGDAVHINKLWLRORNGEDIPVAQTKNINHRRAFAASFRLOQSVTKTDQDLYRCV 270  
 Db 206 ASFOCWAAGR-ABAEERFLLQORSGALVPAAGVRHSHRSFLATFPFLAAVSRABQDLYRCV 264  
 QY 271 TQSERSGVS-NEAQLIVRPPRPAPQOLLGVGPTVLLQLNANSIIGDGPILKEVEY 329  
 Db 265 SQAPRGGTSINFAEFVWKEPPTPIAPPQLLRAGPTVLLIQLNANSIIGDGPVIRKEIEY 324  
 QY 330 RMTSGSWTETHAVNAPTYKLWHLDPDTEYEIRVLLTRPGEGGTGLPGPPLITRTKCAEPM 389  
 Db 325 RMARGPMAEVAHVSQTYKLWHLDPDTEYBISVLLTRPGDGTGRLGPGPFISRTKCAEPM 384  
 QY 390 RTPKTLKIAIOARRIADVHESLGYNITRCHTNVTICHYFRG--HN-----ESRAD 440  
 Db 385 RAPKGLAFABIOARQLTLOWERGLGYNVTCHTYTVSLCYHYTLGSSHNQITPRVCEDDR 444  
 QY 441 CLDMDPKAPOHVNVNHLPPYTNVSLKMLTNPBGRKESEETIOTDDEVPGPVVKSLQGT 500  
 Db 445 CQPLHHEEPAAL-----SERREVVLTNPBGRKEKEVTFQDEDDVPSGIAESLTFT 497  
 QY 501 SPENKIPLNWKLEPLENGIITQYEVSYSSIRSDPAPVAGPPQTQVSNLNSHTHVFPHL 560  
 Db 498 PLSDMIFLWKEEPQEPENGLITOYEISYQSISSDPAVNVQA-TSTISKLRNETVHVFSNL 556  
 QY 561 HPGTTVQFFIRASTVKGFGPATAINVTNINSAFSLPDYEGVDASLNETAITITVLLRPAQ 620  
 Db 557 HPGTTVLFSGARTGKGFGQAALTEITTYISAFSL-DYADMPSPGSENNITVLLRPAQ 615  
 QY 621 AKGAPISAYQIVVEOLH-PHRTKREAGAMECYQVPTVYQNALSGGAPYFAAELPCGNLP 679  
 Db 616 GRAPISVQVIVVEEGSRRLRKREPGQCFVPLTFEALARGLVVDYFGAELASSLP 675  
 QY 680 EPAPFTVGDNRITYKGFNPPLEPRKGNINYFOAMSSVVEKETKTCQVRIATKAATBEPEV 739  
 Db 676 EAMPFTVGDNKTGYGFNPPLEPRKALYIFYQAASHLKGTRLCNIRIARKAACKESKP 735  
 QY 740 IPDPKQTRVVKIAGISA-GILVFIILLVIVIVKSK-----LAKRKD 785  
 Db 736 L-EVSQRSEEMGLITGICAGGLAVLILLGALIIIRKGRDHVAYSYYKPVNMTK---- 790  
 QY 786 AMGNTRQEMTHVNMADRSYADOSTLHAEDPLSLTMDQHNFSRPLNDPLVPTAVLDEN 845  
 Db 791 ATVNYRQEKTHMSAVDRSFTDQSTL---QPPGLSPMDTHGYSTR-----GEQ 835  
 QY 846 HS---ATAESSRLDVPRLYCEGTESPYQTQLHPAIRVADLLOHINLMKTSDSYGFKEEY 903  
 Db 836 RSGGVTEASSLLGSPRPGKRGSPHYTQLHPAVERVADLLOHINOMKTAEGYGFQKEY 895  
 QY 904 ESFFEGOSAWDAKQONRAKRYGNIYADHSRVLQVDEDDPSSDYINANYIDILWY 963  
 Db 896 ESFFEG----WDATKKDKVKGRQEPMPAYDRHRVKLHPMLGDPNADYNANYI----- 946  
 QY 964 RDGVORSHVIATQGVHETVYDFWVMVQEQSACIIVMTNLVEVGRVKCYKWPDPTEV 1023  
 Db 947 -DGHRSNHPFIATQGPKEPVYDFWVMVQEQHSSIVMTKLVEVAGCKSRYWPEDSDT 1005  
 QY 1024 YGDFKVTCEWELAEVYVVTFTLRRGYNEIREVKQFHFTGWPDHGVPYHATGLLSFIR 1083  
 Db 1006 YGDIKIMLVKTEILAEVYVVTFTFALERKYSARVEVRFHTANPEHGVPHYHTGLLAFIR 1065  
 QY 1084 RVKLSNPPSAGPIVHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNVCVKALRSRRINMV 1143

Db 1066 RVKASTPPDAGPIVHCSAGTGTGCVYVLDVMDMAECGVVDIYNVCVTKLSCRCVNMI 1125  
 QY 1144 QTEBQYIFHDALEACLGETAIPVCEPKAAAFDMIRIDSQTNSSHLKDEFOFOTLNSVTP 1203  
 Db 1126 QTEBQYIFHDALEACLGETTIPVSEFKATYKEMIRIDPQSNSSQURREFQTLNSVTP 1185  
 QY 1204 RLQAECSIACLPRNHDKNRPFMDLPPDRCLPLITIDGESSNYINAALMDSYRQPAFI 1263  
 Db 1186 PLDVEYSIALLPRNDRKNRMDVLPDRCLPELISITDGSNNYINAALTDVYTRSAFI 1245  
 QY 1264 VTOYPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQG---CPOYWPBEGMLRYGPIQVECM 1320  
 Db 1246 VTLLHQSTTPDPRWRLVYDYGCTSIYMLNOLNOSNAWPCLOQYWPBEGROOYGLMEVEFM 1305  
 QY 1321 SCMDCCDVINRIFRINLTPRQEQGLVMVOQFYLGHASHREVPSCRSFKLKLILQVEKWQ 1380  
 Db 1306 SGTADEDLVARVFRVQNISRLQESHLVHRHFQFLRWSAYRDTDPSEKAFLLHLLAEVDKQW 1365  
 QY 1381 ECEBEGERTIHLCLNGGRRSGMFCAGIGIVEMVKQNVVDVFAVKTLRNSKPNMVYAP 1440  
 Db 1366 --AESGDGRTIVHCLNGGRRGTSCALRTVLEMIRCHNLVDVSAFATLRNYPKNMVETM 1423  
 QY 1441 EOYRFCDYVALEYLES 1456  
 Db 1424 DQYHFCYDVALEYLEA 1439  
 RESULT 12  
 US-10-087-993-34  
 ; Sequence 34, Application US/10087993  
 ; Publication No. US20020169303A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ullrich, Axel  
 ; Aoki, Naohito  
 ; Kim, Yeong Woong  
 ; Wang, Hong Yang  
 ; Chen, Zhengjun  
 ; Naylor, Oliver  
 ; Kharitonov, Alexei Igorevich  
 ; TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDPI, CLK,  
 ; AND SIRP POLYPEPTIDES AND RELATED  
 ; PRODUCTS AND METHODS  
 ; NUMBER OF SEQUENCES: 38  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSeq for Windows 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/087,993  
 ; FILING DATE: 05-Mar-2002  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/877,150  
 ; FILING DATE: June 17, 1997  
 ; APPLICATION NUMBER: U.S. 60/019,629  
 ; FILING DATE: June 17, 1996  
 ; APPLICATION NUMBER: U.S. 60/023,485  
 ; FILING DATE: August 9, 1996  
 ; APPLICATION NUMBER: U.S. 60/030,860  
 ; FILING DATE: No. US20020169303A1, December 13, 1996  
 ; APPLICATION NUMBER: U.S. 60/034,286  
 ; FILING DATE: December 19, 1996

```
; APPLICATION NUMBER: U.S. 60/030,964
; FILING DATE: No. US20020169303A1ember 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 225/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1430 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-087-993-34

Query Match 55.4%; Score 4325; DB 13; Length 1430;
Beat Local Similarity 58.1%; Pred. No. 1.9e-313;
Matches 839; Conservative 197; Mismatches 345; Indels 64; Gaps 22;

QY 32 AGGCTFD--DGPACDYHQDLYDDFEWVHYSAQEPHYLPPPEMPOGSMYVVDSSNHDPE 88
Db 24 AAGCTFEASDPAVCEYSQAQYDDFQWEQVRIHFGTRAPADLPHGSLMWNTISOHPGQ 83
QY 89 KARLQLPKENDTHCIDPFSYLLYSQKGLNPOTNLILRVNKGPIPLANPINVVTGTGRDW 148
Db 84 RAHVIFQSLSENDTHCVQFSYFLYSRDTG-GTLRVYRVNGGPIASAVNMTGSHGRQW 142
QY 149 LRAELAVSTFWPNEVQVTFEAEVSGRSGYTAIDDIQVLSYPCDKSPHFLRLGDVEVNAG 208
Db 143 HQAELAVSTFWPNEVQVTFEALISDPRRGYMLDILLISYPCAKAPHSRLGDVEVNAG 202
QY 209 ONATFQCTATGRDAVHNKMLQRRNGEDI PVAQTNKINHRPAASFRLOEYTKTDOLYR 268
Db 203 QNASFQCMWAG-EPMRQRFLLQKQSGALVP-AGAFGTATGFLATPPLAAVSRAEQDLYR 260
QY 269 CVTQSGRSGVSNFAQLIVREPRIAPPQLLGVTGPTLLIQLNANSIIGDGPILLKEVE 328
Db 261 CVSQAPRG-GVSNFPELVKEPTPIAPPQLLRAGPTVLIQLNTNSIIGDGPVIRKEIE 319
QY 329 YNMTSGSWTETHAVNAPYKLMHLPDTEYETIRVLLTRPGEQGTG---LPGPLITRYKC 385
Db 320 YRMARGPMAEVAHVSLQTYKLMHLPDTEYETIRVLLTRPGEQGTGRWATPHQ----- 372
QY 386 AEPMET---PKTLAETQARRIADVWESLGYNTLRCHTFNVTICYHYFERG--HNESRA 439
Db 373 -HQMRRAHEGPKGLAFAEIQARQLTQWEPLGYNVTRCHTYVSLCYHTYLGSSHNQIR 431
QY 440 DCLDMDPKAPQHVNVHLPPYTNVSLKMLITNPEGRKSEBETIIQTDDEVPGPVPVKSLOG 499
Db 432 ECVKTEQGVSRVYTIKNLLPYRVNVHVLVTNPEGRKEGKEVTFQTDDEVPSGIAAESLTF 491
QY 500 TSFENKIFLNWKEPELPNGIITQYEVSYSSIRSPDPAPVAGPDPQTVSNLMNSTHVFVHM 559
Db 492 TPLEDMIFLWKEPEPBNGLITQYETISQSISSDPANVPVPRRTISKLRNETHYVFSN 551
QY 560 LHPGTYQFFIRASTVKGGPATAVNTNINISAPSLPDYEGVDASINETATITVLLRPA 619
Db 552 LHPGTYLFSVARTKGGFGQAALTEITTNISAPSF-DYADMPSPLGESNTITVLLRPA 610
QY 620 QAKGAPISQYQVWEQLPHRTRKBRAGAMECYQVPVTVQNALSQGA----PYFFAAELPP 675
Db 611 QCRGAPISYQVIVEE---ERAGCGGTWTGLLPSAID--LRGGAGPRLVHYFGELAA 665
QY 676 GNLPEAPPTVGNRTYKGFVNPPPLAPRGYNYIFQAMSSVEKETKTQCVRIATKAATE 735
Db 666 SSLPEAMPPTVGDNTQYRFGWNPPLPRKAYLITVYQAASHLKGELRLNCIRIARKAACK 725
QY 736 EPEVIPDPKQTDVRVVKIAGISA-GILVFILLVVIVIVKSKLAKKKDKAMGNTRQEM 794
```

```
Db 726 SKRPL-EVSQRSEMGILIGICAGGLAVLILLGAIIVIRKGPVNMTK-ATVNYRQEK 783
QY 795 THMVNANDRSYADOSTLHAEDPLSLTMDQHNFSRPLPNDPLVTAVDENHSATAESSR 854
Db 784 THMISAVDRSFTDQSLQEDERLGLSPMDTHGYSTR-----GDQRSGGVTEASS 832
QY 855 LL-DVPRYLCEGTSPYQTGOLHPAIRVADLLOHINLMKTSDSYGFEKEEYSEFPFGQAS 913
Db 833 LLGSPRRPCRGKSPYHTGOLHPAIRVADLLOHINLMKTAEGYGFQKEYSFPFEG---- 888
QY 914 WDVAKDQNRKAKRYGNIIAVDHSRVILQPVEDDPSDDYINANYIDWLXYDGYQRPESHY 973
Db 889 WDATKKDKVKGSFQEPMPAYDRHVKLHPMLGDPNADYINANYI-----DGYHRSNHF 942
QY 974 IATQGPVHETVYDFWRMVWQESACIWMVNLVEVGRVKCYKYPDDTDEVYDGFVTCVE 1033
Db 943 IATQGPKEVYDFWRMVWQEHCSIVMITKLVVGRVKCSRYWPEDSDTYGDIKIMLVK 1002
QY 1034 MEPLAEVVRFTLERRGYNEIREVKQPHFTGWDHGVVPVYHATGLLSFIRVKLSNPSPA 1093
Db 1003 TETLAEVVRFTLERRGYNEIREVKQPHFTGWDHGVVPVYHATGLLSFIRVKLSNPSPA 1062
QY 1094 GPIVHCSAGAGRTGCVIVIDIMLDMAREBGVVDIYNCVKALRSRRINMVQTEBQYIFIH 1153
Db 1063 GPIVHCSAGAGRTGCVIVIDIMLDMAREBGVVDIYNCVKALRSRRINMVQTEBQYIFIH 1122
QY 1154 DAILEACLCGETATPVCCEKAAAYFDMIRIDSQTNSSHLKDBFQTLNSVTPRLQAECSIA 1213
Db 1123 DAILEACLCGETTIPVSEFKATYKEMIRIDPQSNSSQLRSEFQTLNSVTPPLDVECSIA 1182
QY 1214 CLPNHDKNRFMDMLPDRCLPFLITIDGESSYINAAALMDSYRQPAFIVTQYPLPNTV 1273
Db 1183 LLPNRDNKNSMDVLPDRCLPFLITIDGESSYINAAALMDSYRQPAFIVTQYPLPNTV 1242
QY 1274 KDFWRLVYDGYCTSIVMNLNEVDLSQG---CPQYWPEEGMLRYGPTQVECMSCSDCDVIN 1330
Db 1243 PDFWRLVYDGYCTSIVMNLNQLNQSNAWPCLOYPFQGRQYGLMEVEFMSTADEDLVA 1302
QY 1331 RIFRICMLTRPQEGYLMVQOYQYLGWASHREVPGSKSFLKLILOVEKQWECBEGERT 1390
Db 1303 RVFRVQNISRLQEGDLLVRHFQFLRWASAYRDTDPDSKKAFLLAEVDKWKQ--AESGDGRT 1360
QY 1391 ITHCLNGGSRGSMFCATGIWVWVKRONVDVPHAVKTLRNSKNMVEAPEQYRCYDVA 1450
Db 1361 IVHCLNGGSRGSGTFCACATVLEMIRCHNLVDVFFAAQTLRNYKPNMVMETMQYHFCYDVA 1420
QY 1451 LEYLE 1455
Db 1421 LEYLE 1425

RESULT 13
US-10-296-115-1190
; Sequence 1190, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1190
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1190
```

Query Match	31.6%;	Score 2471.5;	DB 15;	Length 623;
Best Local Similarity	72.3%;	Pred. No. 1.7e-175;		
Matches 451;	Conservative 74;	Mismatches 86;	Indels 13;	Gaps 3;
Qy	834	DPLVPTAVLDENHGHATAESRLRLDVPY-LCEGTESPQTGLHPAIRVADLLQHINLMK	892	
Db	11	DPRVRT-----HTWASDTSLSVQSHYTKREPADVPYQTGLHPAIRVADLLQHITQMK	64	
Qy	893	TSDSYGFKBEYESPFEGQSASWDVAKKDONRKNRYGNIIAYDHSRVILOPVEDDPSSDY	952	
Db	65	CAEGYGKFEYESPFEGQSAPWDSAKKXENRKNRYGNIIAYDHSRVLQTEIGDTNSDY	124	
Qy	953	INANYIDILWLDYQYQSPSHYIATQGPVHETVDFWRVWQEQAGACIVMTNLVEVGRVK	1012	
Db	125	INGNYI-----DGYHRPNHYIATQGPWQETIYDFWRVWVHENTASTIIMTNLVEVGRVK	178	
Qy	1013	CYKWPDPDTVEYGDVKTCVEMEPLAEVVRVTFTLERRGYNEIREVKQPHFTGPHDGV	1072	
Db	179	CKYWPDPDTTEIYKDIKVTLETLLAEVIRTFAVEKRGVHREIRIQPHFTGPHDGV	238	
Qy	1073	YHATGLLSFTRRVKLSNPPSAGPIVWHCSAGAGRTGCVIVIDIMDMAEREGVVDIYNCV	1132	
Db	239	YHATGLLGFVRVKSKSPSAGPIVWHCSAGAGRTGCFIVIDIMDMAEREGVVDIYNCV	298	
Qy	1133	KALSRRRINMVQTEBQYIFTHDAILEACLCGETAIPVCEPKAAFYDMIRIDSQTNSSHLK	1192	
Db	299	RELRSRRVNMVQTEBQYVFTHDAILEACLCGDTSPASQVRSLYDMNKLDPQTNSSQIK	358	
Qy	1193	DEFOTLNSVTPRLOAEDCSIACLPRNHDKNRFMDMLPPDRCLPLIITIDGESSNYNAAL	1252	
Db	359	EEFRTLNMVTPTLRVEDCSIALPRNHEKNRCMDILPPDRCLPLIITIDGESSNYNAAL	418	
Qy	1253	MDSYRQPAAFVTOYPLPNTVKDPRWLAVDYDGCTSIYMLNEVDLSQCPQYWEEGMLRY	1312	
Db	419	MDSYQSPSAFVTOHPLPNTVKDPRWLVLVDYHCTSVVMLNDVDPAQJLCPQYWPENGVRH	478	
Qy	1313	GPIQVECMSCMDCDVINRIFRICNLTRPOEGLMWQOFOYLGWASHREVPGKRSFLK	1372	
Db	479	GPIQVEFVSADLEEDIISRFIRIYNAARPQDGVRMWQOFOELGHPMYRDTFVSKRSFLK	538	
Qy	1373	ILQVEKQWEECEBGEGETIICHLCNGGRRSGMFCAGIGVEMVKRQNVVDVVFHAVKTLRNS	1432	
Db	539	IRQVDKQWEEVNGGEGRTVVHCLNGGRRSGTFFCAISIVCEMLRHQRTVDVVFHAVKTLRNN	598	
Qy	1433	KPNVWEAPEQVRFCYDVALEYLES	1456	
Db	599	KPNMVDLLDQYKFCYEVALEYLNS	622	

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RESULT 14
US-10-296-115-1390
; Sequence 1390, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1390
; LENGTH: 815
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1390

```

Query Match	28.4%	Score	2216;	DB 15;	Length	815;	
Best Local Similarity	54.0%	Pred. No.	3.1e-156;				
Matches	409;	Conservative	126;	Mismatches	216;	Indels	6;
						Gaps	4;

[illegible]

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RESULT 15
US-9-808-602-54
: Sequence 54, Application US/098086020
: Patent No. US20020155115A1
: GENERAL INFORMATION:
: APPLICANT: Vernet, Corine A
: APPLICANT: Fernandes, Elma
: APPLICANT: Shlnkets, Richard A
: APPLICANT: Herрман, John L
: APPLICANT: Majumder, Kumud
: APPLICANT: Mishra, Vishnu
: APPLICANT: Mezes, Peter S
: APPLICANT: MacDougall, John
: TITLE OF INVENTION: No. US20020155115
: FILE REFERENCE: 15966-697 CIP
: CURRENT APPLICATION NUMBER: US/09/8
: CURRENT FILING DATE: 2001-03-14
: PRIOR APPLICATION NUMBER: 09/800,19
: PRIOR FILING DATE: 2001-03-05

```

```

1  APPLICANT: MACDOUGALL, JOHN
2  TITLE OF INVENTION: No. US20020155115a1el Proteins and Nucleic Acids Encoding Same
3  FILE REFERENCE: 15966-697 CIP
4  CURRENT APPLICATION NUMBER: US/09/808,602
5  CURRENT FILING DATE: 2001-03-14
6  PRIOR APPLICATION NUMBER: 09/800,198
7  PRIOR FILING DATE: 2001-03-05

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:40:58 ; Search time 38.7393 Seconds  
(without alignments)  
3618.750 Million cell updates/sec

Title: US-09-887-669-1  
Perfect score: 7809  
Sequence: 1 MDVAAALPAFVALWLLYPW.....EAPQYRFCYDVALEYLESS 1457

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7809	100.0	1457	1 A48066	protein-tyrosine-p
2	7506.5	96.1	1440	2 JC6312	protein-tyrosine-p
3	4812.5	61.6	1452	1 S17669	protein-tyrosine-p
4	4793.5	61.4	1452	1 S17670	protein-tyrosine-p
5	4619	59.1	1436	2 JC5290	protein-tyrosine-p
6	4359	55.8	1442	2 S72441	protein-tyrosine-p
7	1516.5	19.4	1501	2 I58148	protein-tyrosine-p
8	1495	19.1	1499	2 I50212	protein-tyrosine-p
9	1494	19.1	1898	2 S46216	leukocyte antigen-
10	1492.5	19.1	1897	1 TDHULK	leukocyte antigen-
11	1482.5	19.0	1912	2 A56178	protein-tyrosine-p
12	1475.5	18.9	1496	1 A48758	protein-tyrosine-p
13	1453.5	18.6	1863	2 S46217	protein-tyrosine-p
14	1452.5	18.6	1691	1 D54689	protein-tyrosine-p
15	1452.5	18.6	1894	2 C54689	protein-tyrosine-p
16	1452	18.6	1290	2 A56493	leukocyte common a
17	1440.5	18.4	1907	2 S50893	protein-tyrosine-p
18	1438	18.4	2029	1 TDFLTK	protein-tyrosine-p
19	1415.5	18.1	1231	2 S53088	protein-tyrosine-p
20	1345.5	17.2	1437	2 T31093	probable protein-t
21	1337	17.1	1585	2 T19121	probable protein-t
22	1311.5	16.8	2051	2 T30938	receptor tyrosine
23	1240	15.9	582	2 A57068	protein-tyrosine-p
24	1175.5	15.1	796	1 JC1285	protein-tyrosine-p
25	1155	14.8	802	1 A36065	protein-tyrosine-p
26	1145	14.7	832	2 JC8051	protein-tyrosine-p
27	1142	14.6	699	2 JC6332	protein-tyrosine-p
28	1136.5	14.6	829	1 A47373	protein-tyrosine-p
29	1127.5	14.4	700	1 S12053	protein-tyrosine-p

30	1094	14.0	1262	1 B48758	protein-tyrosine-p
31	1057.5	13.5	680	2 JC8052	protein-tyrosine-p
32	1019	13.0	2314	1 A46151	protein-tyrosine-p
33	1009	12.9	1442	1 B48148	protein-tyrosine-p
34	987	12.6	1445	1 A48148	protein-tyrosine-p
35	970	12.4	1422	2 T42636	protein-tyrosine-p
36	946.5	12.1	1301	1 A41822	protein-tyrosine-p
37	931	11.9	1462	1 B36182	protein-tyrosine-p
38	929	11.9	1273	1 TDRTLT	leukocyte common a
39	928.5	11.9	1291	1 A28334	leukocyte common a
40	928	11.9	1304	1 A46546	leukocyte common a
41	908.5	11.6	1200	2 T43148	probable protein-t
42	877	11.2	1409	2 T42522	protein-tyrosine-p
43	870	11.1	1237	2 A54080	hypothetical prote
44	860.5	11.0	1422	2 T30111	probable protein-t
45	767	9.8	711	2 T23738	probable protein-t

ALIGNMENTS

RESULT 1

A48066

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type kappa precursor - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 21-Jan-1994 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
C/Accession: A48066  
R/Jiang, Y.P.; Wang, H.; D'Eustachio, P.; Musacchio, J.M.; Schleisinger, J.; Sap, J.  
Mol. Cell. Biol. 13, 2942-2951, 1993  
A/Title: Cloning and characterization of R-PTP-kappa, a new member of the receptor prote

ion.  
A/Reference number: A48066; MUID: 93233655; PMID: 8474452

A/Accession: A48066

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-1457 <JIA>

A/Cross-references: UNIPROT:P35822; GB:L10106; NID:G2933771; PIDN:AAA40021.1; PID:G293772

A/Experimental source: brain

A/Note: sequence extracted from NCBI backbone (NCBIP:129880)

C/Complex: after cleavage by a furin-like endopeptidase, the two chains remain associated.  
C/Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe

-tyrosine-phosphatase homology

C/Keywords: Glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tran

F/1-28/Domain: signal sequence #status predicted <SIG>

F/29-1457/Product: protein-tyrosine-phosphatase, receptor type kappa, uncleaved #status

F/29-641-644-755/Domain: extracellular #status predicted <EXT>

F/30-133/Domain: MAM homology <MAM>

F/208-271/Domain: immunoglobulin homology <IMM>

F/293-371/Domain: fibronectin type III repeat homology <FN3A>

F/388-477/Domain: fibronectin type III repeat homology <FN3B>

F/489-581/Domain: fibronectin type III repeat homology <FN3C>

F/593-682/Domain: fibronectin type III repeat homology <FN3D>

F/644-1457/Product: protein-tyrosine-phosphatase, receptor type kappa, chain 2 #status p

F/756-772/Domain: transmembrane #status predicted <TMN>

F/773-1457/Domain: intracellular #status predicted <INT>

F/841-1457/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F/922-1148/Domain: protein-tyrosine-phosphatase homology <PTP1>

F/1218-1442/Domain: protein-tyrosine-phosphatase homology <PTP2>

F/100,139,210,415,423,435,461,551,585,589,606,689/Binding site: carbohydrate (Asn) (cova

F/215-269/Diulfide bonds: #status predicted

F/643-644/Cleavage site: Arg-Glu (furin-like endopeptidase) #status experimental

F/1100/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1106/Binding site: substrate phosphate (Arg) #status predicted

F/1394/Active site: Cys (phosphocysteine intermediate) #status predicted

F/1400/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 7809; DB 1; Length 1457;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDVAAALPAFVALWLLYPWLLGSLGQFSAGCTPDDGFGACDYHODLYDDPEWHVUS 60  
|||||

Db 1 MDVAAALPAFVALWLLYPWLLGSSALGQFSAGGCTFDDGPGACDYHQDLYDDPFWVHVS 60  
Qy 61 AQEHYLPPEMPQGSYVMVDSNHDGPKARLQLPTMKENDTHCIDFSLYLLYSQKGLNPG 120  
Db 61 AQEHYLPPEMPQGSYVMVDSNHDGPKARLQLPTMKENDTHCIDFSLYLLYSQKGLNPG 120  
Qy 121 TLNLTILVRNKGPLANPIWNVGTGTRDWLRAELAVSTFWPNEYQVIFAEVSGGRSGVIA 180  
Db 121 TLNLTILVRNKGPLANPIWNVGTGTRDWLRAELAVSTFWPNEYQVIFAEVSGGRSGVIA 180  
Qy 181 IDDIQVLSYPCDKSPHFLRLGDEVEVNAQNATFOCIATGRDAVHNKWLQRRNGEDIPVA 240  
Db 181 IDDIQVLSYPCDKSPHFLRLGDEVEVNAQNATFOCIATGRDAVHNKWLQRRNGEDIPVA 240  
Qy 241 QTKNINHRRAAFSLQVETKTQDLYRCVTSQSERGSGVSNFAQLIVREPPRPPIAPPOLL 300  
Db 241 QTKNINHRRAAFSLQVETKTQDLYRCVTSQSERGSGVSNFAQLIVREPPRPPIAPPOLL 300  
Qy 301 GVGPTYLLIOLNANSIIGDGPITLKEVEYRMTSGSWTETHAVNAPTYKLWHLDPDTEYEI 360  
Db 301 GVGPTYLLIOLNANSIIGDGPITLKEVEYRMTSGSWTETHAVNAPTYKLWHLDPDTEYEI 360  
Qy 361 RVLLTRPGEGGTGLPGPLITRTKCAEPMWRTPKTLKIAEIQARRIAVDWESLGYNITRCH 420  
Db 361 RVLLTRPGEGGTGLPGPLITRTKCAEPMWRTPKTLKIAEIQARRIAVDWESLGYNITRCH 420  
Qy 421 TFNVTICYHYFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKWLMTNPEGKSESET 480  
Db 421 TFNVTICYHYFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKWLMTNPEGKSESET 480  
Qy 481 LIQDDEDVPGVPVKSLOQTSFENKI FLNWKPELPNGIITQYEVSYSSIRSFDPAPVPA 540  
Db 481 LIQDDEDVPGVPVKSLOQTSFENKI FLNWKPELPNGIITQYEVSYSSIRSFDPAPVPA 540  
Qy 541 GPQTVSNLWNSHTHVFHMLHPGTTYQFFIRASTVKFGFPATAINVTNINISAPSLPDYEG 600  
Db 541 GPQTVSNLWNSHTHVFHMLHPGTTYQFFIRASTVKFGFPATAINVTNINISAPSLPDYEG 600  
Qy 601 VDASLNATATTITVLLRPAQAKGAPISAYQIIVVEQLHPHRTKREAGMECYQVPVYQNA 660  
Db 601 VDASLNATATTITVLLRPAQAKGAPISAYQIIVVEQLHPHRTKREAGMECYQVPVYQNA 660  
Qy 661 LSGGAPYFAAELPGNLPERAPFTVGNRTYKGFNPNPLAPRKGYNIYFQAMSSVEKET 720  
Db 661 LSGGAPYFAAELPGNLPERAPFTVGNRTYKGFNPNPLAPRKGYNIYFQAMSSVEKET 720  
Qy 721 KTQCVRIATKAAATEBEPEVIPPAPKQTDVRVKIAGISAGILVFILLLLVIVIVKSKLA 780  
Db 721 KTQCVRIATKAAATEBEPEVIPPAPKQTDVRVKIAGISAGILVFILLLLVIVIVKSKLA 780  
Qy 781 KKRKDMAGNTRQEMTHVMNADRSYADOSTLHAEDPLSLTFMDQHNFPRLPNDPLVPTA 840  
Db 781 KKRKDMAGNTRQEMTHVMNADRSYADOSTLHAEDPLSLTFMDQHNFPRLPNDPLVPTA 840  
Qy 841 VLDEHNSATAESRLLDVPRYLCEGTESPYQGLHPAIRVADILLOHINLMKTSYSGFK 900  
Db 841 VLDEHNSATAESRLLDVPRYLCEGTESPYQGLHPAIRVADILLOHINLMKTSYSGFK 900  
Qy 901 BEYESFFEQQSASWDVAKKDONAKRNYGNIITAYDHSRVILQPVDEDDPSSDYINANYIDI 960  
Db 901 BEYESFFEQQSASWDVAKKDONAKRNYGNIITAYDHSRVILQPVDEDDPSSDYINANYIDI 960  
Qy 961 WLRYDGYQRP SHYIATQGPVHETVDFWRVMWQESACIWMVTNLVEVGRVKCYKWPDD 1020  
Db 961 WLRYDGYQRP SHYIATQGPVHETVDFWRVMWQESACIWMVTNLVEVGRVKCYKWPDD 1020  
Qy 1021 TEVYGDPKVTCVMEPELAYVYRTTLERRGYNEIREVKQFHTGMPDHGVPYHATGLLS 1080  
Db 1021 TEVYGDPKVTCVMEPELAYVYRTTLERRGYNEIREVKQFHTGMPDHGVPYHATGLLS 1080  
Qy 1081 FIRRVKLSNPPSAGPIVTVHCSAGAGRTGCIYVIDIMLMDAEREVVYDIYNCVKALRSRRI 1140  
Db 1081 FIRRVKLSNPPSAGPIVTVHCSAGAGRTGCIYVIDIMLMDAEREVVYDIYNCVKALRSRRI 1140

Qy 1141 NMVQTERQYIFIHDAILEACLCGETAIPVCEPKAAYFDMIRIDTSQTNSSHLKDBFOTLNS 1200  
Db 1141 NMVQTERQYIFIHDAILEACLCGETAIPVCEPKAAYFDMIRIDTSQTNSSHLKDBFOTLNS 1200  
Qy 1201 VTPRLQAEDECSIACLPRNHDKNRPMMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPA 1260  
Db 1201 VTPRLQAEDECSIACLPRNHDKNRPMMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPA 1260  
Qy 1261 AFIVTQYPLPNTVKDFWRLVVDYGCSTISVMLNEVDLSQGCPCQYWPPEGMLRYGPIQVECM 1320  
Db 1261 AFIVTQYPLPNTVKDFWRLVVDYGCSTISVMLNEVDLSQGCPCQYWPPEGMLRYGPIQVECM 1320  
Qy 1321 SCSMDCDVINRIIFRICNLTRPOEGYLMVQOYQILGNWASHREVPGSKSFLKLLIQVEKWQ 1380  
Db 1321 SCSMDCDVINRIIFRICNLTRPOEGYLMVQOYQILGNWASHREVPGSKSFLKLLIQVEKWQ 1380  
Qy 1381 ECEGEGRITIIHCLNGGSGMFCAGIIVVEMVKRQNVVDVFAVKTLRNSKPNMVEAP 1440  
Db 1381 ECEGEGRITIIHCLNGGSGMFCAGIIVVEMVKRQNVVDVFAVKTLRNSKPNMVEAP 1440  
Qy 1441 EQYRFCDVDALEYLESS 1457  
Db 1441 EQYRFCDVDALEYLESS 1457

## RESULT 2

JC6312

protein-tyrosine-phosphatase (EC 3.1.1.3.48) receptor-type - human

C:Species: Homo sapiens (man)

C:Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jan-2000

C:Accession: JC6312

R:Yang, Y.; Gill, M.C.; Choi, E.Y.; Park, S.H.; Pyun, K.H.; Ha, H.

Gene 186, 77-82, 1997

A:Title: Molecular cloning and chromosomal localization of a human gene homologous to th  
A:Reference number: JC6312; MUID:97199372; PMID:9047348

A:Accession: JC6312

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1440 &lt;YAN&gt;

A:Cross-references: GB:L77886

C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe

-tyrosine-phosphatase homology

C:Keywords: phosphoric monoester hydrolase

F:31-194/Domain: NAM homology &lt;NAM&gt;

F:209-272/Domain: immunoglobulin homology &lt;IMM&gt;

F:294-372/Domain: fibronectin type III repeat homology &lt;3FR&gt;

F:911-1131/Domain: protein-tyrosine-phosphatase homology &lt;PTP&gt;

Query Match 96.1%; Score 7506.5; DB 2; Length 1440;

Best Local Similarity 96.3%; Pred. No. 0;

Matches 1404; Conservative 19; Mismatches 16; Indels 19; Gaps 3;

Qy 1 MD-VAAALPAFVALWLLYPWLLGSSALGQFSAGGCTFDDGPGACDYHQDLYDDPFWVHVS 59  
Db 1 MD-TTAAAVPAFVALLLSPPWLLGSAQGSAGGCTFDDGPGACDYHQDLYDDPFWVHVS 60  
Qy 60 SAQEPHYLPPEMPQGSYVMVDSNHDGPKARLQLPTMKENDTHCIDFSLYLLYSQKGLNP 119  
Db 61 SAQEPHYLPPEMPQGSYVMVDSNHDGPKARLQLPTMKENDTHCIDFSLYLLYSQKGLNP 120  
Qy 120 GTLNILVRNKGPLANPIWNVGTGTRDWLRAELAVSTFWPNEYQVIFAEVSGGRSGVI 179  
Db 121 GTLNILVRNKGPLANPIWNVGTGTRDWLRAELAVSTFWPNEYQVIFAEVSGGRSGVI 180  
Qy 180 AIDDIQVLSYPCDKSPHFLRLGDEVEVNAQNATFOCIATGRDAVHNKWLQRRNGEDIPV 239  
Db 181 AIDDIQVLSYPCDKSPHFLRLGDEVEVNAQNATFOCIATGRDAVHNKWLQRRNGEDIPV 240  
Qy 240 AQTKNINHRRAAFSLQVETKTQDLYRCVTSQSERGSGVSNFAQLIVREPPRPPIAPPOLL 299  
Db 241 AQTKNINHRRAAFSLQVETKTQDLYRCVTSQSERGSGVSNFPQLIVREPPRPPIAPPOLL 300

300 LGVGPYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPYKYLWHLDPDTEYE 359  
Db LGVGPYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPYKYLWHLDPDTEYE 360  
360 IRVLLTRPGEGGTGLPGPPLITRTKCAEPWRTPKTKIAETQARRIADVWESLYNITRC 419  
Db IRVLLTRPGEGGTGLPGPPLITRTKCAEPWRTPKTKIAETQARRIADVWESLYNITRC 420  
420 HTFNVTICYNHYFRGHNSRADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESBE 479  
Db HSFNVITICYNHYFRGHNSKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESBE 480  
480 TIIQTDSDVPGVPVKSLQGTSPFNKIFLWKEPLENGIITQYEVSYSSIRSDPAVPV 539  
Db TIIQTDSDVPGVPVKSLQGTSPFNKIFLWKEPLENGIITQYEVSYSSIRSDPAVPV 540  
540 AGPPQTVSNLWNSHHVFMHLPGTQYOFFIRASTVKGFPGPATVNTVNTISAPSLPDYE 599  
Db AGPPQTVSNLWNSHHVFMHLPGTQYOFFIRASTVKGFPGPATVNTVNTISAPSLPDYE 600  
600 GVDASLNETAITITVLLRPAQAAGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVITYQ 659  
Db GVDASLNETAITITVLLRPAQAAGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVITYQ 660  
660 ALSGAPYFAAELPGNLPEPAPFTVGNRTYKGFNWPPLAPRGNIYFOAMSVYEKE 719  
Db AMSGAPYFACRTPPGNLPEPAPFTVGNRTYKGFNWPPLAPRGNIYFOAMSVYEKE 720  
720 TKTCQVRIATKAAATEPEVLPDPAKQTDVVKIAGISAGILVFLILLVIVIVKSKL 779  
Db TKTCQVRIATKAAATEPEVLPDPAKQTDVVKIAGISAGILVFLILLVIVIVKSKL 780  
780 AKKRKDMANGTROBMTVMNAMDRSYAQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPT 839  
Db AKKRKDMANGTROBMTVMNAMDRSYAQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPT 840  
840 AVLDENHSATBSRLLDVPRYLCEGTESPYQTQLHPAIRVADLLOHIMLMTSDSYGF 899  
Db ENHSATBSRLLDVPRYLCEGTESPYQTQLHPAIRVADLLOHIMLMTSDSYGF 898  
900 KEEVESFEGQSASWDVAKKQDNKRNRYGHIITAYDHSRVLQVDEDPSSDIYANAYID 959  
Db KEEVESFEGQSASWDVAKKQDNKRNRYGHIITAYDHSRVLQVDEDPSSDIYANAYID 960  
960 IWLRYDGYQRPVSHYIATQGPVHETVYDFWVMVWQESQACIVMTNLVEGRVKCYKWP 1019  
Db DGYQRPVSHYIATQGPVHETVYDFWVMVWQESQACIVMTNLVEGRVKCYKWP 1002  
1020 DTEVYDGFVKTCVEMEPALAEYVVRFTFLRRGYNEIREVKQFHTGMPDHGVPVHATGLL 1079  
Db DTEVYDGFVKTCVEMEPALAEYVVRFTFLRRGYNEIREVKQFHTGMPDHGVPVHATGLL 1062  
1080 SFIRRVKLSNPPSAGPIVHCHSAGAGTCYIVIDIMLDAEREGVVDIYNCUKALBSRR 1139  
Db SFIRRVKLSNPPSAGPIVHCHSAGAGTCYIVIDIMLDAEREGVVDIYNCUKALBSRR 1122  
1140 INNVQTEEQYIFIHDAILEACLGETAIPVCEFKAAAYFDMIRIDSQTNSSHLKDEFOTLN 1199  
Db INNVQTEEQYIFIHDAILEACLGETAIPVCEFKAAAYFDMIRIDSQTNSSHLKDEFOTLN 1182  
1200 SVTPRLQAECDSCIACLPRNHDKNRFDMLPPDRCLPLIITIDGESSNYINAAALMDSYRQ 1259  
Db SVTPRLQAECDSCIACLPRNHDKNRFDMLPPDRCLPLIITIDGESSNYINAAALMDSYRQ 1242  
1260 AAFIVTQYPLNVTVKDFWRLVYDGTCSIWMLNEVDLSQCGPQWPWPEGMLRGPIQVEK 1319  
Db AAFIVTQYPLNVTVKDFWRLVYDGTCSIWMLNEVDLSQCGPQWPWPEGMLRGPIQVEK 1302  
1320 MSCMDCDVNIRFRIENLNRPOBYLWVQOFOYLGWASHREVPGRSKFLKILQVEKW 1379  
Db MSCMDCDVNIRFRIENLNRPOBYLWVQOFOYLGWASHREVPGRSKFLKILQVEKW 1362  
1380 QEBCEBEGRTIITHCLNGGSGMFCAGIIVWEMVKRQNVVDVFAVKTLLRNSKPNMVEA 1439

Db 1363 QEBCEBEGRTIITHCLNGGSGMFCAGIIVWEMVKRQNVVDVFAVKTLLRNSKPNMVEA 1422  
QY 1440 PEQYRFCYDVALEYLESS 1457  
Db 1423 PEQYRFCYDVALEYLESS 1440  
RESULT 3  
S17669  
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type mu precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 22-Nov-1993 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
C/Accession: S17669  
FEB5 Lett. 290, 123-130, 1991  
A:Title: Cloning, expression and chromosomal localization of a new putative receptor-like  
A:Reference number: S17669; MUID:92008644; PMID:1655529  
A/Accession: S17669  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1452 <CEB>  
A:Cross-references: UNIPROT:P28827; EMBL:X58288; NID:g32455; PIDN:CAA41226.1; PID:g32456  
A>Note: the authors translated the codon TAT for residue 1340 as His, TTC for residue 13.  
C/Genetics:  
A:Gene: GDB:PTPRM; PTPRL1  
A:Cross-references: GDB:1128093; OMIM:176888  
A:Map position: 18p11.2-18p11.2  
C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe  
-tyrosine-phosphatase homology  
C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tran  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-1452/Product: protein-tyrosine-phosphatase, receptor type mu #status predicted <MAT  
F;21-745/Domain: extracellular #status predicted <EXT>  
F;22-184/Domain: MAM homology <MAM>  
F;139-262/Domain: immunoglobulin homology <IMM>  
F;284-364/Domain: fibronectin type III repeat homology #status atypical <FN3A>  
F;379-470/Domain: fibronectin type III repeat homology <FN3B>  
F;482-574/Domain: fibronectin type III repeat homology <FN3C>  
F;586-674/Domain: fibronectin type III repeat homology <FN3D>  
F;746-762/Domain: transmembrane #status predicted <TM>  
F;763-1452/Domain: intracellular #status predicted <INT>  
F;842-1452/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F;923-1143/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F;1213-1437/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F;72, 92, 131, 249, 406, 414, 448, 454, 534, 544, 598, 651, 681/Binding site: carbohydrate (Asn) (co  
F;206-260/Disulfide bonds: #status predicted  
F;1095/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1101/Binding site: substrate phosphate (Arg) #status predicted  
F;1389/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1395/Binding site: substrate phosphate (Arg) #status predicted  
Query Match 61.6%; Score 4812.5; DB 1; Length 1452;  
Best Local Similarity 61.4%; Pred. No. 7.4e-316;  
Matches 891; Conservative 209; Mismatches 322; Indels 29; Gaps 9;  
QY 22 LIGSALQFSAGACTGDDGACDYHQDLYDDFEWVHVSQAEPHYLPPEMPOGSMYVVD 81  
Db 14 LLTLAGETFGGCLDEPYSTCGYQSGEGDDFNWQVNTLTXTSDPWPSSSLMLVNA 73  
QY 82 SNHDPGEKARLQPTWKENDTHCIDFSYLLYSQKLNPGTILNLRVKNKGLANPINVT 141  
Db 74 SGRPEGORAHLLLPOLKENDTHCIDFHYFVSSKSNPPGLLVVVKVNGPLGNPINNIS 133  
QY 142 GFTGRDLWRAELAVSWFNPNEYQVIEAEVSGSGRYIADDDIQVLSYPCDKSPHFRLG 201  
Db 134 GDPTRTNRAELAISTFWPNFYQVIEV-ITSGHQGYLAIDVKVLGHPCTRTPHFLRIQ 192  
QY 202 DVVNAGQATFOCIATGRDAVKNLWLRQNGEDIPVAOTKKNINHRFAASPRLOQVTK 261  
Db 193 NVEVNAQGFATFOCSAIGRTVAGDLWLQGLIDVRDAPLKEIKVTSSRRFIASFNVNTTK 252  
QY 262 TDQDLXRCVTQSRGSGVSNFAQLIVREPPRIAPPQLLGVGPTYLLIQLNANSIIGDGP 321

Db 253 RDAGKYRCWIRTEGGVGISYNAELVVEPPVPIAPPQLASVGATYMLQLNANSINGDGP 312  
Qy 322 IILKEVEYRMTSGSTWETHAVNAPYKLUHLDDPDTEYEIRVULLTRPGEGGTGLPGPLIIT 381  
Db 313 IVAREVEYCTASGWNDRQPDVSTSYKICHLDDPDTEYEISVLLTRPGEGGTGSGPALRT 372  
Qy 382 RTKCAEPNRTPTKLAIEIOARRIADVDESIGYNTTRCHTFENVITCYHYFRGHNESRAD- 440  
Db 373 RTKCADPWRGPRKLEVEVKEKQIIRWEPFGYNVTRCHSNLTVHYCIYGGQEQVREE 432  
Qy 441 -CLMDMPKAPQHVNVNHLPPYTNVLSKMLITNPEGRKESEETIIOTDEDVPGVPVKSLOQ 499  
Db 433 VSMDFENSHPOHTITNLSPYTNVSVKLIILMNPGRKESQELIVOTDEDLPGAVPTESIQ 492  
Qy 500 TSFENKIFLNKKEPLNEINGITQYEVSYSSSTRSPDPAVPVAGPPQTVTVNLNNSNTHVPMH 559  
Db 493 STFEKIEFLQWREPTQTYGVITLYEITYKAVSSFPDEIDLNSQSRVSKLGNETHFLPFG 552  
Qy 560 LHPGTTYOFFTRASTVKGFGATAINVTNTISAPSLPDYEGVDASLNSTATITVLLRPA 619  
Db 553 LYPGTTYFTIRASTAKFGGPPATNQFTTKISAPSNPAYE-LETPLNQTDNTVTVMKRP 611  
Qy 620 QAKGAPISAYQIVVQQLPHRTRKREAGAMECYQVPVTVQNALSGGAPYFFAAELPPGNLP 679  
Db 612 HSRGAPSVQIVVEEPRRTKTEILKCYVPVPIHFQNASLLNSQYFFAAEPADSIO 671  
Qy 680 EPAPTVGDNRTYKGFWMNPLAPRKGYNIFYOAMSSVEKEFKTCQVRIATKAAATEBEV 739  
Db 672 AAQPTTIGNKTYNGYMNTPLLPYKSYRIYFOAASRANGETKIDCVQVATKGAATPKD-- 729  
Qy 740 TPDPAKQTRVVYKIASIGALIVFTLLLVIVIVVKKSLAKRKADANGTROETHMVN 799  
Db 730 VPEPEKQTDHTVKIAGVAGIAGILLFVILFGLVVLVKKRKLAKRKETWSSTRQEMTVMN 789  
Qy 800 AMDRYADQSTLHARDPLSLTFMDQHNPSPRLNDP-----LVPTAVL-DSNH 846  
Db 790 SNDKSYAEQGTNCDE---AFSPMDTHNLNGRSVSPSSFTKMTNTLSVSPNSYYPDETH 846  
Qy 847 SATASSRLLDVPRY-LCEGTESPYQTQLHPAIRVADLLQHINLMKTSDSYGFKEEYES 905  
Db 847 TWASDTSSLVQSHTYKKREPADVPYQTQGLHPAIRVADLLQHIITQMKCAEGYGFKEEYES 906  
Qy 906 FPEGQASWDVAKDONAKRNYGNI IAYDHSRVILQPVEDDPSDYINANYVIDLWLYRD 965  
Db 907 FPEGQASPDWSAKDONAKRNYGNI IAYDHSRVRLQITEGDTSNDYINGNYI-----D 960  
Qy 966 GYORPSHYIATQGPVHETVYDFWRVMWQEQSACIVVMVNLVEGRVKCYKWPDDTEVYG 1025  
Db 961 GYHRPNHYIATQGPQETIYDFWRVMWHENTASIIIMVNLVEGRVKCKYWPDDTEIYK 1020  
Qy 1026 DPKVTCVMEPIAEYVYVFTLLERGYNEIREVKQFHFTGWPDPHGVPYHATGLLSFIRRV 1085  
Db 1021 DIKVTLLIETELLAEYVIRTFAVEKRGVHEIRIQHFHFTGWPDPHGVPYHATGLLGFVRQ 1080  
Qy 1086 KLSNPSAGPIVHCSAGRGTGCVIIVIMLDMAREBGVDIYNCVKALSRRLNMVQT 1145  
Db 1081 KSKSPSAGPLVHCSAGRGTGCFIVIDIMLDMAREBGVDIYNCVRELSSRRNMVQT 1140  
Qy 1146 BEQYFIHDAILEACLCGTALPVCEFKAAYPDMIRIDSQTNSSHLKDBEFQTLNSVTPRL 1205  
Db 1141 BEQYFIHDAILEACLCGDTSPASQVRSLYYDMNKLDPQTNSSQIKKEFRILNMVTPIL 1200  
Qy 1206 QAEDCSIACLPRNHDKRMFMDLPDRCLPFLITIDGESSNYINAAALMDSYRQPAFIVT 1265  
Db 1201 RVEDCSIALPRNHEKNRQMDILPDRCLPFLITIDGESSNYINAAALMDSYRQPSAFIVT 1260  
Qy 1266 QYPLNTVKDFWRLVYDYCTSIYMLNEVDLSQGCPOYWPREGMLRYGPIQVECHSCSMD 1325  
Db 1261 QHPLPNTVKDFWRLVLDYHCTSVMLNDVDPALQCPQYWPENGVRHGHGPIQVEFVSADLE 1320  
Qy 1326 CDVINIRIFRICNLTRPQEGYLMVQFOYILGWASHREVPGSKSFLKLILOVEKWBECBE 1385

Db 1321 EDIISIRIFRIYNAARPDQGYRMVQOQFQFLGPMVYRDTFVSKRSFKLIRQVDKMQEYNG 1380  
Qy 1386 GEGBTIITHCLNGGGRSGMFCAGIIGVWVKRQNVVDVFAVKTLRNSKPNMVAPEQVRF 1445  
Db 1381 GEGTVVHCLNGGGRSGTFCASISVCEMLRHQRVTVDFHAVKTLRNNKPNMVDLLDQYKF 1440  
Qy 1446 CYDVALEYLES 1456  
Db 1441 CYEVALBYLNS 1451  
RESULT 4  
S17670  
Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type mu precursor [validated] - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Nov-1993 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: S17670  
R:Gebbinck, M.F.B.G.; van Etten, I.; Hateboer, G.; Suijkerbuijk, R.; Beijersbergen, R.L.;  
FEBS Lett. 290, 123-130, 1991  
A:Title: Cloning, expression and chromosomal localization of a new putative receptor-like  
A:Reference number: S17669; MUID:92008644; PMID:1655529  
A:Accession: S17670  
A:Molecule type: mRNA  
A:Residues: 1-1452 <GEB>  
A:Cross-references: UNIPROT:P28828; EMBL:X58287; NID:G53234; PIDN:CAA41225.1; PID:G53235  
C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe  
C:tyrosine-phosphatase homology  
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; trar  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-1452/Product: protein-tyrosine-phosphatase, receptor type mu #status predicted <MAI  
F:21-745/Domain: extracellular #status predicted <EXT>  
F:22-184/Domain: MAM homology <MAM>  
F:199-262/Domain: immunoglobulin homology <IMM>  
F:284-362/Domain: fibronectin type III repeat homology <FN3A>  
F:379-470/Domain: fibronectin type III repeat homology <FN3B>  
F:482-574/Domain: fibronectin type III repeat homology <FN3C>  
F:586-674/Domain: fibronectin type III repeat homology <FN3D>  
F:746-762/Domain: transmembrane #status predicted <TMN>  
F:763-1452/Domain: intracellular #status predicted <INT>  
F:842-1452/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:923-1143/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F:1213-1437/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:72\_92\_131\_249\_406\_414\_448\_454\_534\_544\_598\_651\_681/Binding site: carbohydrate (Asn) (co  
F:206-260/Disulfide bonds: #status predicted  
F:1095/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1101/Binding site: substrate phosphate (Arg) #status predicted  
F:1389/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1395/Binding site: substrate phosphate (Arg) #status predicted  
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Best Local Similarity 61.3%; Pred. No. 1.4e-314; Mismatches 32; Indels 29; Gaps 9;  
Matches 889; Conservative 208; Mismatches 32; Indels 29; Gaps 9;  
Qy 22 ILGALGAFSAGGCTFDDGPGACDHYQDLYDDFEWVHVSAQEPHYLPPEMPOGSMVVDVS 81  
Db 14 LLLTAAGTTFSGCLFDEPYSTCGYSQADEDDFNWEQVNTLTKTPTSDPMPGSGFNLVNT 73  
Qy 82 SNHDPGEKARQLPTMKENDTHCIDFSVLLYSQKGLNFGTILNLRVKNKGLPLANINWVT 141  
Db 74 SGKPEQRAHLLPOLKENDTHCIDFHYFVSSKSNAPGLLNLYVKNVNGPLGNPIMNIS 133  
Qy 142 GFTGRDWLRALVSTFWPNEYQVTFEAEVSGRSRGTATDDIOVLVSYPCCDKSPHFLRLG 201  
Db 134 GDFTRTHRAELAISTFWPNFYQVIFEV-VTSGHGYLAIIDEVKVLGHPTKTRTPFLRIQ 192  
Qy 202 DVEVNAGQATFQCIATGRDAVHNKMLQRRNGEDI PVAQTKNINHRPFAASFRLOEVTK 261  
Db 193 NVEVNAGQATFQCSAIGRTVAGDLWLQGDVDRDAPLKEIKVTSRRFIASFNVNVTTK 252  
Qy 262 TDQDLRYCVTQSEGRSGVSNFAQLIVRPPRPPIAPPQLLGVTYLLQLNANSIIGDGP 321  
Db 253 RDAGKYRCWIRTEGGVGISYNAELVVEPPVPIAPPQLASVGATYMLQLNANSINGDGP 312





[illegible]

A>Note: in Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattus r. Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J. Biochem. J. 302, 39-47, 1994

A>Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase from rat liver

A>Accession number: S46216; MUID:94347119; PMID:8068021

A>Accession: S46218

A>Status: translation not shown

A>Molecule type: mRNA

A>Residues: 1-1501 <ZHA>

A>Cross-references: EMBL:U12329; NID:G294573; PIDN:AAC37657.1; PID:G294574

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; Cys

C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosine phosphatase

F:47-109/Domain: immunoglobulin homology <IMM1>

F:149-209/Domain: immunoglobulin homology <IMM2>

F:246-300/Domain: immunoglobulin homology <IMM3>

F:413-506/Domain: fibronectin type III repeat homology <3FR>

F:882-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:969-1190/Domain: protein-tyrosine-phosphatase homology <PTP1>

F:1258-1481/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status predicted

F:1148/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted

F:1433/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted

F:1439/Binding site: substrate phosphate (Arg) #link PTP2 #status predicted

Query Match 19.4%; Score 1516.5; DB 2; Length 1501;  
Beat Local Similarity 29.8%; Pred. No. 1.6e-93;  
Matches 420; Conservative 205; Mismatches 471; Indels 315; Gaps 46;

QY 204 EVNAGQNTFOCIATGRDAVHNKMLQRRNG---EDIPVAQTKNHNRRFAASFLRQEV 259  
DB 242 EIMPGNNVITCAVGSMPYVK-WHQGEDITPEDMPVG--RNV-----LELT 288

QY 260 TKTDQDLRYCVTSQSRGSGVNSFAQLIVREPRPIAPPQLLGVGTYLLTLQNLNANSTIGD 319  
DB 289 DVKDSANTCVAMSSLGV-IEAVAQITVKSFLKPCGTPVVTENTATSIITWDSGN--P 344

QY 320 GPIILKEVEYRMTS--GSWTETHAVNAPYIKLWHLDPDTEYEIRVLLTRPGEGTGLPGP 377  
DB 345 DPVSYYVIEYKSKDQGPYQIKEDITTRYSTGGLSNPSEYEIYW--SAVNSIGQGPPSE 402

QY 378 PLITRTKCAEPMRTKTKLIAIQARRIADVDES-----LGYNITRCHTENVVTICYH 429  
DB 403 SVVTRTGGQASAPAPNVQARMLSATTIMQWEEPEVNGLRIGYRV----- 449

QY 430 YFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESBETIIQT----- 484  
DB 450 YV-----TMEPEHPVGNWQKH-NVD-DSLTLTTVGSLLDEDETYTVRVLAFTS 493

QY 485 --DEDVPGVPVKSLOG-----TSPENKIFLNWKEPLEPNGIITQYEVSYS-- 529  
DB 494 VGDGLSDPIQVTKTOGVPQGPMNIRAEAKSETSIGLSWAPRQES--VIKYELLFREGD 551

QY 530 ----IRSFDPAPVAGPPQTVSNLWNSTHHVFMHLPGCTTYOFFTRASTVKGFGPATAI 584  
DB 552 RGREGVRFDP-----TTAFVVEDLKPNTEYAFRLAARSQGLGAFTAV 595

QY 585 NVTNINISAPS-----LPD-----YEGVDASLN-ETATTIT 613  
DB 596 VCQRTLQAI SPKNFKVGMIMKTSVILLSWEFFPDYNSPTPKIQYINGLTLVDVGRITKKLI 655

QY 614 VLLAP-----AQAKGAPISAYQIVVEQLHPHRTKREA-----GAME 649  
DB 656 THLKPHTYTNFVLTNRGSSGLGQTV-----TARTAFNMLSGKPSVAPKPDNDGSIV 708

QY 650 CY----QVPVTYQNALSGGAPYYFAAELP-----PCNLTP----- 679  
DB 709 VYLPDQGSPTVQV-----YFVIMVPLRKSRCGQFPILLGSPEDMDLBEILIQDLSRL 760

QY 680 -----BPAPFTVGDNRTYKGFVWNPPLAPRKGYNITFOAMSS 715  
DB 761 QRRSLRHSRQLEVPYPTAARFSILPAVPHPGNQYQYGGFGRNGRLGEPGHRHYVLFVLAV 818





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QY 331 MTSGSWTETHAVNAPTYKLWHLDPDTEYEIRV-LLTRPGEGETGLPGPPLITRYKCAEPM 389
Db 774 TISG-----LTPETYSITVAAYTTKGDGAR-----SKPKVVTITGAVPG 813
QY 390 RTPKTLKIAEIQARRIADW-----ESLGYNITRCHTFENVITCYHYFGRHESRADC 441
Db 814 R--PTMVSTTAMHTALLQWHPKLPGLGELGYRL-----QYRADEARNT 858
QY 442 LMDPKAPQHVNVHLPPTVNVSLKMLNPNBGRKESBETIIOETDEVPGPVP-----VKSL 497
Db 859 IDFGKDDQHFTVTLGHKGATYIFRLAAKNRAGPGSEFEKEITTPEDAPSGFPQNLRTVGL 918
QY 498 QGTSPENKIFLNWKEPL--EPNGIITQVEYSYSIRSPDPAVPVAGPPQTVSNLWNSTHH 555
Db 919 TTSTTE-----LAWDPFLAERNGRITNTVTVYVRDINS-----QHELQNVTVGDVHL 964
QY 556 VFMLHPGTGYOFFTRASTVKGFGP-----ATAINVTTNISAPS 594
Db 965 TLLGLKPDTTVDIKVRAHTSGAGPLSPSIQSRTPMEQVFAKNPRVAAAMKTSVLLSWE 1024
QY 595 LPD-----YEGVDASLN-----ETATTITVLLRPAQAKG-----623
Db 1025 VPDYSKSAVPFKILYNGQSEVDGHSRKLJADLPNTSEYFVLNMRGTSAGGLQLHLSVI 1084
QY 624 -----APISA-----YQIVV-----633
Db 1085 RTAPDLLPKPLPASAFIEDGRFSLSPQVOPSLVRWFYIVVPIRVDVGGNLLAPRWST 1144
QY 634 -EQLH-----PHRTKEAGAMECYQVPVTVYQNALSGGAPYFAAELPPGNL 678
Db 1145 PEELELLELEAIEGEBEKQRRRRQAERLK-----PYVAAQV--DEL 1185
QY 679 PEPAPFTYGDNRITYKGFNPPPLAPRKXNYIYFQAMSSVEKETK-----TQCVRATK 730
Db 1186 PE--FTFLGDKNRYGFNRPPLSDLSYQCFVLASLKEPMDQKRYASSPYSDIIVVQVTP 1243
QY 731 AAATEPEVEIPDPAKQTRVVKIAGISAGILVFILLILLVIVVVKSLAKRKRDMGMT 790
Db 1244 AQQKEPEML-----WVTGFLAVILILIVIAI-----LLFKK-----1278
QY 791 RQEMTHVMNAMDR---SVADQSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPTAVLDENHS 847
Db 1279 ---RTHSSSSKDEQSIGLKDSLLAHSDFVEMRNLN-----1311
QY 848 ATAESSRLLDVPRYLCEGTESPYQTQL--HPAIRVADLQHLINLMKTSDSYGFKEEYES 905
Db 1312 -----YQTPGMRDHPPIPIITDLADNIERLKANDGLKFSQEYES 1349
QY 906 PFEQASWDVAKQDONRAKNRYGNIAYDHSRVLQPVEDDDPSDDYINANYIDILWLYRD 965
Db 1350 IDPGQQFTWENSNSFNPKRYANVIAVDHSRVLITSIDGVPGSDYINANYI-----D 1403
QY 966 GYORPSHYIATQGPVHETVYDFWRMVWQEOSACIWMVTNLVGVKVCYKWP--DDTEVY 1024
Db 1404 GYRKQNAVIATQGPIDETMGDFWRMVWQRIATVVMTRLEBSRKVKCDQYWPARGTETY 1463
QY 1025 GDFKVTCEVMEPLABYVVRITFLRRRGYNEIREVQFHFTGPDWPGVPHYATGLLSPIRR 1084
Db 1464 GLIQVTLVDVTVELATYTRMTFALHKSQSGSEKELAQFQFMAPDPDHGVPEYPTPILAFLLR 1523
QY 1085 VKLSNPPSAGPIVWCHSAGAGTCGYIVIDIMLMAERGGVVDIYVNCVKALRSRRINMVQ 1144
Db 1524 VKACNPLDAGPMVWCHSAGVGTGCFIVIDAMLERMKHEKTVDIYGHVTCRMSQRNVMVQ 1583
QY 1145 TEEQYIFTHDALEACLCGETAI PVCEFKAAFYDMIRIDISQNTNSHLKDEFOTLNSVTPR 1204
Db 1584 TEDQVTFIHEALEAAMCHTEBVLARNLYAHITQKLGQVPPGESVTAMELEFKLL--AGSK 1641
QY 1205 LOAEDCSIACLRNDKRNPFMDPPDCLPLFITIDG--ESSNYINAAALMDSYRQPAAFI 1263
Db 1642 ARASRFISANLPCNFKNRLNVMFVELTRVCLQPIRGVGGSDYINAGFLDGYRQOKAVI 1701
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QY 1264 VTQYPLPNTVKDFWRLVVDYVGCTSI VMLNEVDL--SQSCPOYWPBEGMLRYGPIQVECMS 1321
Db 1702 ATQGPLAESTEDFWRLMWEHNSTII VMLTKUREMGREKCHOYWPAERSARQYFVVDPM 1761
QY 1322 CSMDCDVINRIFCNILNTRPQEGY-LMVQQOYQYLGWASHREVPGSKRSFLKLLILQVEKWQ 1380
Db 1762 --EYNNPQYILREFKVTDAARDGOSRTIROQFQDM-PEQGVPKTGEFIDFIGQVHKTK 1817
QY 1381 BECEGEGERTIIHCLNGGSGRSMFCAGIIVVMVKRQNVVDVFAVKTILRNSKPNMVEAP 1440
Db 1818 EQFGQ-DGPIVHCSAGVGTGVTITLSIVLERMRVYEGVDMFQTVKTLRTQRPAMVQTE 1876
QY 1441 EYRFEYVDVALEYLES 1456
Db 1877 DQYQLCYRAALEYLG 1892

RESULT 10
TDHULK
leukocyte antigen-related protein precursor - human
N:Alternate names: leukocyte common antigen homolog
N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: S03841; JI0051
R:Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 168, 1523-1530, 1988
A:Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region ho
A:Reference number: JI0051; MUID:89035978; PMID:2972792
A:Accession: S03841
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1897 <STR>
A:Cross-references: UNIPROT:P10586; EMBL:Y00815; NID:G34266; PIDN:CAA68754.1; PID:G34267
C:Genetics:
C:Gene: GDB:PTPRF; LAR
A:Cross-references: GDB:120138; OMIM:179590
A:Map position: lp34-lp34
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
og
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
P:1-16/Domain: signal sequence #status predicted <SIG>
P:17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>
P:17-1250/Domain: extracellular #status predicted <EXT>
P:37-99/Domain: immunoglobulin homology <IMM1>
P:139-199/Domain: immunoglobulin homology <IMM2>
P:236-230/Domain: immunoglobulin homology <IMM3>
P:308-330/Domain: fibronectin type III repeat homology <FN3A>
P:403-489/Domain: fibronectin type III repeat homology <FN3B>
P:501-583/Domain: fibronectin type III repeat homology <FN3C>
P:596-685/Domain: fibronectin type III repeat homology <FN3D>
P:698-798/Domain: fibronectin type III repeat homology #status atypical <FN3E>
P:810-893/Domain: fibronectin type III repeat homology <FN3F>
P:905-989/Domain: fibronectin type III repeat homology <FN3G>
P:1001-1078/Domain: fibronectin type III repeat homology <FN3H>
P:1251-1274/Domain: transmembrane #status predicted <TM>
P:1275-1897/Domain: intracellular #status predicted <INT>
P:1385-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>
P:1365-1586/Domain: protein-tyrosine-phosphatase homology <PTP1>
P:1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>
P:444-97,146-197,243-288/disulfide bonds: #status predicted
P:107,240,285,711,956/Binding site: carbohydrate (Asn) (covalent) #status predicted
P:1538/Active site: Cys (phosphocysteine intermediate) #status predicted
P:1544/Binding site: substrate phosphate (Arg) #status predicted
P:1829/Active site: Cys (phosphocysteine intermediate) #status predicted
P:1835/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.1%; Score 1492.5; DB 1; Length 1897;
Best Local Similarity 28.9%; Pred. No. 9.6e-92;
Matches 469; Conservative 211; Mismatches 551; Indels 393; Gaps 59;
QY 68 PPMPQG-----SYMVVD-----SHNDPGEKARLQLPTMKENDTHCIDFS--YL 110
```

Db 426 PPEPENGILRGYRYVYTPDSRRPPNNAWKHNTDAG-----LLTVGSLLPGLTYSLRVL 479  
Qy 111 LYSQKLNPGFLNILVRNKGGLANPINWVTFGRDMLRAELAVSTFW-----PNE-----Y 163  
Db 480 AFTAVGDPSPPTIQVTKQGVPAQP-----ADFOAE--VESDTRIQLSWLLPPQERIMY 533  
Qy 164 QVIFEAEVSGSGSVIAIDDIQVLSYPC-DKSPHFL-----RLG-----DVEVNA 207  
Db 534 ELVTAABAEDEQKHVTFDPTS--SYTLEDLKPOTLYRFQLAARSDMGVGVFTTPIEART 591  
Qy 208 GQNA-----TFQCIATGRDAVHNKML-----QRRNGEDIPVACTKININRRFAASRFLQ 257  
Db 592 AQSPTSPAPKVCMSVSGTTRVYS-WVPPPADSRNG-----VITQYSAHEAVDGEDGR 646  
Qy 258 EVT-----KTDQDL-----YRCVTQ--SERGSGVSNPAQLIVREPPRIAPQLLG 301  
Db 647 HVVDGISREHSSMDLVGLEKTEYRVVRAHTDVGPGPSESSPVLVRTDEDVSPGPRAKVE 706  
Qy 302 VGP-----TYLLIQLNAN-----SIIGDGPILLKEVEYR 330  
Db 707 VEPLNSTAVHYKLPVPSKOHGQIRGVQVTVYRLE-NGBRPGLPIIQD--VMLAEAQWR 763  
Qy 331 MTSGSWTETHAVNAPTVKLMLHLDPDTEYIRV-LLTRPGEGLTLPGLPLITRTKCAEPM 389  
Db 764 PEESDEYET-----TISGLTETTYSVTVAAATYTKGDAR--SKPLVITVTGAVPG 812  
Qy 390 RTPKTLXIAEQARRIAVDM-----ESLGYNITRCHTNFNTVICYHYFRGHNESRADC 441  
Db 813 R--PTWMTISTAMNTALLQWHPKXELGCLLYRQCYRA-----DEARPNT 857  
Qy 442 LDMDPKAPQVNVNHLPPYTNVSLKMLITNPEGKSESEETIOTDEDVPGVP-----VKSL 497  
Db 858 IDFGKDDQHFVTVLGKHGTYTIFPLAANKRAGLGEFEKEIRTPEDLPSPQPQLHVTGL 917  
Qy 498 QGTSFENKILFNWKEPL--BPNGLIITQVSEYSSIRSFDPAPVAGPQTVSNLWNSTH 555  
Db 918 TTSTTE-----LANDPPVLAENGRIISYTVVFRDNG-----QQELQNTTDTTRF 963  
Qy 556 VFMLHPGTYQFFIRASTVKFGP-----ATAINVTNIGAPS 594  
Db 964 TLTLGLKDDTYDIKVRATWSKSGSPLSPISQSRTPVEQVFAKNFRVAAMAKTSVLLSWE 1023  
Qy 595 LPD-----YEGVDASLN-----ETATTITVLLRPAQAKG-----623  
Db 1024 VPDSYSKAVPFLKLYNGQSVEDGHSRKLADIQPNTEYSFVLNMRGSSAGGLQHLVSI 1083  
Qy 624 -----APISAY-----OIVVEQLHPHRTKEAGAM--648  
Db 1084 RTAPDLLPHKPLPASAVIEDGRFPLSMHVQDPSLVRFVIVVVI-----DRVGGSLMT 1138  
Qy 649 -----ECYQVPVTVYNALSGGAPY-----YFAAELPPGNLPEPAPPTVGDNR 690  
Db 1139 PRWSTPELELDELLEALEIOGEBEQRRRRQAEKLPYVAAQLDV--LPE--FTLGDGX 1194  
Qy 691 TYKGFNPPPLAPRGYNIYFOAMSSVKEKY-----TQCVRIATKAAATEPEVVPD 742  
Db 1195 NYRGFYNRPLSPDLSYQCFVLASLKEPMDQKRYASSPYSEIVVQVTPAQOQEBEPL--1252  
Qy 743 PAKQTDVVKIAGISAGILVFILLVIVIVVKSLAKRKDKAMGNTRQEMTHVNMAD 802  
Db 1253 -----WVTGVPVAVILLIIVIAI-----LLFKRK-----RTHSPSSKD 1286  
Qy 803 R---SYAQDQSTLHAEDPLSLTFMDQHNFSPLPNDPLVPTAVLDENHSATAESSRLDVP 859  
Db 1287 EQSIGLKSLLAHSSDPVEMRLN-----1310  
Qy 860 RYLCEGTESYQGTQL--HPAIRVADLLQHINLMKTSDSYGFKEEYSEFFEGOSASWDVA 917  
Db 1311 -----YQTPGMRDHPPIPTDLADNLIERLKANDGLKFSQYESIDPGQOQFWENS 1360  
Qy 918 KQONRAKNYGNIIAYDSRVLQPVEDDPSDDYINANVIDIWLRYDGRQORSHYIATQ 977  
Db 1361 NLEVNFKNRYANVIAYDHSRVLITSDIGVPGSDYINANYI-----DGYRKQNAVYIATQ 1414

Qy 978 GPVHETVYDFRMVWVWQESACIVMVTNLVEYGRVKCYKYP-DDTEYVGDFKVCVEMEP 1036  
Db 1415 GLPETMGDFRMVWMEQRTATVVMTRLEEKSRVKCQYWPARGTETCGLIQVTLDDTVE 1474  
Qy 1037 LAEYVVTFTLERGGYNEIBEYKQFHETGTHGPDHGVPHATGLLSFIRVKLSNPSAGPI 1096  
Db 1475 LATYVTRFALHKSSEKRELRQFQPMAMPDGHGVBPYPTPILAFRLRVKACNPLDAGPM 1534  
Qy 1097 VVHCSAGRTGTCYIVIDIMDMAEREGVVDIYVNCVKALASRRRINMVQTEEQYIFIHDAI 1156  
Db 1535 VVHCSAGRTGTCYIVIDIMLERMKEKHTVDIYGHVTCMRSQRYNMVQTEQYVFIHEAL 1594  
Qy 1157 LEACLCGETAIPVCEFAAYFDMIRIDSQNSSHLKDDEFQTLNVTPLRLQABDCSIACLP 1216  
Db 1595 LEAATCGHTVPARNLYAHIQKLGQVPPGESVTAAMELEFKLLAS--SKAHTSRRTISANLP 1652  
Qy 1217 RNDHKNRPMDLPRDCLPELITIDG--ESSNYINAAIMDSYROPAAETVQYPLNPTVKD 1275  
Db 1653 CNFKNRLVNMIPVELTRVCLQPIRGVEGSDYINASFIDGYRQOKAYIATQGLAEATED 1712  
Qy 1276 FWRLLVYDYGCTSIYMLNEVDL--SQGCPQYWPEEGMLRYGPIQVECMSCSMDCOVINRIF 1333  
Db 1713 FWRMLMEHNSITIIYMLTKLEMGEKCHQYWPASRSARYQYFVVDPA--EYMWPOYIL 1769  
Qy 1334 RICNLTRPOEGY-LMWQOQYVLGWASHREYVPGSKRSFLKILQVEKWQEBCEGEGRIT 1392  
Db 1770 REFKVTARDQGSRTIRQFQTDW-PEQGVFKTEGFIQVGHKTEQFGQ-DGPITV 1827  
Qy 1393 HCLNGGSRGSMFCAIGIIVEMVRQNVVDVFAVKTLNRSKPNMVEAPEQYRFCDYVALE 1452  
Db 1828 HCSAGVGRGVFTTSLIVLERMYEGVVDVFQTVKTLRTQRPAMVQTEQYQLCYRAALE 1887  
Qy 1453 YLES 1456  
Db 1888 YLGS 1891

## RESULT 11

A56178

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human  
N;Alternate names: protein-tyrosine-phosphatase BPTP-2

C;Species: Homo sapiens (man)

C;Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text\_change 09-Jul-2004

C;Accession: A56178; S12052; B44929

R;Pulido, R.; Krueger, N.X.; Serra-Pages, C.; Saito, H.; Streuli, M.

J. Biol. Chem. 270, 6722-6728, 1995

A;Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.

A;Reference number: A56178; MUID:95204468; PMID:7896816

A;Accession: A56178

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1912 <PUL>

A;Cross-references: UNIPROT:P23468; GB:L38929; NID:g755652; PIDN:AAC41749.1; PID:g755653

R;Krueger, N.X.; Streuli, M.; Saito, H.

EMBO J. 9, 3241-3252, 1990

A;Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatase

A;Reference number: S12049; MUID:9106018; PMID:2170109

A;Accession: S12052

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 390-1912 <KRU>

A;Cross-references: GB:X54133; NID:g35789; PIDN:CAA38068.1; PID:g35790

A;Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-T-R;Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yachi

Cancer Res. 52, 737-740, 1992

A;Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.

A;Reference number: A44929; MUID:92119637; PMID:1370651

A;Accession: B44929

A;Molecule type: mRNA

A;Residues: 1756-1804, 'C', 1806-1845 <ADA>

A;Cross-references: GB:S78086; NID:g243545; PIDN:AAB21147.1; PID:g243546

A:Experimental source: pre-B cell NALM-6  
A:Note: sequence extracted from NCBI backbone (NCBIN:78086, NCBIP:78087)  
A:Note: the authors did not report the entire codon for residue 90  
C:Genetics:  
A:Gene: GDB:PTPRD  
A:Cross-references: GDB:131384; OMIM:601598  
A:Map position: 9p24-9p24  
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; ogy  
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
F:38-100/Domain: immunoglobulin homology <IMM1>  
F:140-209/Domain: immunoglobulin homology <IMM2>  
F:250-304/Domain: immunoglobulin homology <IMM3>  
F:711-811/Domain: fibronectin type III repeat homology <3FR>  
F:1293-1912/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:1669-1892/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:1553/Active site: Cys (phosphotyrosine intermediate) #status Predicted  
F:1559/Binding site: substrate phosphate (Arg) #status predicted  
F:1844/Active site: Cys (phosphotyrosine intermediate) #status predicted  
F:1850/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.0%; Score 1482.5; DB 2; Length 1912;  
Best Local Similarity 27.2%; Pred. No. 4.6e-91;  
Matches 464; Conservative 222; Mismatches 534; Indels 487; Gaps 57;

Qy 51 YDDFEW-----VHSAQEPHYLP-----PEMPQ 73  
| | | | |  
Db YSDYEFVVAVNNIGRGPSEPVLTQTSEQAPSSAPRDVQARMLSSITILVQWKEPEEPN 445  
| | | | |  
Qy 74 QS-----YVVDSSNDHPGEKARLQPTMKN--DTHCIDFSYLL-----YSQGLNPGT 121  
| | | | |  
Db GOIQYRVYTMPTQHVNN-----WMKHNVADSQITIGNLVPOKTVSVKVL----- 493  
| | | | |  
Qy 122 LNILVRNKGPLANIPNVTGFTGRDLRAELAVTFWPNBYQVTFEAEVSGSGSYIAI 181  
| | | | |  
Db 494 -AFTSIGDGPLSSDI-----QVITQTGVPG----- 517  
| | | | |  
Qy 182 DDIOVLSVPCD-KSPHFRLGDEVNAGQATFQCIATGRDAVHNKMLQRRNGEDIPA 240  
| | | | |  
Db 518 ---QPLNKAPESETSILLSTWTPRSDTIANYELVY-KDGEH-----GSE----- 559  
| | | | |  
Qy 241 QTKNINRRFAASFLQVTKTDQDLYRCVTOSESGSVNFAQLIVRS-PPRPTAPQOL 299  
| | | | |  
Db 560 QRITTEP---GTSYRLQGLKPNLSYFLRAASPOGLGAST-AEISAKTMOSKPSAPPQD 615  
| | | | |  
Qy 300 LGV---GPTYLILQNLNANSIIGDGPILK-EVEYRMTSGSWTETHAV-----NAPTYKLW 350  
| | | | |  
Db 616 ISCTSPSSITLVSWQPPVPEKQNGIITEYSIKYTAVDGEDDKPHEILGIPSDTTKYLLE 675  
| | | | |  
Qy 351 HLDPTVEIRVLLTRPGGGTGLPGPLITTKCAEMRTPTKIAEIQARRIADWE 410  
| | | | |  
Db 676 QLEKWEY--RITVTAHTDVGCPESLSVLIRTNEDVSPGPPRKEVEAVNSTSVKVSWR 733  
| | | | |  
Qy 411 S-----LGYNITRCHTFNVICVHYFRGN----- 435  
| | | | |  
Db 734 SVPNKHQGIQYQV-----HYVRMENGEPKGQPMKDKVMDLADQWEDDTT 781  
| | | | |  
Qy 436 -----ESRADCLDMDPK-----APQHVNNHLPVTVNS 463  
| | | | |  
Db 782 EHDMLISGLQETSILVTATYTKDGARSFKPLVSTTGAVPGKPRLVNH-----TQWN 837  
| | | | |  
Qy 464 LKMLTNP-----GRK-----ESETTIQTD----- 485  
| | | | |  
Db 838 TALIQWHPVDTFGLQYRLKFGKDMPELTLTFSEKEDHPTATDIHKGASYVFLISA 897  
| | | | |  
Qy 486 -----EDVGPVPVKSLOGTSFENKIEFNKKEPL--EPNGIITQYVS 526  
| | | | |  
Db 898 RNKVGGEEMVKEISIPSEVPPTGFPQNLHSEGTSTTSVQLSQWPPVLAERNGLIITKYL 957  
| | | | |  
Qy 527 YSIRSFDPAVPVAG---PPQTVSNLWNSTHVFVHMLHPTGTYQFFIRASTVKGFGP--- 580  
| | | | |  
Db 958 YRDINI--PLLPMEQLIVADITMTLTG-----LKPDITYDVKVRHAHTSKGPGYSP 1007  
| | | | |

RESULT 12

A48758

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor-linked form p1 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)

Qy 581 -----ATAINVTNISAPSLPD-----YEGVDASL 605  
| | | | |  
Db 1008 SVQRTPLPVDQVPAKNFHVXAMKTSVLLSWEIPENTNSAMPFKILLYDDGKQWVEVDGRA 1067  
| | | | |  
Qy 606 NETATTITVLLRPAQ-----AKGAP----- 625  
| | | | |  
Db 1068 TQ---KLIVNLKPEKSYSVLITNRGNSAGGLQHRVTAKTADPDLRTKPAFIGKTNLDQMI 1124  
| | | | |  
Qy 626 -----ISAYQIVVEQLPHRTK-----REAGAMECYQV-----PVTYQN 659  
| | | | |  
Db 1125 TVQLPEVPANENIKGYIIIVPLKSKRGKFTKPWESPEMELDELLKEISKRKRISRYGR 1184  
| | | | |  
Qy 660 ALSCGAPYFAAELPPGNLPEPAPFTVGDNRITYKGFWNPPPLAPRKGNIYFQAMSSVEKE 719  
| | | | |  
Db 1185 EVE--LKPYYAAHFD---VLPTFTLGDDKHGFGFTNKQLQSGQEV-VFFVLAWMEHAE 1237  
| | | | |  
Qy 720 TKTCQVRIATKAAATEBPEVIPAKQTDRTVRVVKIAGISAGIL--VFILLLLWVIVVKKS 777  
| | | | |  
Db 1238 SK---MYATSPYSDPVVMDLDPQITDBEGLIIVWVGPVLAVVFIICIVIALLYKRK 1293  
| | | | |  
Qy 778 KL-AKKRKDAMGNTRQEMTHMVNAMDRSYADQSTLHAEADPLSLTFMDQHNFSPRLPNDPL 836  
| | | | |  
Db 1294 RAESDSRKSSIPNNKEIPSH-----HPTDPVELRLRN----- 1325  
| | | | |  
Qy 837 VPTAVLDENHSATAESRLLDVPRLCEGTSPYQTGOL--HPAIRVADILLQHINLMKTS 894  
| | | | |  
Db 1326 -----FQTPGMASHPPFIPLELADHLERLXAN 1352  
| | | | |  
Qy 895 DSYGKBEYSEFFEGQSASMDVAKQDNRAKNRYGNIAYDHSRVILQVDEDDPSDDYIN 954  
| | | | |  
Db 1353 DNLAFSYESIDPGQQTWEHSNLEVNKPKNYANVIAIDHSRVLLSAISGIPGSDYVN 1412  
| | | | |  
Qy 955 ANYIDILWLDYGRQPSHYIATQGPVHTVDFWRWVWQBOBOSACIVMTNLVEVGRVKCY 1014  
| | | | |  
Db 1413 ANYI-----DGYRKNAVYATQGLSLPETFQDFWRMIWEQRSATVMMTKLEERSVRKD 1466  
| | | | |  
Qy 1015 KYWPD-DTEVVYGDFAKTCVEMEPLAEYVVRFTLLERGCYNEIREVKQPHFTGWPDHGVPY 1073  
| | | | |  
Db 1467 QYWSRGTFTHGLVQVLTLLDTVELATYCVRTFALYKNGSSSEKREVRQQTAMPDHPGVE 1526  
| | | | |  
Qy 1074 HATGLLSFIRRVKLSNPPSAGPIVHCSAGAGRTGCIYIDIMLDMABREGVVDIYNCVK 1133  
| | | | |  
Db 1527 HPTFLAFLRVKTCNPPDAGPMVHCSAGVGTGCFIVIDAMLERIKHEKTVDIYGHVT 1586  
| | | | |  
Qy 1134 ALRRRINMVTESQYIPIHDAILEACLCGETAIPVCEFAKAYPMIIRIDQSTNSHLKD 1193  
| | | | |  
Db 1587 LMRQNRNVVQTEQYIFIHDALEAVTCGTEVPARNLYAIQKLTQIETGENVTGMEL 1646  
| | | | |  
Qy 1194 EFQTLINSVTPRLOAEDCSIACLPRNHDKNRFMDMLPPDRCLPFLITIDQ-BSSNYINAAL 1252  
| | | | |  
Db 1647 EFKRLAS--SKAHTSRFISANLPCNKNRILVNIIMPYESTRVCLQPIRGVSGSDYINASF 1704  
| | | | |  
Qy 1253 MDSYRQPAAFIVTQVPLPNTVKDFWRLVYDYGCTSIIVMLNEVDL--SOGCPQYWPPEGML 1310  
| | | | |  
Db 1705 IDGYRQKAYATATQGLAETTEDFWRLWEHNSITIVMLTKLREMGREKCHQYWPAAERSA 1764  
| | | | |  
Qy 1311 RYGPITQVECMSCMDCDVINRIFRNICNTRPQEGY-LMVQOPQYILGWASHREVPQSKRSF 1369  
| | | | |  
Db 1765 RYQYFVVDpMA--EYNNPQVILREFKVTDAARDQGSRTVRQQTDM-PEQGVPKSGEGF 1820  
| | | | |  
Qy 1370 LKLLILOVEKQBECEBEGERTIIHCLNGGGBSGMFCAGIIVVMKRNQNVVDVEHAVKTL 1429  
| | | | |  
Db 1821 IDFIQGVHKTKEFGQ-QDGPISVHCSAGVGTGVFTISILVERMRVGEVVDIFQTVKML 1879  
| | | | |  
Qy 1430 RNSKNMYEAPQYRQCYDVALEYLES 1456  
| | | | |  
Db 1880 RTQRPMVQTEQYQFSRAALEYLG 1906  
| | | | |





QY	1437	VEAPEQRFCVDVALEYLS	1456
DB	1838	VQTEDEYQCFQALEYLGS	1857
RESULT 14			
D54689	protein-tyrosine-phosphatase (BC 3.1.3.48), receptor type delta, splice form D precursor N;Alternate names: MPTP delta type D N;Contains: protein tyrosine phosphatase, receptor type delta, splice form A C;Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 A;Accession: D54689; A54689 R;Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H. Mol. Cell. Biol. 13, 5513-5523, 1993 A;Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized A;Reference number: A54689; MUID:93360986; PMID:8355697 A;Accession: D54689 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1691 <MIZ> A;Cross-references: UNIPROT:Q64487 A;Experimental source: brain A;Note: sequence inconsistent with nucleotide translation A;Note: sequence inconsistent with NCBI backbone (NCBIN:137486, NCBIP:136537) A;Accession: A54689 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-398,799-1691 <MIZ> A;Experimental source: brain A;Note: sequence inconsistent with nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:136522, NCBIP:136524) C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology: ogy C;Keywords: alternative apolipin homology<IMM3> F;42-95/Domain: immunoglobulin homology<IMM3> F;114-196/Domain: fibronectin type III repeat homology<FN3> F;1075-1691/Domain: leukocyte common antigen cytosolic domain homology<LAC> F;1449-1671/Domain: protein-tyrosine-phosphatase homology<PTP2> F;1333/Active site: Cys (phosphotyrosine intermediate) #status predicted F;1339/Binding site: substrate phosphate (Arg) #status predicted F;1623/Active site: Cys (phosphotyrosine intermediate) #status predicted F;1629/Binding site: substrate phosphate (Arg) #status predicted		
Query Match 18.6%; Score 1452.5; DB 1; Length 1691;			
Best Local Similarity 28.7%; Pred. No. 4e-89;			
Matches 414; Conservative 205; Mismatches 466; Indels 359; Gaps 42;			
QY	253	SFLQEVTKDQLRYCVTOSRGSGVSNPAQLIVREPPRIAPPOLLGV--GPTYLLI	309
DB	361	SYRLQGLKPNLSYFRLSATSPOQGAIST-AETISARTMQPSAPPDQISCTSPSSILV	419
QY	310	QLNANSIGDGPIILK-EVEYRTSGSWETHAV-----NAPTYKLWHLDPDTEYIRVL	363
DB	420	SWOPPVVKONGIIITSLKYAAVDGEDYKPHEIIGNSSDTTKYLLEQEKWTXY--RIT	477
QY	364	LTRFGEGGTGLPGPLITRTKCAEPWRTPKTLIAEIQARRIAVDWES-----LG	413
DB	478	VTAHTDVGPWPESLVLRDDEVSPGPRKEVEAVNATAVKVSRSPVPNKHQOQIRG	537
QY	414	YNITRCHTFNVTTICYHYFRGHNS-----RADCLDM-----	444
DB	538	YQV-----HYVMKNGEPKSAMLKVMADADAQDMIISGLQPETSYSLTVTAYT	585
QY	445	-----DPKAQHVVNHLPPTVNLSKMLTNPE-----G	473
DB	586	TKGDGARSKPLVSTTGTSVGFKPRLVINH----TQMNTALIQWHPPVDTFGLGYRLKFG	641
QY	474	RK-----ESBETIIQTID-----EDVGGPV	492
DB	642	RKDMEPLTLTFSEKEDHFATDIHKCASVVFPLSARNKVGFGEEMVKVISVPEEIPITGF	701
QY	493	PVKSLOQTGFENKIFLNWKEPL--EPNGIITOYEVSYSIRSFPDPAVPVAG---PPQTVS	547

Db 1682 YLGS 1685

RESULT 15

CS4689

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor

N:Alternate names: MPP delta type B/C

N:Contains: protein tyrosine phosphatase, receptor type delta, splice form C

C:Species: Mus musculus (house mouse)

C:Date: 25-Apr-1995 #sequence\_revision 19-May-1995 #text\_change 09-Jul-2004

C:Accession: CS4689; B54689

R:MiZuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.

Mol. Cell. Biol. 13, 5513-5523, 1993

A:Title: MPP delta, a putative murine homolog of HTP delta, is expressed in specialized

A:Reference number: A54689; MUID:93360986; PMID:8355697

A:Accession: CS4689

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1894 <MIZ>

A:Cross-references: UNIPROT:Q64487

A:Experimental source: brain; splice form B

A:Note: sequence inconsistent with nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBI:137487)

A:Accession: B54689

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <MIZ>

A:Experimental source: brain; splice form C

A:Note: sequence inconsistent with nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBI:136530)

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; ocy

C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd

F:45-107/Domain: immunoglobulin homology <IMM1>

F:245-299/Domain: immunoglobulin homology <IMM2>

F:317-399/Domain: fibronectin type III repeat homology <FN3A>

F:1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:1536/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1542/Binding site: substrate phosphate (Arg) #status predicted

F:1826/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1832/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.6%; Score 1452.5; DB 2; Length 1894;

Best Local Similarity 28.7%; Pred. No. 4.8e-89;

Matches 414; Conservative 205; Mismatches 466; Indels 359; Gaps 42;

QY 253 SPRLQEVTKTDQDLVRCVTSQSERGSGVNFALIVREPPRIAPQLLGV---GPTYLLI 309

Db 564 SYRLOGLPNSLYYFRLSATSPQGLGAST-ABISARTWQKSPAPQDISCTSPSTSLIV 622

QY 310 QLNANSIIGDGPILIK-EVEYEMTSGSWTETHAV-----NAPTKYKLHLPDPTYEIRVL 363

Db 623 SQPPPPVEKQNGIITEYSLKYAAVDGEDYKPEHIGNSDDTKYLLEQLEKWTET--RIT 680

QY 364 LTRPQEGGTLQPPPLITTKCAEPWPTKTKIAIQAIRIANDWES-----LG 413

Db 681 VTAHTDVGWPBESLSVLTDEDPSPPKVEAVEAVNATAVKVSWRSPVPNKQHGQIRG 740

QY 414 YNITRCHTFNVTVCHYFRGHNES-----RADCLDM----- 444

Db 741 YQV-----HYVKMENGEPKSAMLKDVMLADAQMDIISGLQPETSYSLVTAVT 788

QY 445 -----DPKAPQVWVHLPPYTVNLSKMLTNP-----G 473

Db 789 TKGDGARKPKLVSTVTSVPGKPRLVINH-----TQNTALIQWHPVDTFGLQGYRLKEG 844

QY 474 RK-----ESEETIQT-----EDVPGPV 492

Db 845 RKMDEPLTLTLEPSEKEDHPTATDIHKGASYVFRLSARNKVGFGGEEMVKREISVPEIPTGF 904

QY 493 PVKSLQGTSFENKIFLNWKEPL--EPNGIITQYEVSYSSIRSFDDPAVPVAG---PPQTVS 547

Db 905 PQLHSEGTSTSTSVQLSQPPVLAERNGVITKTYLLYRDINV--PLLPMEHLIVPADTSM 962

QY 548 NLWNSTHHVFMHLHPGTTYOFFFRASTVKGFGPATAINVTNINISAPSLPDYEGVDASL-- 605

Db 963 TLTG-----LKSDDTYDVVKVRAHTSKRGP-----YSPSVQFRTLP-----VDQSMFA 1005

QY 606 ----NETATTITVLLR----PAQAKGAPISAYQI-----VVQOLPHPTKR----EAGAMEC 650

Db 1006 KNFHVKAMKTSVLLSWEIENYNNPALSKFFMMQKMWEEVDGRATQKLVNKLPEKS 1065

QY 651 YQVPVTVQNALSGGAPYFAELPPG-----NLPE----- 680

Db 1066 YSPVLTVNRGSAGGLQHRVTAKTAPDVLRTKPAFIGTKNLDGMTVQLPDVPAENIKGY 1125

QY 681 -----P 681

Db 1126 YIIIVPLKSRGKFIKPWESPDEMEDELLEKEISRKRISRYGREVELKPYIAAHFDVLP 1185

QY 682 APFTVGNRTYKGFNPPLAPRKGYNIYFQAMSVSEKETKTQCVRIATKAAATEPEVIP 741

Db 1186 TEFTLGDDKHGGFTNKOLQGQY-VFFVLAVMDHAESK-----MYATSPYSDPVSMDL 1240

QY 742 DPAKQTDORVVKIAGISAGIL--VEILLVIVIVIKSKL-AKKRKDAMGNTROEMTHV 798

Db 1241 DPQPIITDBEGLIWMVGPVLAVFIIICIVIAILLYKRAESESRSKSLPNSKEVPSH-- 1298

QY 799 NAMDRSYADOSTLHAEDPLSLTFMDQHNFSRPLPNDPLVPTAVLDENHSATAESRLLDV 858

Db 1299 -----HPTDFVELRLN----- 1310

QY 859 PRYLCEGTSPYQGL--HPAIRVADLLQHLNLMKTSDSYGPKEEYESFEGOSASWDV 916

Db 1311 -----FQPPGMASHPPPILELADHIEELKANLNKFSQEVESIDPGQOFTWEH 1359

QY 917 AKQDNRAKNRYGNIAYDHSRVILQPVDDPSDDYINANYIDILWYLDGQYRPSHIAT 976

Db 1360 SNLEVNPKRYANVIAVDHRSVLLSALGIPGSDYVNAVY-----DGYRKQNAVYAT 1413

QY 977 QGPVHTYDPMVMWQEQSACIWMVNLVEVGRVKYKWPD-DTEVYGDFKTCVEME 1035

Db 1414 QGSLPETFGDFWRIM-EQEAETVMVMTKLESRVRKCDQYWPSPRGTTGVLGVQLTLDTV 1472

QY 1036 PLAEEVVRTFTLERRGYNEIREVKQHFHTGHPDHPVHATGLLSFIRRVKLSNPPSAGP 1095

Db 1473 ELT-YCVRTFALYNGSSEKRRKVKQFOFTAMPDGHGVPEHPPTFLAFLRRVKTCPDAGP 1531

QY 1096 IVVHCSAGAGRTGCVIIVIDIMDMAEREGVVVDIYNCVKALRSRRINMVQTEEQYIFIHDA 1155

Db 1532 MVVHCSAGVGRGTCFVIDAMLERIKHEKTVDIYGHVTLMAQRNVMVQTEDQYIFIHDA 1591

QY 1156 ILEACLCGETAIPVCEPKAAVDMIRDSQNSSHLKDEFOFOTLNSVTPRLQAECSIACL 1215

Db 1592 LLEAVTCGTEVPARNLYAYIQKLTQIBTGENVGTMELEFKRLAS--SKAHTSRFISANL 1649

QY 1216 PRNHDKSRFMDLPPDRCLPELITIDG-ESSNYIINAALMDSYROPAAFIQVPLPNTVK 1274

Db 1650 PCNFKFRLNIMPYESGRVCLQPIRGVSGSDYNASLDGTYRQOKAVIATQGLPAETTE 1709

QY 1275 DFWRLLVDYDGTSTVMLNEVDL--SQGCPQVWPEGMRLRYGPIQVCMSCMDCDVINRI 1332

Db 1710 DFWRMLHEHNTIIVMLTKLEMGREKCHQWPAERSARYQYFVVDPA-----EYNMPQVI 1766

QY 1333 FRIENLTPQBGYLMVOQFOYGLWASHREVPGSKRSFLKLIQVKEWQEECEBGRITII 1392

Db 1767 LRBFKVTDARDQSRVRFQFTDW-PEQGVPKSGEGFIDFICQVHKTEQEQ-DEPISV 1824

QY 1393 HCLNGGSGSMFCALIGIVEMVKQNVVDVFAVKTLENSKPNMVEAPEQVFCYDVALE 1452

Db 1825 HCSAGVGTGFTILSIVLERMYEGVVVDIFQTVKQLRTQRPAMVQTEDQYFCRAALE 1884

QY 1453 YLES 1456

Db 1885 YLGS 1888

Search completed: June 1, 2005, 13:56:28  
Job time : 51.7393 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:32:43 ; Search time 169.044 Seconds  
(without alignments)  
4413.635 Million cell updates/sec

Title: US-09-887-669-1  
Perfect score: 7809  
Sequence: 1 MDVAAAALPAFVALWLLYPW.....EAPQYRFCVDVALEYLESS 1457

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7809	100.0	1457	1 PTPK_MOUSE	P35822 mus musculus
2	7592.5	97.2	1440	2 Q6WJ2	Q86w67 mus musculus
3	7589.5	97.2	1440	2 Q6WJ2	Q86w67 mus musculus
4	7582	97.1	1439	1 PTPK_HUMAN	Q15262 homo sapien
5	4822.5	61.8	1486	2 Q6WJ2	Q86w67 mus musculus
6	4812.5	61.6	1452	1 PTPM_HUMAN	P28827 homo sapien
7	4793.5	61.4	1452	1 PTPM_MOUSE	P28828 mus musculus
8	4732.5	60.6	1390	2 Q6V148	Q86v60 homo sapien
9	4675	59.9	1434	2 Q6V148	Q6v148 gallus gall
10	4619	59.1	1436	2 Q00197	Q00197 homo sapien
11	4610	59.0	1436	2 Q22850	Q22850 homo sapien
12	4602.5	58.9	1439	2 P78399	P78399 homo sapien
13	4597	58.8	1436	2 Q35564	Q35564 mus musculus
14	4591	58.8	1436	2 P70125	P70125 mus musculus
15	4579	58.6	1454	1 PPT_MOUSE	Q99m80 mus musculus
16	4542.5	58.2	1463	1 PPT_HUMAN	O14522 homo sapien
17	4497.5	57.6	1434	2 Q6E5N7	Q6e5n7 brachydanio
18	4426	56.7	844	2 Q8C462	Q8c462 mus musculus
19	4359	55.8	1442	2 Q22735	Q22735 homo sapien
20	4339	55.6	1430	1 PTPU_HUMAN	Q92729 homo sapien
21	3482.5	44.6	1195	2 Q9PUX2	Q9pum2 xenopus lae
22	2665	34.1	492	2 Q8IV94	Q8iv94 homo sapien
23	2630.5	33.7	990	2 Q6PDN0	Q6pdn0 mus musculus
24	2534	32.4	502	2 Q6WJ2	Q86w67 mus musculus
25	2270	29.1	465	2 Q9IB99	Q9ib99 potamotrygo
26	1918	24.6	617	2 Q66JY9	Q66jy9 mus musculus
27	1689.5	21.6	542	2 P70643	P70643 rattus norv
28	1527.5	19.6	1788	2 Q9IA70	Q9ia70 xenopus lae
29	1526	19.5	1502	2 Q9UM81	Q9um81 homo sapien
30	1514.5	19.4	1501	2 Q9QW00	Q9qw00 rattus sp.
31	1511.5	19.4	1501	2 Q7TT17	Q7t17 mus musculus

32	1508	19.3	1529	2	Q6PG86	Q6pg86 mus musculus
33	1506.5	19.3	1887	2	Q9QW67	Q9qw67 rattus sp.
34	1500	19.2	278	2	Q8C819	Q8c819 mus musculus
35	1495	19.1	1499	2	Q90815	Q90815 gallus gall
36	1495	19.1	1898	2	Q9EQ17	Q9eq17 mus musculus
37	1494	19.1	1898	2	Q84604	Q84604 r protein-t
38	1492.5	19.1	1897	1	PTPF_HUMAN	P10586 homo sapien
39	1487.5	19.0	1948	1	PTNS_HUMAN	Q13332 homo sapien
40	1485.5	19.0	1254	2	Q8VBV0	Q8vbv0 mus musculus
41	1482.5	19.0	1912	1	PTPD_HUMAN	P23468 homo sapien
42	1480	19.0	1898	2	Q86W50	Q86w50 homo sapien
43	1477	18.9	273	2	Q99KV5	Q99kv5 mus musculus
44	1477	18.9	1191	2	Q7Z3X4	Q7z3x4 homo sapien
45	1461	18.7	1889	2	Q7Q0X2	Q7q0x2 anopheles g

#### ALIGNMENTS

##### RESULT 1

PTPK\_MOUSE  
ID\_PTPK\_MOUSE STANDARD; PRT; 1457 AA.  
AC P35822;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DB Receptor-type protein-tyrosine phosphatase kappa precursor  
DB (EC 3.1.3.48) (R-PTP-kappa).  
GN Name=Ptpk; Synonyms=Ptpk;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RI; TISSUE=Brain;  
RX MEDLINE=93233655; PubMed=8474452;  
RA Jiang Y.P., Wang H., D'Eustachio P., Musacchio J.M., Schlessinger J., Sap J.;  
RA "Cloning and characterization of R-PTP-kappa, a new member of the receptor protein tyrosine phosphatase family with a proteolytically cleaved cellular adhesion molecule-like extracellular region.";  
RL Mol. Cell. Biol. 13:2942-2951(1993).  
CC -I- FUNCTION: Regulation of processes involving cell contact and adhesion such as growth control, tumor invasion, and metastasis.  
CC Forms complexes with beta-catenin and gamma-catenin/plakoglobin.  
CC Beta-catenin may be a substrate for the catalytic activity of PTP-kappa.  
CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -I- TISSUE SPECIFICITY: High levels in liver and kidney. Lower levels in lung, brain and heart. Not seen in spleen and testis.  
CC -I- DEVELOPMENTAL STAGE: Developmentally regulated with highest expression found in developing areas or in areas capable of developmental plasticity.  
CC -I- PFM: This protein undergoes proteolytic processing.  
CC -I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Receptor class 2B subfamily.  
CC -I- SIMILARITY: Contains 4 fibronectin type III domains.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -I- SIMILARITY: Contains 1 MAM domain.  
CC -I- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; L10106; AAA40021.1; --

DR	PIR; A48066; A48066.	QY	121	TLNLLVRVNGKPLANPIWNVTGFTGRDWLRAELAVSTFWPNEYQVIFAEYSGGSGYIA	180
DR	HSSP; P28827; 1RPM.	QY	121	TLNLLVRVNGKPLANPIWNVTGFTGRDWLRAELAVSTFWPNEYQVIFAEYSGGSGYIA	180
DR	MGD; MGI:103310; Ptpk.	QY	181	IDDIQVLSYPCDKSPHFLRLGDVEVNAQONATFQCIATGRDAVHNKWLQRRNGSDI PVA	240
DR	InterPro; IPR003961; FN_III.	QY	181	IDDIQVLSYPCDKSPHFLRLGDVEVNAQONATFQCIATGRDAVHNKWLQRRNGSDI PVA	240
DR	InterPro; IPR008957; FN_III-like.	QY	241	QTKNINHRFAASFRLOEVTKTDQDLRCVTSQSERGSGVSNPAQLIVREPPRIAPPOLL	300
DR	InterPro; IPR003599; IG.	QY	241	QTKNINHRFAASFRLOEVTKTDQDLRCVTSQSERGSGVSNPAQLIVREPPRIAPPOLL	300
DR	InterPro; IPR007110; IG-like.	QY	301	GVGPTYLLIQLNANSIIGDGPILLKEVEYRTSGSWTETHAVNAPTYKLMHLDPDTEYI	360
DR	InterPro; IPR000998; MAM.	QY	301	GVGPTYLLIQLNANSIIGDGPILLKEVEYRTSGSWTETHAVNAPTYKLMHLDPDTEYI	360
DR	InterPro; IPR000387; TYR_phosphatase.	QY	361	RVLLTRPGEGETGLPGPPLITRTKCAEPMRTPKTLKIAEIQARRIADWESLGYNITRCH	420
DR	InterPro; IPR000242; Tyr_PP.	QY	361	RVLLTRPGEGETGLPGPPLITRTKCAEPMRTPKTLKIAEIQARRIADWESLGYNITRCH	420
DR	Pfam; PF00041; fn3; 2.	QY	421	TFNVTICVHYFRGHNESRADCLMDPKAPQHVNVHLPPYTNVSLKMLITNPEGRKESSET	480
DR	Pfam; PF00629; MAM; 1.	QY	421	TFNVTICVHYFRGHNESRADCLMDPKAPQHVNVHLPPYTNVSLKMLITNPEGRKESSET	480
DR	PRINTS; PRO00020; MAMDOMAIN.	QY	481	IIQTDDEVPVGVKSLQCTSFENKIFLNWKEPLEPNCIIITQYEVSYSSIRSFDPAPVA	540
DR	PRINTS; PRO00700; PRTPHPHTASE.	QY	481	IIQTDDEVPVGVKSLQCTSFENKIFLNWKEPLEPNCIIITQYEVSYSSIRSFDPAPVA	540
DR	SMART; SM00060; FN3; 3.	QY	541	GPPQTVSNLWNSTHVFMHLHPGTYQFFIRASTVKGFGPATAINVTNINAPSLPDYEG	600
DR	SMART; SM00409; IG; 1.	QY	541	GPPQTVSNLWNSTHVFMHLHPGTYQFFIRASTVKGFGPATAINVTNINAPSLPDYEG	600
DR	SMART; SM00137; MAM; 1.	QY	601	VDASINETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQNA	660
DR	SMART; SM00194; PTPC; 2.	QY	601	VDASINETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQNA	660
DR	PROSITE; PS0853; FN3; 4.	QY	661	LSGGAPYFAAEELPPGNLPEPAPFTVGNRTYKGFNPPPLAPRKGYNIYFQAMSSVEKET	720
DR	PROSITE; PS0835; IG LIKE; 1.	QY	661	LSGGAPYFAAEELPPGNLPEPAPFTVGNRTYKGFNPPPLAPRKGYNIYFQAMSSVEKET	720
DR	PROSITE; PS00740; MAM 1; 1.	QY	721	KTQCVRIATKAAATEEPEVI PDPKATQDTRVVKIAGISAGILVFI LLLLVII VVKSKLA	780
DR	PROSITE; PS0060; MAM 2; 1.	QY	721	KTQCVRIATKAAATEEPEVI PDPKATQDTRVVKIAGISAGILVFI LLLLVII VVKSKLA	780
DR	PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.	QY	781	KRRKDMAGNTQEMTHMVNMDRSYADQSTLHAEDPLSLTFMDQHNFPRLPNDPLVPTA	840
DR	PROSITE; PS00556; TYR_PHOSPHATASE 2; 2.	QY	781	KRRKDMAGNTQEMTHMVNMDRSYADQSTLHAEDPLSLTFMDQHNFPRLPNDPLVPTA	840
DR	PROSITE; PS00555; TYR_PHOSPHATASE PTP; 2.	QY	841	VLDENHSATAESSRLLDVPRYLCEGTSPYQTLHPAIRVADLLOHINLMKTSYSGPK	900
KW	Glycoprotein; Hydrolase; Immunoglobulin domain; Protein phosphatase;	QY	841	VLDENHSATAESSRLLDVPRYLCEGTSPYQTLHPAIRVADLLOHINLMKTSYSGPK	900
KW	Receptor; Repeat; Signal; Transmembrane.	QY	901	EYESFPEGQASWDVAKDQNRKNGNI IAYDHSRVILQPVDEDDPSSDYINANYIDI	960
FT	SIGNAL 1 25 Potential.	QY	901	EYESFPEGQASWDVAKDQNRKNGNI IAYDHSRVILQPVDEDDPSSDYINANYIDI	960
FT	CHAIN 26 1457 Receptor-type protein-tyrosine phosphatase kappa.	QY	961	WLYRDGYQRP SHYIATQGVHETVDFWRVMWQEQSACI VMVTNILVEGRVKCYKWPDD	1020
FT	DOMAIN 26 752 Extracellular (Potential).	QY	1021	TEVYGDFFKTCVMEPPLAEYVVRTTLERRGNEIREVKQHFHTGPDHGVPHATGLLS	1080
FT	TRANSMEM 753 774 Potential.	QY	1021	TEVYGDFFKTCVMEPPLAEYVVRTTLERRGNEIREVKQHFHTGPDHGVPHATGLLS	1080
FT	DOMAIN 775 1457 Cytoplasmic (Potential).	QY	1081	FIRRVKLSNPSPSAGPIVHCSAGARTGCIYVIDIMLMAEREGVVDIYNCVKALRSRI	1140
FT	DOMAIN 30 193 MAM.	QY	1081	FIRRVKLSNPSPSAGPIVHCSAGARTGCIYVIDIMLMAEREGVVDIYNCVKALRSRI	1140
FT	DOMAIN 195 280 Ig-like C2-type.	QY	1141	NMVQTEQYIIFTHDAILEACLCGETAIPVCBFAAYFDMIRIDSQTNSSHLKDEFQTLNS	1200
FT	DOMAIN 290 382 Fibronectin type-III 1.	QY	1141	NMVQTEQYIIFTHDAILEACLCGETAIPVCBFAAYFDMIRIDSQTNSSHLKDEFQTLNS	1200
FT	DOMAIN 388 484 Fibronectin type-III 2.	QY			
FT	DOMAIN 489 598 Fibronectin type-III 3.	QY			
FT	DOMAIN 589 688 Fibronectin type-III 4.	QY			
FT	DOMAIN 922 1158 Protein-tyrosine phosphatase 1.	QY			
FT	DOMAIN 1218 1452 Protein-tyrosine phosphatase 2.	QY			
FT	ACT_SITE 1100 1100 Phosphocysteine intermediate (By similarity).	QY			
FT	ACT_SITE 1394 1394 Phosphocysteine intermediate (By similarity).	QY			
FT	DISULFID 215 269 N-linked (GlcNAc... ) (Potential).	QY			
FT	CARBOHYD 100 100 N-linked (GlcNAc... ) (Potential).	QY			
FT	CARBOHYD 139 139 N-linked (GlcNAc... ) (Potential).	QY			
FT	CARBOHYD 210 210 N-linked (GlcNAc... ) (Potential).	QY			
FT	CARBOHYD 415 415 N-linked (GlcNAc... ) (Potential).	QY			
FT	CARBOHYD 423 423 N-linked (GlcNAc... ) (Potential).	QY			
FT	CARBOHYD 435 435 N-linked (GlcNAc... ) (Potential).	QY			
FT	CARBOHYD 461 461 N-linked (GlcNAc... ) (Potential).	QY			
FT	CARBOHYD 551 551 N-linked (GlcNAc... ) (Potential).	QY			
FT	CARBOHYD 585 585 N-linked (GlcNAc... ) (Potential).	QY			
FT	CARBOHYD 589 589 N-linked (GlcNAc... ) (Potential).	QY			
FT	CARBOHYD 606 606 N-linked (GlcNAc... ) (Potential).	QY			
FT	CARBOHYD 689 689 N-linked (GlcNAc... ) (Potential).	QY			
SQ	SEQUENCE 1457 AA; 164185 MW; 19D4B99B7ECE8605 CRC64;	QY			
Query Match					100.0%; Score 7809; DB 1; Length 1457;
Best Local Similarity					100.0%; Pred. No. 0;
Matches 1457; Conservative					0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MDVAAALPAFVALWLLYPNLLGSLGQFSAGGCTFDDGPGACDYHQDLYDDFEWVHS	60			
Db	1 MDVAAALPAFVALWLLYPNLLGSLGQFSAGGCTFDDGPGACDYHQDLYDDFEWVHS	60			
QY	61 AQEPHYLPPEMPQGSYMWVDSSNHDPEKARLQLPTMKENDTHCIDFSYLLYSQKGLNPG	120			
Db	61 AQEPHYLPPEMPQGSYMWVDSSNHDPEKARLQLPTMKENDTHCIDFSYLLYSQKGLNPG	120			

Qy 1201 VTPRLQEDCSIACLPRNHDKNRFDMLPPDRCLPFLITIDGSSNINAAALMDSYRQPA 1260  
 Db 1201 VTPRLQEDCSIACLPRNHDKNRFDMLPPDRCLPFLITIDGSSNINAAALMDSYRQPA 1260  
 Qy 1261 AFIVTQPLPNTVXDFWRLVVDYDCTSVMLNEVDLSQGCPOYWPBEGMLRYGPIQVECM 1320  
 Db 1261 AFIVTQPLPNTVXDFWRLVVDYDCTSVMLNEVDLSQGCPOYWPBEGMLRYGPIQVECM 1320  
 Qy 1321 SCSDCDVINRIFRICNLTRPQGYLMVQOQYILGWASHREVPGSKRSFLKLILOVEKWQ 1380  
 Db 1321 SCSDCDVINRIFRICNLTRPQGYLMVQOQYILGWASHREVPGSKRSFLKLILOVEKWQ 1380  
 Qy 1381 ECEBEGGRTIHCNGGSGRSGMFCAGIVVEMVKRQNVVDVFAVKTILRNSKNVVEAP 1440  
 Db 1381 ECEBEGGRTIHCNGGSGRSGMFCAGIVVEMVKRQNVVDVFAVKTILRNSKNVVEAP 1440  
 Qy 1441 EQYRFCYDVALEYLESS 1457  
 Db 1441 EQYRFCYDVALEYLESS 1457

RESULT 2  
 Q86WJ2 ID Q86WJ2 PRELIMINARY; PRT: 1440 AA.  
 AC Q86WJ2  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Mutant receptor type protein tyrosine phosphatase K (EC  
 DE 3.1.3.48)  
 DE Name=PTRPK;  
 GN Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Melanoma;  
 RX MEDLINE=22679345; PubMed=12794170;  
 RA Novellino L., Renkvist N., Rini F., Mazzocchi A., Rivoltini L.,  
 RA Greco A., Deho P., Squarcina P., Robbins P.F., Parmiani G.,  
 RA Castelli C.;  
 RT "Identification of a mutated receptor-like protein tyrosine  
 RT phosphatase kappa as a novel, class II HLA-restricted melanoma  
 RT antigen.";  
 RL J. Immunol. 170:6363-6370(2003).  
 DR EMBL; AF533875; AAC49502.1; -;  
 DR HSSP; P28827; IRPM.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR003961; FN.III.  
 DR InterPro; IPR008957; FN.III-like.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR000998; MAM.  
 DR InterPro; IPR00387; Tyr\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00047; ig; 1.  
 DR Pfam; PF00629; MAM; 1.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00020; MAMDOMAIN.  
 DR PRINTS; PR00700; PRTPHPTASE.  
 DR SMART; SM00060; FN3; 3.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00137; MAM; 1.  
 DR SMART; SM00194; PTPc; 2.  
 DR PROSITE; PS50853; FN3; 3.  
 DR PROSITE; PS50835; IG\_LIKE; 1.

DR PROSITE; PS00740; MAM\_1; 1.  
 DR PROSITE; PS0060; MAM\_2; 1.  
 DR PROSITE; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_ptp; 2.  
 KW Glycoprotein; Hydrolase; Receptor.  
 SQ SEQUENCE 1440 AA; 162271 MW; B140BC621878586A CRC64;

Query Match 97.2%; Score 7592.5; DB 2; Length 1440;  
 Best Local Similarity 97.5%; Pred. No. 0;  
 Matches 1421; Conservative 12; Mismatches 6; Indels 19; Gaps 3;

Qy 1 MD-VAAALPAFVALMILLYPWPILLGSLGQFSAAGGCTFDDGPGACDTHODLYDDPFWHV 59  
 Db 1 MDTAAALPAFVALLLSLSPWLLGSAQGGFSAGGCTFDDGPGACDTHODLYDDPFWHV 60  
 Qy 60 SAQEPHYLPPEMPCGYSVMVVDSSNHDPEKARLQPTMKENDTHCIDFSYLLYSQKGLNP 119  
 Db 61 SAQEPHYLPPEMPCGYSYIVDSSDHDPEKARLQPTMKENDTHCIDFSYLLYSQKGLNP 120  
 Qy 120 GTLNILVRNKGPLANIMNVGTGTRDMLRAELAVSTFWPNEYQVIFEAESGSGSYI 179  
 Db 121 GTLNILVRNKGPLANIMNVGTGTRDMLRAELAVSTFWPNEYQVIFEAESGSGSYI 180  
 Qy 180 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQATFQCIATGRDAVHNKLMLORRNGEDIPV 239  
 Db 181 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQATFQCIATGRDAVHNKLMLORRNGEDIPV 240  
 Qy 240 AQTKNINHRFAASFRLOEVTQDQDLRYCVTOSERGSGVSNFAQLIVRPPRIAPQOL 299  
 Db 241 AQTKNINHRFAASFRLOEVTQDQDLRYCVTOSERGSGVSNFAQLIVRPPRIAPQOL 300  
 Qy 300 LGVGPTVLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDEYE 359  
 Db 301 LGVGPTVLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDEYE 360  
 Qy 360 IRVLLTRPGEGETGLPGPPLITRTKCAEPMTPTKTKIAEIQAARRIADVDESLEYNITRC 419  
 Db 361 IRVLLTRPGEGETGLPGPPLITRTKCAEPMTPTKTKIAEIQAARRIADVDESLEYNITRC 420  
 Qy 420 HTFNVTICVHYFRGHNESRADCLMDPKAPQHVNVHLPPTYNVSLSKMLTNPEGRKSEEE 479  
 Db 421 HTFNVTICVHYFRGHNESKADCLMDPKAPQHVNVHLPPTYNVSLSKMLTNPEGRKSEEE 480  
 Qy 480 TIIQTDEDVPGVPVKSLOQTSFENKIFLNKWKPLENGIITQYEVSYSSIRSDPAVPV 539  
 Db 481 TIIQTDEDVPGVPVKSLOQTSFENKIFLNKWKPLENGIITQYEVSYSSIRSDPAVPV 540  
 Qy 540 AGPPQTVSNLWNSTHVFHMLHPGTTVQFFIRASTVKGFGPATINVTNISAPSLPDYE 599  
 Db 541 AGPPQTVSNLWNSTHVFHMLHPGTTVQFFIRASTVKGFGPATINVTNISAPSLPDYE 600  
 Qy 600 GVDASLNETHATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQN 659  
 Db 601 GVDASLNETHATITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPTVYQN 660  
 Qy 660 ALSCGAPYFAELPPGNLPEPAPFTVGDNRKTYGFWNPPLAPRKGNINIFQAMSSVEKE 719  
 Db 661 AMSGAPYFAELPPGNLPEPAPFTVGDNRKTYGFWNPPLAPRKGNINIFQAMSSVEKE 720  
 Qy 720 TKTCQVRIATKAAATEEPEVIPPAPKQTRDVVKIAGISAGILVFILLVIVIVKSKL 779  
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 Qy 780 AKRKQDAMGNTRQEMTHVMNMDRSYADQSTLHAEDPLSLTFMDQHNFSRLPNDPLVPT 839  
 Db 781 AKRKQDAMGNTRQEMTHVMNMDRSYADQSTLHAEDPLSLTFMDQHNFSRLPNDPLVPT 832  
 Qy 840 AVLDEHNSATAESSRLLDVPRYLCEGTSPYQGLHPAIRVADLLQHLINLMKTSDSYGF 899  
 Db 833 ----ENHSATAESSRLLDVPRYLCEGTSPYQGLHPAIRVADLLQHLINLMKTSDSYGF 888  
 Qy 900 KEEYESFFEQOSASWDVAKKQDNRAKNRYGNIITAYDHSRVILQPVEDDPSDDINANYID 959

Db 889 KEEYESFEGQSASWDVAKQNRKRNRYGNIIADHSRVILQPVEDDPSSDIYANNTI- 947  
Qy 960 IWLXRDGQRSHYIATQPVHETVYDFWRMVMWQSQSACIVMVTNLVVEGRVKCYKWPD 1019  
Db 948 ----DGQRSHYIATQPVHETVYDFWRMVMWQSQSACIVMVTNLVVEGRVKCYKWPD 1002  
Qy 1020 DTEVYGDPKVTCVEMEPALAEYVVRTFTLRRGYNEIREVKQPHFTGWPDPHGVPHATGLL 1079  
Db 1003 DTEVYGDPKVTCVEMEPALAEYVVRTFTLRRGYNEIREVKQPHFTGWPDPHGVPHATGLL 1062  
Qy 1080 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCTIVIMLDMAEREGVVDIYNCVKALRSRR 1139  
Db 1063 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCTIVIMLDMAEREGVVDIYNCVKALRSRR 1122  
Qy 1140 INNVQTEREQYIFIHDAILEACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDBEFQTLN 1199  
Db 1123 INNVQTEREQYIFIHDAILEACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDBEFQTLN 1182  
Qy 1200 SVTPRLQEDCSIACLPRNHDKNRPMMLPPDRCLPFLITIDGESSNVTINAAALMDSYRQP 1259  
Db 1183 SVTPRLQEDCSIACLPRNHDKNRPMMLPPDRCLPFLITIDGESSNVTINAAALMDSYRQP 1242  
Qy 1260 AAFIVTQYPLPNTVKDFWRLVYDYGCTSIWMLNEVDLSQGCPOYWPBEGMLRYGPIQVEK 1319  
Db 1243 AAFIVTQYPLPNTVKDFWRLVYDYGCTSIWMLNEVDLSQGCPOYWPBEGMLRYGPIQVEK 1302  
Qy 1320 MSCSMDCDVINRIFRICNLTRPOEGLVMVQOYILGWASHREVPGSKSFKLILIQVEKW 1379  
Db 1303 MSCSMDCDVINRIFRICNLTRPOEGLVMVQOYILGWASHREVPGSKSFKLILIQVEKW 1362  
Qy 1380 QBECEGEGRTIIHCLNGGSGMPCFCAIGIVVMYKQNVVDVHFVAKTLRNSKPNMVEA 1439  
Db 1363 QBECEGEGRTIIHCLNGGSGMPCFCAIGIVVMYKQNVVDVHFVAKTLRNSKPNMVEA 1422  
Qy 1440 PEQYRFDVDALEYLESS 1457  
Db 1423 PEQYRFDVDALEYLESS 1440  
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Q68DT8 PRELIMINARY; PRT; 1440 AA.  
ID Q68DT8  
AC Q68DT8;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE Hypothetical protein DKFZp686C2268.  
GN Name=DKFZp686C2268;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP SEQUENCE FROM N.A.  
RC TISSUE=Endometrium carcinoma cell line;  
RG The German cDNA Consortium;  
RA Ottenwaelder B., Obermaier B., DeutschenBaur S., Schaiipp A.,  
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CB749277; CAH18132.1; -.  
DR InterPro; IPR003961; FN.III.  
DR InterPro; IPR008957; FN.III-like.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR000998; MAM.  
DR InterPro; IPR003595; PTPc motif.  
DR InterPro; IPR000367; Tyr\_phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00041; fn3; 2.  
DR Pfam; PF00629; MAM; 1.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00020; MAMDOMAIN.

PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00137; MAM; 1.  
DR SMART; SM00194; PTPc; 2.  
DR SMART; SM00404; PTPc motif; 2.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR PROSITE; PS00740; MAM\_1; 1.  
DR PROSITE; PS00660; MAM\_2; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 2.  
DR PROSITE; PS0056; TYR\_PHOSPHATASE 2; 2.  
DR PROSITE; PS0055; TYR\_PHOSPHATASE\_PTP; 2.  
KW Glycoprotein; Hypothetical protein.  
SQ SEQUENCE 1440 AA; 162129 MW; 41BA5E4D6E0C0359 CRC64;  
Query Match 97.2%; Score 7589.5; DB 2; Length 1440;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 1420; Conservative 12; Mismatches 7; Indels 19; Gaps 3;  
Qy 1 MD-VAAALPAFVALWILYWPILGSLGQPSAGGCTPDDGPGACDYHQDLYDDFEWVHV 59  
Db 1 MDTTAAALPAFVALWILYWPILGSLGQPSAGGCTPDDGPGACDYHQDLYDDFEWVHV 60  
Qy 60 SAQSPHYLPPMPGSGSYMVVDSSNHDGCEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 119  
Db 61 SAQSPHYLPPMPGSGSYMVVDSSNHDGCEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 120  
Qy 120 GTNLILVRVNGKPLANPINWVTGTGRDMLRAELAVSTFWPNEYQVIFEAEVSGRSGYI 179  
Db 121 GTNLILVRVNGKPLANPINWVTGTGRDMLRAELAVSTFWPNEYQVIFEAEVSGRSGYI 180  
Qy 180 AIDDIQVLSYPCDSKSPHRLRGDVEVNAQNATQCIATGRDADAVHNKWLQRRNGEDIPV 239  
Db 181 AIDDIQVLSYPCDSKSPHRLRGDVEVNAQNATQCIATGRDADAVHNKWLQRRNGEDIPV 240  
Qy 240 AOTKNINHRRAAFRLQEVTKTDQDLYRCVCTQSERGSGVSNFAQLIVREPPRIAPPQL 299  
Db 241 AOTKNINHRRAAFRLQEVTKTDQDLYRCVCTQSERGSGVSNFAQLIVREPPRIAPPQL 300  
Qy 300 LGVGPTYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 359  
Db 301 LGVGPTYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 360  
Qy 360 IRVLLTRPGEGETGLPGPPLITRTKCAEPMPTPKTLKIAETQARRIADVWSLGNITRC 419  
Db 361 IRVLLTRPGEGETGLPGPPLITRTKCAEPMPTPKTLKIAETQARRIADVWSLGNITRC 420  
Qy 420 HTFNVTICYHYFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEE 479  
Db 421 HTFNVTICYHYFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEE 480  
Qy 480 TIIQTDEDVPGVPVKSLQGTSFENKIFLNKKEPLEPNGIITQYEVSVSSIRSPDPAVPV 539  
Db 481 TIIQTDEDVPGVPVKSLQGTSFENKIFLNKKEPLEPNGIITQYEVSVSSIRSPDPAVPV 540  
Qy 540 AGPPQTVSNLWNSTHVVFMHLHPGTYTQFFTRASTVKFGPATAINVTNINSAPLDPYE 599  
Db 541 AGPPQTVSNLWNSTHVVFMHLHPGTYTQFFTRASTVKFGPATAINVTNINSAPLDPYE 600  
Qy 600 GVDASLNATATTITVLLRPAQAKGAPISAYQIYVVEQLHPHRTKRGAGAMECYQVPTVYQN 659  
Db 601 GVDASLNATATTITVLLRPAQAKGAPISAYQIYVVEQLHPHRTKRGAGAMECYQVPTVYQN 660  
Qy 660 ALSGAPYFAAEALPPGNLPEPAPFTVGDNRNRTYKGFWMNPPPLAPRKGYNIYFOAMSVEKE 719  
Db 661 AMSGAPYFAAEALPPGNLPEPAPFTVGDNRNRTYKGFWMNPPPLAPRKGYNIYFOAMSVEKE 720  
Qy 720 TKTQCVRIATKAAATEEPEVIPPDAKQTDNRVVKIAGISAGILVFLILLVLIIVKSKL 779  
Db 721 TKTQCVRIATKAAATEEPEVIPPDAKQTDNRVVKIAGISAGILVFLILLVLIIVKSKL 780  
Qy 780 AKKRKDMGNTROEMTHVMNAMDRSYADQSTLHAEDPLSLTFMDQHNTPRLPNDPLVPT 839

Db 781 AKKRDANGNTRQEWTHWVWMDRSYADQSTLHAEDPLSITFMDQHNFSRY----- 832  
Qy 840 AVLDEHSATASRLLDVPRYLCEGTSPYQTLHPAIRVADLLQHINLMKTSDSYGF 899  
Db 833 -----ENHSATASRLLDVPRYLCEGTSPYQTLHPAIRVADLLQHINLMKTSDSYGF 888  
Qy 900 KEEYESFEGOSASMDVAKDONAKRYGNIIAYDHSRVLTQVEDDPSDDYINANYID 959  
Db 889 KEEYESFEGOSASMDVAKDONAKRYGNIIAYDHSRVLTQVEDDPSDDYINANYI- 947  
Qy 960 IWLXRDGYQRPESHYATQGPVHETVYDFWRMVWQEQSACIWMVTLNVEGVKCYKWPD 1019  
Db 948 -----DGVRPESHYATQGPVHETVYDFWRMVWQEQSACIWMVTLNVEGVKCYKWPD 1002  
Qy 1020 DTEVYGFKVTCEMEPLAEYVTRFTLRRGYNEIREVKQFHTGMPDGVPHATGLL 1079  
Db 1003 DTEVYGFKVTCEMEPLAEYVTRFTLRRGYNEIREVKQFHTGMPDGVPHATGLL 1062  
Qy 1080 SFTIRVKLSNPPSAGPIVHCSAGAGRTGCYIVIDIMLDMAERGVVDIYNCVKALRSR 1139  
Db 1063 SFTIRVKLSNPPSAGPIVHCSAGAGRTGCYIVIDIMLDMAERGVVDIYNCVKALRSR 1122  
Qy 1140 INMVQTEBQYIFIHDAILEACLCGETAIPVCEPKAAVDFMDIRIDSTQNSHLKDEFOTLN 1199  
Db 1123 INMVQTEBQYIFIHDAILEACLCGETAIPVCEPKAAVDFMDIRIDSTQNSHLKDEFOTLN 1182  
Qy 1200 SVTPRLQAECDSCIACLPNHDKNRMDMLPDRCLPFLITIDGSSNYINAALMDSYRQP 1259  
Db 1183 SVTPRLQAECDSCIACLPNHDKNRMDMLPDRCLPFLITIDGSSNYINAALMDSYRQP 1242  
Qy 1260 AAFITVQYPLNTVKDFWRLVYDYGCTSIWMLNEVDLSQGPQYWPPEGMLRYGPIQVEK 1319  
Db 1243 AAFITVQYPLNTVKDFWRLVYDYGCTSIWMLNEVDLSQGPQYWPPEGMLRYGPIQVEK 1302  
Qy 1320 MSCSMDCDVLNIRIFRINLTPRQBYLWVQFQYLGWASHREVPGSKRSFLKLILQVEKW 1379  
Db 1303 MSCSMDCDVLNIRIFRINLTPRQBYLWVQFQYLGWASHREVPGSKRSFLKLILQVEKW 1362  
Qy 1380 QEECEGEGRTHIHLNGGGRSGMFCAGIIVENVKRQNVVDVPHAVKTLRNSKPNMVEA 1439  
Db 1363 QEECEGEGRTHIHLNGGGRSGMFCAGIIVENVKRQNVVDVPHAVKTLRNSKPNMVEA 1422  
Qy 1440 PEQYRFCYDVALEYLESS 1457  
Db 1423 PEQYRFCYDVALEYLESS 1440

RESULT 4  
PTPK HUMAN STANDARD; PRT; 1439 AA.  
AC Q15262; Q14763;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Receptor-type protein-tyrosine phosphatase kappa precursor  
DE (EC 3.1.3.48) (R-PTP-kappa).  
GN Name=PTPRK; Synonyms=PTPK;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96279245; PubMed=8663237; DOI=10.1074/jbc.271.28.16712;  
RA Fuchs M., Mueller T., Lerch M., Ullrich A.;  
RT "Association of human protein-tyrosine phosphatase kappa with members  
of the armadillo family.";  
RL J. Biol. Chem. 271:16712-16719(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Forebrain;  
RX MEDLINE=97199372; PubMed=9047348; DOI=10.1016/S0378-1119(96)00684-1;  
RA Yang Y., Gil M.C., Choi E.Y., Park S.H., Pyun K.H., Ha H.;

RT "Molecular cloning and chromosomal localization of a human gene  
homologous to the murine R-PTP-kappa, a receptor-type protein tyrosine  
phosphatase.";  
RL Gene 186:77-82(1997).  
CC -1- FUNCTION: Regulation of processes involving cell contact and  
adhesion such as growth control, tumor invasion, and metastasis.  
CC Forms complexes with beta-catenin and gamma-catenin/plakoglobin.  
CC Beta-catenin may be a substrate for the catalytic activity of PTP-  
kappa.  
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
tyrosine + phosphate.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein; at adherens  
junctions.  
CC -1- TISSUE SPECIFICITY: High levels in lung, brain and colon; less in  
liver, pancreas, stomach, kidney, placenta and mammary carcinoma.  
CC -1- PIM: This protein undergoes proteolytic processing.  
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
CC Receptor class 2B subfamily.  
CC -1- SIMILARITY: Contains 4 fibronectin type III domains.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -1- SIMILARITY: Contains 1 MAM domain.  
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
CC -----  
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CC -----  
DR EMBL; Z70660; CAA94519.1; -;  
DR EMBL; L77886; AAC37599.1; -;  
DR HSJP; P28827; IRPM.  
DR Genew; HGNC:9674; PTPRK.  
DR MIM; 602545; -;  
DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
DR GO; GO:0005001; F: transmembrane receptor protein tyrosine pho. . .; TAS.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN-III-like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR000998; MAM.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00041; fn3; 2.  
DR Pfam; PF00047; ig; 1.  
DR Pfam; PF00629; MAM; 1.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00020; MAMDOMAIN.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR PROSITE; PS50853; FN3; 3.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR PROSITE; PS00740; MAM\_1; 1.  
DR PROSITE; PS30060; MAM\_2; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS50055; TYR\_PHOSPHATASE\_ptp; 2.  
KW Glycoprotein; Hydrolase; Immunoglobulin domain; Protein phosphatase;  
KW Receptor; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 26  
FT CHAIN 27 1439  
FT Receptor-type protein-tyrosine  
FT phosphatase kappa.  
FT Extracellular (Potential).  
FT Potential.  
FT CYTOPLASMIC (Potential).  
FT MAM.  
FT IG-like C2-type.  
FT Fibronectin type-III 1.  
FT Fibronectin type-III 2.  
FT Fibronectin type-III 3.  
FT Fibronectin type-III 4.  
FT Protein-tyrosine phosphatase 1.  
FT Protein-tyrosine phosphatase 2.



RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,  
 RA Klausner R.D., Collins P.S., Wagner L., Schaefer C.F., Bhat N.K.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting M., Madan A., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Director MGC Project;  
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC079621; AAH79621.1;  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR008957; FN\_III-like.  
 DR InterPro: IPR008979; Gal\_bind\_like.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR000998; MAM.  
 DR InterPro: IPR003595; PTPc\_motif.  
 DR InterPro: IPR000387; Tyr\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00041; fn3; 3.  
 DR Pfam: PF00047; ig; 1.  
 DR Pfam: PF00629; MAM; 1.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00020; MAMDOMAIN.  
 DR PRINTS: PR00700; PTPPHPTASE.  
 DR SMART: SM00060; FN3; 3.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00137; MAM; 1.  
 DR SMART: SM00194; PTPc; 2.  
 DR SMART: SM00404; PTPc\_motif; 2.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 DR PROSITE: PS00740; MAM\_1; 1.  
 DR PROSITE: PS50060; MAM\_2; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Glycoprotein.  
 SQ SEQUENCE 1486 AA; 167143 MW; 3698D67AD522D01A CRC64;  
 Query Match 61.8%; Score 4822.5; DB 2; Length 1486;  
 Best Local Similarity 60.4%; Pred. No. 2.4e-317;  
 Matches 896; Conservative 208; Mismatches 320; Indels 59; Gaps 9;  
 QY 22 LIGSALQFSGAGCTFDGFCADYHQDLYDDFEWVHVSQAQEPHYLPENPQGSYMWVDS 81  
 DB 14 LLTAAGETSGGCLFDEPYSTCGYSQADDEDFWEQVNTLTKTPTSPFWPWSGFMVLNT 73  
 QY 82 SNHDPGKARLQLPTMKENDTHCIDFSYLLYSOKGLNPGTNTILVRNKGPLANPWNVT 141  
 DB 74 SGRPEGORALLLPOLKENDTHCIDFHYFVSSKSNAPGLLVVYKVNCPGNPWNIS 133  
 QY 142 GFTGRDRLRAELAVSTFWPNEYQVIFEAIVSGRSGYIATDDTQVLSYGCDSKSPHFLRLG 201  
 DB 1203 SLYYDMNKLDPTQNSSQIKEEFRTLNMTPTLRVEDCSIALPRNHEKNRCKMDILPPDR 1262

Db 134 GDPTRTWHRALALSTFWPNFYQVIFEV-VTSGHQGYLAIDEVKVLGHPCTRTTHFLRIQ 192  
 QY 202 DVEVNAGQATFOCIATGRDAVHNKMLQRRNGSDIIPVAQTKNINHRFAASFFLQEVTK 261  
 Db 193 NVEVNAGQATFOCSAIGRTVAGDRLMLQGDVEDAPLKEIKVTSRRFIASFVNVVTK 252  
 QY 262 TDQDLRYCVTQSRGSGVSNPAQLIVREPPRPPIAPPOLLGVGPYLLIQLNANSIIGDGP 321  
 Db 253 RDAGKYRCMCTGEGVGISNYAELVWKEPVPPIAPPOLASVGATYMLIQLNANSINGDGP 312  
 QY 322 IILKEVEYRMTSGSWTETHAVNAPTYKWLHLDPPDEYEVRLVLRPGEGGGLPGPPLIT 381  
 Db 313 IVAREVEYCTASSGWNDRQPDVSTSYKIGHLDPDEYEVSVLLTRPGEGGTSGPAPART 372  
 QY 382 RTKCAEPMRPTKTLKIAEIQARRIADVWSGLGYNITRCHTFNVITICYHYFRGHESRAD- 440  
 Db 373 RTKCADPMRGPRLKEVVEVKSQRTIRWEFGYVNVTRCHSVNLTVHYGYVGGEQVREE 432  
 QY 441 -CLDMDPKAPQHVNVNHLPPYTNVSLKMLNPEGRKESEBETIQTDDSDVPGVPVKSLQ 499  
 Db 433 VSWDTONSHPOHTITNLSPYTNVSVKLLILNPEGRKESQELTVQTDDELPCAVPTESTQG 492  
 QY 500 TSFENKIFLNWKEPLEPENGIIIOYEVSYSSIRSPDPAVPVAGPPQTVSNLWNSTHHFMH 559  
 Db 493 SAFEKIFLQWRREPTQYGVITLYEITYKAVSSFDPDEIDLSNOSGRVSKLGNETHFLFFG 552  
 QY 560 LHPGTTYQFFIRASTVKFGFPATAINVTINISAPSLPDYEGVDASLANETATTITVLRLPA 619  
 Db 553 LYFGTTYFTIRASTAKGFGPPATNQFTTKISAPSEPAYE-FETPLNQDNTVTIVMLKPA 611  
 QY 620 QAKGAPISAYQIVVQQLHPHRTKREAGAMECYQVPTYQNALSGAPYFAAEALPPGNLP 679  
 Db 612 QSRGAPSVVQIVVEBERPRRTKTKTEILKCYVPVHFQNASILNSQYFAAEFPADSLQ 671  
 QY 680 EPAPFTVGNRTYKGFVWNPPLAPRKGNIIYFOAMSSVEKETKTCQVRIAKAA----- 732  
 Db 672 AAQFTTIGDNKTYNGYWNTEPLPHKSYRIYQAAASRANGETKDKCVRVATKAAIIVTQLT 731  
 QY 733 -----ATEPEVPIPDPAKOTDRVVKIAGISAGILVFILLVIVIVVK 776  
 Db 732 TPYIRIAPAGDGLTCAVTPKVPPEKQTDHTVKIAGVIAGILLVIFLGVVLVWKK 791  
 QY 777 SKLAKKRKADMGNTROEMTHVNMADRSYADQSTLHAEDPLSLTFMDQHNFSR----- 830  
 Db 792 RKLAKKRKETMSSTRQEMTVMNSMDKSYAEQGTNCDE---AFSFMGTHNLNGRSVSPPS 848  
 QY 831 -----LPN-----DPLVPTAVLDENHATAESSRLLDVPRY-LCEGTESPTQG 873  
 Db 849 SFTMKTNTLSTSVNSYYPDPFVPTAILDETHMTASDTSLSAQPHYTYKREAADVPYQTG 908  
 QY 874 QLHPAIRVADLLQHLINLMKTSDSYGFKEEYESFFEGQSASDWDVAKKDONAKRYGNIIA 933  
 Db 909 QLHPAIRVADLLQHLITQMKCAEGYGFKEEYESFFEGQSAPWDSAKDENRKNRYGNIIA 968  
 QY 934 YDHSRVILQPVEDDPSSDYINANYIDWLRYDGYQRPISHYIATQGPVHETVYDFWRVWQ 993  
 Db 969 YDHSRVRLQMLEGDNNSDYINGNYI-----DGYHNPVHYIATQGPQETIYDFWRVWVH 1022  
 QY 994 EQSACIWMVNLVEGRVKCYKWPDDTEVYGVFKVTCVEMEPLEAVVTVFTLERRGYN 1053  
 Db 1023 ENTASIMVNLVEGRVKCYKWPDDTEIYKIDIKVTLIDTELLAEVIRTFPAVEKRGH 1082  
 QY 1054 EIREVQKQFHTGPDHGVPHATGLLSFTRRVKLSNPSPSAGPIVHVSACAGRTGCYIVI 1113  
 Db 1083 EIREIQKQFHTGPDHGVPHATGLLGFVRQVKSPPNAGPLVHVSACAGRTGCYIVI 1142  
 QY 1114 DIMLDMAREGVVDIYNCVKALRSRRINMVQTEQYIFIHDAILEACLCCGTAIPVCEFK 1173  
 Db 1143 DIMLDMAREGVVDIYNCVRELRSRRVNVQTEQYVFIHDAILEACLCCGTSIPASQVR 1202  
 QY 1174 AAYFDMIRIDSQNSHLKDEPOTLNSVTPRLQABDCSIACLPRNHDKNRPMOMLPPDR 1233  
 Db 1203 SLYYDMNKLDPTQNSSQIKEEFRTLNMTPTLRVEDCSIALPRNHEKNRCKMDILPPDR 1262

QY 1234 LPFLITIDGSSNYINAALMDSYQPAFIIVTOYPLNTVDFWRLVYDYCTSIIVMLNE 1293  
DB 1263 LPFLITIDGSSNYINAALMDSYQPSAFIVTOYPLNTVDFWRLVLDYHCTSIIVMLND 1322  
QY 1294 VDLGQCQYWPPEGMLRYGPIQVECMSCMDVDINRIFRICNLTRPQEGYLMVQQFOY 1353  
DB 1323 VDPALQCFQYWPENGVRHGHGFIQVEFVSADLEEDIISRIPIYNASRFDQDGRHVVQQFOF 1382  
QY 1354 LGWASHREVPSKGSFLKLIQVEKWQDECEGRTIIHCLNGGGRSGMFCATGIVVEM 1413  
DB 1383 LGWPMYRDPVPSKGSFLKLIQVDKWQDEYNGGEGRTVVHCLNGGGRSGTFCATSIIVCEM 1442  
QY 1414 VKRQNVVDVPHAVKTLRSKNMVEAPROYFCYDVALEYLES 1456  
DB 1443 LRHQRTVDVPHAVKTLRNKNKPMVDLLDOYKFCYEVALEYLNS 1485

RESULT 6  
PTPM\_HUMAN  
ID PTPM\_HUMAN STANDARD; PRT; 1452 AA.  
AC P28827;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48)  
DE (R-PTP-mu).  
GN Name=PTPRM; Synonyms=PTPRL1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92008644; PubMed=1655529; DOI=10.1016/0014-5793(91)81241-Y;  
RA Gebbink M.F.B.G., van Eten I., Hateboer G., Suijkerbuijk R.,  
RA Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.;  
RT "Cloning, expression and chromosomal localization of a new putative  
RT receptor-like protein tyrosine phosphatase.";  
RL FEBS Lett. 290:123-130(1991).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 879-1156.  
RX MEDLINE=98010572; PubMed=9346878; DOI=10.1074/jbc.272.44.27505;  
RA Hoffmann K.M., Tonks N.K., Barford D.;  
RT "The crystal structure of domain 1 of receptor protein-tyrosine  
RT phosphatase mu.";  
RL J. Biol. Chem. 272:27505-27508(1997).  
CC -!- FUNCTION: May play a key role in signal transduction and growth  
CC control.  
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
CC tyrosine + phosphate.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
CC Receptor class 2B subfamily.  
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 NAM domain.  
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC EMBL; X58288; CAA41226.1; -.  
DR PIR; S17669; S17669.  
DR PDB; IRPM; X-ray; A/B=879-1156.  
DR Genew; HGNC:9675; PTPRM.  
DR MIM; 176888; -.  
DR GO; GO:0005887; C-integral to plasma membrane; TAS.

GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.  
GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR000998; NAM.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; TYR\_PP.  
DR Pfam; PF00041; fn3; 3.  
DR Pfam; PF00629; MAM; 1.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00020; MAMDOMAIN.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00137; MAM; 1.  
DR SMART; SM00194; PTPc; 2.  
DR PROSITE; PS50853; FN3; 3.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR PROSITE; PS00740; MAM\_1; 1.  
DR PROSITE; PS50060; MAM\_2; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
KW 3D-structure; Glycoprotein; Hydrolase; Immunoglobulin domain;  
KW Protein phosphatase; Receptor; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 20 Potential.  
FT CHAIN 21 1452 Receptor-type protein-tyrosine  
FT DOMAIN 21 742 phosphatase mu.  
FT TRANSMEM 743 764 Extracellular (Potential).  
FT DOMAIN 765 1452 Potential.  
FT DOMAIN 22 184 Cytoplasmic (Potential).  
FT DOMAIN 186 277 Ig-like C2-type.  
FT DOMAIN 281 371 Fibronectin type-III 1.  
FT DOMAIN 379 477 Fibronectin type-III 2.  
FT DOMAIN 482 581 Fibronectin type-III 3.  
FT DOMAIN 589 671 Fibronectin type-III 4.  
FT DOMAIN 923 1153 Protein-tyrosine phosphatase 1.  
FT DOMAIN 1213 1447 Protein-tyrosine phosphatase 2.  
FT ACT\_SITE 1095 1095 Phosphocysteine intermediate (By  
FT ACT\_SITE 1389 1389 similarity).  
FT ACT\_SITE 1389 1389 Phosphocysteine intermediate (By  
FT DISULFID 206 260 similarity).  
FT CARBOHYD 72 72 Potential.  
FT CARBOHYD 92 92 N-linked (GlcNAc . .) (Potential).  
FT CARBOHYD 131 131 N-linked (GlcNAc . .) (Potential).  
FT CARBOHYD 249 249 N-linked (GlcNAc . .) (Potential).  
FT CARBOHYD 406 406 N-linked (GlcNAc . .) (Potential).  
FT CARBOHYD 414 414 N-linked (GlcNAc . .) (Potential).  
FT CARBOHYD 454 454 N-linked (GlcNAc . .) (Potential).  
FT CARBOHYD 534 534 N-linked (GlcNAc . .) (Potential).  
FT CARBOHYD 544 544 N-linked (GlcNAc . .) (Potential).  
FT CARBOHYD 598 598 N-linked (GlcNAc . .) (Potential).  
FT CARBOHYD 651 651 N-linked (GlcNAc . .) (Potential).  
FT CARBOHYD 681 681 N-linked (GlcNAc . .) (Potential).  
FT STRAND 880 881  
FT TURN 882 884  
FT TURN 885 905  
FT HELIX 906 906  
FT TURN 916 919  
FT TURN 921 926  
FT TURN 930 931  
FT TURN 936 938  
FT STRAND 939 941  
FT TURN 946 947  
FT TURN 949 952  
FT TURN 953 961  
FT STRAND 962 963  
FT TURN 963 963

FT STRAND 964 971  
 FT HELIX 976 978  
 FT TURN 979 988  
 FT STRAND 989 990  
 FT STRAND 993 996  
 FT TURN 1001 1002  
 FT TURN 1003 1004  
 FT STRAND 1005 1006  
 FT STRAND 1016 1019  
 FT TURN 1020 1021  
 FT STRAND 1022 1032  
 FT TURN 1033 1034  
 FT STRAND 1035 1044  
 FT TURN 1045 1046  
 FT STRAND 1051 1058  
 FT HELIX 1071 1083  
 FT TURN 1086 1087  
 FT STRAND 1091 1094  
 FT HELIX 1100 1118  
 FT STRAND 1120 1121  
 FT HELIX 1123 1133  
 FT TURN 1135 1136  
 FT HELIX 1141 1155  
 SQ SEQUENCE 1452 AA; 163633 MW; 08175D3595A6C7E0 CRC64;

Query Match 61.6%; Score 4812.5; DB 1; Length 1452;  
 Best Local Similarity 61.4%; Pred. No. 1.3e-316;  
 Matches 891; Conservative 209; Mismatches 322; Indels 29; Gaps 9;

QY 22 LLGSALGFAGGCTFDGACADYHODLYDDFEWVHVSQAQEPHYLPPEMPOGSMYVDS 81  
 DB 14 LLLTAAGTETSGGCLFDEPSTCYQSSEGGDFWNEQVNTLTKTPTSPMPGSLMLVNA 73  
 QY 82 SNHDPGEKARLQLPTMKENDTHCIDFSYLLYSQKGLNPGTNILVRNKGKPLANPIWNT 141  
 DB 74 SGREGQRAHLLLPQAKENDTHCIDFHYFVSSKNSPPGLNVVYKVNNGPLNPNIS 133  
 QY 142 GFTGRDLRAELAVSTWPNYQVIFAEVSGSGSYAIDDIQVLSYPCDKSPHFLRLG 201  
 DB 134 GDPTRTNRAELAISTWPNFYQVIFEV-ITSGHQGYLAIDEVKVLGHPCPTRTTHFLRIQ 192  
 QY 202 DVEVNAQONATFOCIATGRDAVHNKMLQRRNGEDI PVAQTKNINHRFPASFLQEVTK 261  
 DB 193 NVEVNAQOFATFOCSAIGRTVAGDRLLQGLDIDVADAPLKEIKVTSSRRFASFENVNTTK 252  
 QY 262 TDQDLXRCVTSQSGSVSNFAOLI VREPREPIAPOLLGVGPTYLLIQLNANSIIGDGP 321  
 DB 253 RDAGKYRMTREGGVI SNVAELVVKPEPVPPIAPPQASVGATYLIQLNANSINGDGP 312  
 QY 322 IILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPPDTEYEIRVLLTRPGEGGTGLPGPLIT 381  
 DB 313 IVAREVEYCTASGSWDRQPDVSTSYKIGHLDPPDTEYEISVLLTRPGEGGTGSFPAIRT 372  
 QY 382 RTKCAEMPTPKTLIAEIQARRIANDWESLGNITRCHTFNVITICHYPRGHNESRAD- 440  
 DB 373 RTKCADPMRGPRKLEVVVEVSRQITIRWEPFGYVNTVCHSYNLTVHYCYQVGQEQVREE 432  
 QY 441 -CLDMDPKAPQVHVNHLPPVYTNVSLKMLTNPEGRKESEETIOTDSDVDPVPVKSLQ 499  
 DB 433 VSWDTENSHQHIITNLSPTNVSVKULNMPEGRKESQELIVQTDDEDLPGAFTVESIQG 492  
 QY 500 TSPENKIFLWKEPLENGIITQYEVSYSTRSDPAPVPPQTVSNLWNSHHVFMH 559  
 DB 493 STFEKIFLQWREPTQYVITLYEITYKAVSSFDPEIDLNSQSGRYSKLGNETHFLFFG 552  
 QY 560 LHPGTTTQPIRSTVKGFGATAINVTNISAPSLPDYEGVDASLNETAATTIVLRLPA 619  
 DB 553 LYPGTTTSFIRASTAKGFGPPATNQFTTKISAPSMPEAYE-LETPLNQTDNTVTVMLKPA 611  
 QY 620 QAKGAPISAYQIVVEQLHPRHTKEACAMECYQVPTVYQNALSGAPYFAAELPPGNLP 679  
 DB 612 HSRGAPVSVYQIVVEERPRRTKTKTEILKCYVPVPIHFQNASLNSQYFAAEPADSLQ 671

QY 680 EPAPFTVGDNRITYKGFWNPPPLAPRKGNYIYFQAMSSVEKETKTCVRIATKAAATEPEV 739  
 DB 672 AAQPTTIGDNKTYNGYNTPLLPYKSYRIYFQAASTRANGETKIDCVQVATKGAATPKP- 729  
 QY 740 IPDPAKOTDRVVKTAGISAGILVPIILLVIVIVVKSLAKKBDKANDGNTROEMTHVN 799  
 DB 730 VPEPEKQTDHTVKTAGIAGILLEVIIPLGVVLVWKKRKLAKKRKETNSSRQEMTVNVN 789  
 QY 800 AMDRSYADQSTLHAEDPLSLTFMDQHNPSRLPNDP-----LVPTAVL-DENH 846  
 DB 790 SMDKSYAEQGTNCDE---AFSFMDTNLNGRSVSSPSSFTMKTNTLSTSVENSYYPDETH 846  
 QY 847 SATABSRLLDVPRY-LCEGTESPYQTQLHPAIRVADLLOHINIMKTSDSYGKBEYES 905  
 DB 847 TMASDTSSLVQSHTYKKREPADVEYQTQLHPAIRVADLLOHITQMKCAEGYKBEYES 906  
 QY 906 FFEQOSASWDVAKDONRKNRYNIITAYDHSRVILQVDPDDPSSDIYNNYIDWLRYD 965  
 DB 907 FFEQOSAPWSAKDENRKNRYNIITAYDHSRVRLQTIEGDTNSDINGNYI-----D 960  
 QY 966 GYORPSHYIATQGPVHETVYDFWRMVMQEOSACIIVMTNLVEVGRVKCYKWPDDTEVYG 1025  
 DB 961 GYHRPNHYIATQGPVHETVYDFWRMVMQEOSACIIVMTNLVEVGRVKCYKWPDDTEVYG 1020  
 QY 1026 DFKVTCEVMEPLAEBYVVRTFTLERRGYNEIREVQKQFHTGWPDHGVPYHATGLLSFIRV 1085  
 DB 1021 DIKVTLIETBLAEBYVVRTFAVEKRGVHEIREIQFHTGWPDHGVPYHATGLLSFIRV 1080  
 QY 1086 KLSNPSAGPIVHCSAGAGTCYIVIDIMLMAEREGVVYIYNCVKALRSRINNVOT 1145  
 DB 1081 KKSPPSAGPIVHCSAGAGTCYIVIDIMLMAEREGVVYIYNCVKALRSRINNVOT 1140  
 QY 1146 EEOYFIFHDAILEACLGCTAIPVCEFAAYFDMIRIDSTQNTSSHLKDEFOTLNSVTPRL 1205  
 DB 1141 EEOYFIFHDAILEACLGCTAIPVCEFAAYFDMIRIDSTQNTSSHLKDEFOTLNSVTPRL 1200  
 QY 1206 QABDCSTACLPNRHDKRNFMDLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAFIVT 1265  
 DB 1201 RVEDCSIALLPNRHDKRNFMDLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAFIVT 1260  
 QY 1266 QYPLNVTKDFWRLVVDYGTCTSIYMLNEVDLSQCPQYWPBEGMLRYGPIQVECMSCMD 1325  
 DB 1261 QHPLNVTKDFWRLVVDYGTCTSIYMLNEVDLSQCPQYWPBEGMLRYGPIQVECMSCMD 1320  
 QY 1326 CDVNRIFRICNLTROPQGYLWQOFOYLWASHREVPKRSFLKLILOVEKWKQECCE 1385  
 DB 1321 EDIISRIFRINYAARPDQGYRMVQOQFQFGLWPMYTRDTPVSKRSLKLIQVDDKQEEYNG 1380  
 QY 1386 GEGRTIHLCLNGGSGRMFCAIGIVEMVKRQNVVDVFAVKTLRNSKPNMVEAPEQYRF 1445  
 DB 1381 GEGRTVHVCLNGGSGSGTFCASIVCEMLRHQRTVDVFAVKTLRNNKPNMVDLDDQYKF 1440  
 QY 1446 CYDVALEYLES 1456  
 DB 1441 CYEVALEYLNS 1451

RESULT 7  
 PTPM\_MOUSE  
 ID PTPM\_MOUSE STANDARD; PRT; 1452 AA.  
 AC P28828;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48)  
 DE (R-PTP-mu).  
 GN Name: Ptpm;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Lung;  
RX MEDLINE=92008644; PubMed=1655529; DOI=10.1016/0014-5793(91)81241-Y;  
RA Gebbink M.F.B.G., van Eeten I., Hateboer G., Suijkerbuijk R.,  
RA Beijersbergen R., Gaurs van Kessel A., Moolenaar W.H.;  
RT "Cloning, expression and chromosomal localization of a new putative  
RT receptor-like protein tyrosine phosphatase.";  
RL FEBS Lett. 290:123-130(1991).  
CC -!- FUNCTION: May play a key role in signal transduction and growth  
CC control.  
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
CC tyrosine + phosphate.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Most abundant in lung, less in brain and  
CC heart.  
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
CC Receptor class 2B subfamily.  
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 MAM domain.  
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X58287; CAA41225.1; -.  
CC PIR; S17670; S17670.  
CC HSP; P28827; IREP.  
CC MGD; MGI:102694; Ptpm.  
CC InterPro; IPR003961; FN III.  
CC InterPro; IPR008957; FN III-like.  
CC InterPro; IPR008979; Gal\_bind\_like.  
CC InterPro; IPR003599; Ig-like.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR000998; MAM.  
CC InterPro; IPR00387; Tyr phosphatase.  
CC InterPro; IPR000242; Tyr PP.  
CC Pfam; PF00041; fn3; 3.  
CC Pfam; PF00047; ig; 1.  
CC Pfam; PF00629; MAM; 1.  
CC Pfam; PF0102; Y\_phosphatase; 2.  
CC PRINTS; PR0020; MAMDOMAIN.  
CC PRINTS; PR00700; PRTYPHPTASE.  
CC SMART; SM00060; FN3; 3.  
CC SMART; SM00409; IG; 1.  
CC SMART; SM0137; MAM; 1.  
CC SMART; SM00194; PTPC; 2.  
CC PROSITE; PS0853; FN3; 3.  
CC PROSITE; PS0835; IG LIKE; 1.  
CC PROSITE; PS00740; MAM 1; 1.  
CC PROSITE; PS50060; MAM 2; 1.  
CC PROSITE; PS00383; TYR PHOSPHATASE 1; 2.  
CC PROSITE; PS50056; TYR PHOSPHATASE 2; 2.  
CC PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.  
CC Glycoprotein; Hydrolase; Immunoglobulin domain; Protein phosphatase;  
KW Receptor; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 20 Potential.  
FT CHAIN 21 1452 Receptor-type protein-tyrosine  
FT phosphatase mu.  
FT DOMAIN 21 742 Extracellular (Potential).  
FT TRANSMEM 743 764 Potential.  
FT DOMAIN 765 1452 Cytoplasmic (Potential).  
FT DOMAIN 22 184 MAM.  
FT DOMAIN 186 277 Ig-like C2-type.  
FT DOMAIN 281 371 Fibronectin type-III 1.  
FT DOMAIN 379 477 Fibronectin type-III 2.  
FT DOMAIN 482 581 Fibronectin type-III 3.  
FT DOMAIN 589 671 Fibronectin type-III 4.  
FT DOMAIN 923 1153 Protein-tyrosine phosphatase 1.

FT	DOMAIN	1213	1447	Protein-tyrosine phosphatase 2.
FT	ACT_SITE	1095	1095	Phosphocysteine intermediate (By similarity).
FT	ACT_SITE	1389	1389	Phosphocysteine intermediate (By similarity).
FT	DISULFID	206	260	Potential.
FT	CARBOHYD	72	72	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	92	92	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	131	131	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	249	249	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	406	406	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	414	414	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	454	454	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	534	534	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	544	544	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	598	598	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	651	651	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	681	681	N-linked (GlcNAc. .) (Potential).
SQ	SEQUENCE	1452 AA;	163594 MW;	F99D0FC67922CF1E CRC64;

Query Match 61.4%; Score 4793.5; DB 1; Length 1452;  
Best Local Similarity 61.3%; Pred. No. 2.4e-315;  
Matches 889; Conservative 208; Mismatches 325; Indels 29; Gaps 9;

Qy	22	LLGSALGQFSAGGCTDDGACDYNHODLYDDFEWVHVSQAQEPHYLPPMPQSGSMVVD	81
Db <td>14</td> <td>LLTAAGETSGGCLFDEPYSTCGYQADEDDFNEQVNTLTPTSDPMMSSGSMVNT</td> <td>73</td>	14	LLTAAGETSGGCLFDEPYSTCGYQADEDDFNEQVNTLTPTSDPMMSSGSMVNT	73
Qy <td>82</td> <td>SNHDPGSKARLQLPTMKENDTHCIDFSYLLYSQKGLNPGLTNILVRVKNKGLANPIMNVT</td> <td>141</td>	82	SNHDPGSKARLQLPTMKENDTHCIDFSYLLYSQKGLNPGLTNILVRVKNKGLANPIMNVT	141
Db <td>74</td> <td>SGKEGQRAHLLLPQKXENDTHCIDFHYFVSSKSNAPGLLVVYKVNNGPLGNPINIS</td> <td>133</td>	74	SGKEGQRAHLLLPQKXENDTHCIDFHYFVSSKSNAPGLLVVYKVNNGPLGNPINIS	133
Qy <td>142</td> <td>GFTGRDLRAELAVSTFWPNEYQVIFAEVSGSGSYIAIDDIQVLSVPCDKSHFLRLG</td> <td>201</td>	142	GFTGRDLRAELAVSTFWPNEYQVIFAEVSGSGSYIAIDDIQVLSVPCDKSHFLRLG	201
Db <td>134</td> <td>GDPTRTWRAELAISTFWPNFYQVIFEV-VTSHGQGLAIDEVKVLGHPCTRTTHFLRIQ</td> <td>192</td>	134	GDPTRTWRAELAISTFWPNFYQVIFEV-VTSHGQGLAIDEVKVLGHPCTRTTHFLRIQ	192
Qy <td>202</td> <td>DVEYNAGNATFOCIATGRDAVHNKMLQRENGEDIIPAQTKNINHRHFAERLQEVTK</td> <td>261</td>	202	DVEYNAGNATFOCIATGRDAVHNKMLQRENGEDIIPAQTKNINHRHFAERLQEVTK	261
Db <td>193</td> <td>NVEYNAGQFATFOCSAIGRTVAGDRLMLQGLIDVDRDLPEIKVTSRRFISAFNVNTTK</td> <td>252</td>	193	NVEYNAGQFATFOCSAIGRTVAGDRLMLQGLIDVDRDLPEIKVTSRRFISAFNVNTTK	252
Qy <td>262</td> <td>TDQLYRCVCTSERGSGVSNFAQLIVREPPPIAPPQLLGVGPTVLLQLNANSIIGDP</td> <td>321</td>	262	TDQLYRCVCTSERGSGVSNFAQLIVREPPPIAPPQLLGVGPTVLLQLNANSIIGDP	321
Db <td>253</td> <td>RDAGYRCMCTEGVGISNVAELVVKPEVPPIAPPQLASVGATYWLQLNANSINGDP</td> <td>312</td>	253	RDAGYRCMCTEGVGISNVAELVVKPEVPPIAPPQLASVGATYWLQLNANSINGDP	312
Qy <td>322</td> <td>IILKEVYRMTSGSWTETHAVNAPYKLUHLDPTEYBIRVLLTRPGEGGTGLPGPLIT</td> <td>381</td>	322	IILKEVYRMTSGSWTETHAVNAPYKLUHLDPTEYBIRVLLTRPGEGGTGLPGPLIT	381
Db <td>313</td> <td>IVAREVEYCTASGSWDRQPVDSYKIGHLDLPTEYBISVLLTRPGEGGTGSPGALRT</td> <td>372</td>	313	IVAREVEYCTASGSWDRQPVDSYKIGHLDLPTEYBISVLLTRPGEGGTGSPGALRT	372
Qy <td>382</td> <td>RTKCAEPMRTPTLKIAEIQAARIADVDSIGYNTTRCHTFNVTICVHYFRGHNESRAD</td> <td>440</td>	382	RTKCAEPMRTPTLKIAEIQAARIADVDSIGYNTTRCHTFNVTICVHYFRGHNESRAD	440
Db <td>373</td> <td>RTKCADPMRGPRKLEVEVKSQITIRWEPFGYNVTRCHSYNLTVHYGYQGGQGVREE</td> <td>432</td>	373	RTKCADPMRGPRKLEVEVKSQITIRWEPFGYNVTRCHSYNLTVHYGYQGGQGVREE	432
Qy <td>441</td> <td>-CLDMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEETIIOTDEDPGPPVKSQ</td> <td>499</td>	441	-CLDMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESEETIIOTDEDPGPPVKSQ	499
Db <td>433</td> <td>VSMDTDSHPQHTITNLSPYTNVSKLILMNPGRKESQELTVQDDELPGAVPTESIQ</td> <td>492</td>	433	VSMDTDSHPQHTITNLSPYTNVSKLILMNPGRKESQELTVQDDELPGAVPTESIQ	492
Qy <td>500</td> <td>TSFNKIFLNWKEPLENGIITQYEVSVSSIRSDPAVPVAGPPOTVNLNWNSTHVMH</td> <td>559</td>	500	TSFNKIFLNWKEPLENGIITQYEVSVSSIRSDPAVPVAGPPOTVNLNWNSTHVMH	559
Db <td>493</td> <td>SAFEKIFLOWREPTQYTVITLVEITYKAVSSFDPEIDLNSQSGRVSKLGNETHFLPFG</td> <td>552</td>	493	SAFEKIFLOWREPTQYTVITLVEITYKAVSSFDPEIDLNSQSGRVSKLGNETHFLPFG	552
Qy <td>560</td> <td>LHFGTTYQFFIRASTVKGFGPATINVTNINISAPSLPDYEGVDASLNETATITVLLRPA</td> <td>619</td>	560	LHFGTTYQFFIRASTVKGFGPATINVTNINISAPSLPDYEGVDASLNETATITVLLRPA	619
Db <td>553</td> <td>LYPGTTSYFIRASTAGFGFPATNQFTTKISAFSPMPAYE-FETPLNQTDTNVTVMKPA</td> <td>611</td>	553	LYPGTTSYFIRASTAGFGFPATNQFTTKISAFSPMPAYE-FETPLNQTDTNVTVMKPA	611
Qy <td>620</td> <td>QAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQNALSGGAPYFAAELPFGNLP</td> <td>679</td>	620	QAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQNALSGGAPYFAAELPFGNLP	679
Db <td>612</td> <td>QSRGAPSVYQIVVEEERPRTKTTELKCYVPPIHFQNASILNSQYFAAEFFADSIQ</td> <td>671</td>	612	QSRGAPSVYQIVVEEERPRTKTTELKCYVPPIHFQNASILNSQYFAAEFFADSIQ	671
Qy <td>680</td> <td>EPAPFTVGDNRTYKGFWMNPPLAPRGYNYIYQAMSSVEKETKQTCVRIATKAAATEEPEV</td> <td>739</td>	680	EPAPFTVGDNRTYKGFWMNPPLAPRGYNYIYQAMSSVEKETKQTCVRIATKAAATEEPEV	739
Db <td>672</td> <td>AAQPFITGDNKTYGWNTPLLPHKSYRIYQAASRANGETKIDCVRVATKGAATPKP--</td> <td>729</td>	672	AAQPFITGDNKTYGWNTPLLPHKSYRIYQAASRANGETKIDCVRVATKGAATPKP--	729
Qy <td>740</td> <td>IPDPAKQTDVRVVKIAGISAGILVFIILLVVIIVVKSKLAKRKDKAMGNTREQMTHVN</td> <td>799</td>	740	IPDPAKQTDVRVVKIAGISAGILVFIILLVVIIVVKSKLAKRKDKAMGNTREQMTHVN	799

730 VPEKQDHTVTKIAGVIAGILLFVILGLVVLVKKRKLAKRKTMSSTRQMTVMVN 789  
800 AMRSYADQSTLHAEDSLTDFMDQHNFSPLRPNP-----LVPTAVL-DENH 846  
790 SMDKSYAEQGTNCDE--AFSEMTGNLNGRSVSSPSTFTWTKTTLSTSPVNSYYPDETH 846  
847 SATAESRLLDVPRY-ICEGTESYQYQGLHPAIRVADILLOHINLMKTSYSYKEYES 905  
847 TMSDTSLSLAQPHYTKKREADVYQYQGLHPAIRVADILLOHITQMKCAGYGFKEYES 906  
906 FFEQOSASWVAKKQONKRNRYNIIAYDHSRVLQVDEDPSSDYINANYIDWLRYD 965  
907 FFEQOSAPWSAKDENMKRNRYNIIAYDHSRVLQVDEDPSSDYINANYIDWLRYD 960  
966 GYRPSHYIATQGVPHVETVDFWMMWQBSACIVYIDIMLMAEREGVVDIYNCVKALRSRINNVQT 1025  
961 GYRPNHYIATQGVPHVETVDFWMMWQBSACIVYIDIMLMAEREGVVDIYNCVKALRSRINNVQT 1020  
1026 DFKVTCEMPELARYVVRTTLERRGYNREIVKQFHTGWDHGVPHYHATGLLSFTRRV 1085  
1021 DIKVTLDITELLAEYVIRTFVAVKRGHIREIRQFHTGWDHGVPHYHATGLLSFTRRV 1080  
1086 KLSNPPSAGPIVHCSAGAGTGCYIVIDIMLMAEREGVVDIYNCVKALRSRINNVQT 1145  
1081 KKSPPNAGPLVHCSAGAGTGCYIVIDIMLMAEREGVVDIYNCVKALRSRINNVQT 1140  
1146 EEQVFIHDAILEACLCGETAIPCEPKAAYFDMIRDSOTNSHLKDEFTLNSVTPRL 1205  
1141 EEQVFIHDAILEACLCGETSIPASVRSYLYDNKLDPTQNSQIKBEFTLNMVTPRL 1200  
1206 QABDCSIALPRNHDKNRMDMLPPDRCLPLFITIDGESSNYINAAALMDSYRQPAAFIVT 1265  
1201 RVEDCSIALPRNHDKNRMDMLPPDRCLPLFITIDGESSNYINAAALMDSYRQPAAFIVT 1260  
1266 QYPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQCPQYWPBEGMLRGPIQVECMSCMD 1325  
1261 QHPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQCPQYWPBEGMLRGPIQVECMSCMD 1320  
1326 CDVNIIRFICNLTRPOEGLVWQOYVGLWASHREVPGRKSRPLKILQVEKQWCEEE 1385  
1321 EDIISIRIFRYNARSPODGHVWQOYVGLWASHREVPGRKSRPLKILQVEKQWCEEE 1380  
1386 GEGRTIHLCLGGGRSGMFCAGIVEMVRQNVVDVFAVKTILRNSKPNMVEAPEQYRF 1445  
1381 GEGRTVHCLGGGRSGMFCAGIVEMVRQNVVDVFAVKTILRNSKPNMVEAPEQYRF 1440  
1446 CYDVALEYLES 1456  
1441 CYEVALEYLES 1451

## RESULT 8

Q86V60 PRELIMINARY; PRT; 1390 AA.  
AC Q86V60  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE PRPM protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBTaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
FAhey J., Helton E., Kettman M., Maman A.C., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC051651; AAH51651.1; -;  
DR HSPB; P28827; IRPM.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR InterPro; IPR003599; Ig-like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR000998; MAM.  
DR InterPro; IPR000387; Tyr\_phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00041; fn3; 2.  
DR Pfam; PF00047; ig; 1.  
DR Pfam; PF00629; MAM; 1.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00020; MAMDOMAIN.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00194; PTPC; 2.  
DR PROSITE; PS00853; FN3; 3.  
DR PROSITE; PS00835; IG LIKE; 1.  
DR PROSITE; PS00740; MAM 1; 1.  
DR PROSITE; PS00650; MAM 2; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 2.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE 2; 2.  
DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
KW Glycoprotein; Hydrolase.  
SQ SEQUENCE 1390 AA; 156936 MW; D8173543CDD9F79 CRC64;  
Query Match 60.6%; Score 4732.5; DB 2; Length 1390;  
Best Local Similarity 62.2%; Pred. No. 3.1e-311;  
Matches 872; Conservative 205; Mismatches 396; Indels 29; Gaps 9;  
Qy 71 MPOGSYVMVDSSNHDCEKARLQPTMKENDTHCIDFSYLLYSQKGLNPGTFLNLVRVVK 130  
Db 1 MPGSFMLVNASGRPEGQRAHLLLPQKENDTHCIDPHYFVSSKSNPPGLNLVYVKNV 60  
Qy 131 GPLANPNTVNTGFTGRDLRAELAVSTFWPNEVQVIFAEVSGVSGRSYIAIDDIQVLSYP 190  
Db 61 GPLGNFNIWISGDPARTWNAELAISTFWNFQVIFEV-ITSGHQYLAIDEVKVLGHP 119  
Qy 191 CDKSPHFLRLGDEVVNAGQWATFCIATGSDAVHKLWLQRRNGEDIPVATQKNINHRF 250  
Db 120 CTRTPHFLRIQNVENVNAGQWATFCIATGSDAVHKLWLQRRNGEDIPVATQKNINHRF 179  
Qy 251 AAFRLQEVTKTQDLYRCVTSQSGVSNFAQLIVREPRPIAPQILGCVGPTLLIQ 310  
Db 180 IASFNVVNTTKRDAGKYRCMIRTEGGVGISNYAELVVKPEVPFIAPPQLASVGTATLMIQ 239



Db 84 AHLFLQALSENDRTHCLQSFYFWYGRDGHSPGTLISAYVVMGPGVGSVAVNWSGSHGRQWH 143  
Qy 150 RAEIAVSTFWNEXYQVIFAEVSGRSGYIAIDDIQVLSPYCDKSPHFLRLGDEVEVNAQ 209  
Db 144 QAEIAVSLFWPSEYQVLFVAVISSERRGYLGLDILLNLYPCSKAPHFSLRLGDEVEVNAQ 203  
Qy 210 NATQCIATGDAVHKLMLORNGEDIPIVATQKNINHRRAAPASPRLOEVTKTODLYRC 269  
Db 204 NATQCCVAAAGKAAEAEFLMORQSGEVVPAASVXHISHRRFLATFOLDDEVSKGQDLYRC 263  
Qy 270 VTQSERGSGVSNFAQLVREPRPIAPPOLLGVGPTVLLIOLNANSIIGDGPILKEVEY 329  
Db 264 VTQSRGSGVSNFAELIVKEPPTIAPPOLLRASTVLLIOLNANSIIGDGPVIRKIEY 323  
Qy 330 RMTSGSWETHAVNAPTYKMLHLPDDEYEIRVLLTRPGEGLGPPLLTRKCAEPM 389  
Db 324 RMTSGPSEVHAVNMOTYKMLHLPDDEYEIRVLLTRPGEGLGKGPPLISRTKCAEPM 383  
Qy 390 RTPKTLIAEIQARRIADVMSLGNITRCHTFNWTICYHYF--RGHNSRADCLMDMPK 447  
Db 384 RAPKGLAFSEIQSRLQTLQWEPGLNLTCHTYSVSLCYRYLVGSLNQTFFRECAKMER 443  
Qy 448 APOHVVHLPDYTNVSLKMLITNPEGRKESEETIIQDDEVPGVPVVKSLQGTFFENKIP 507  
Db 444 ANRTIKNLLPYRNIHVKLLISNPEGRKEGKVTFQDDEVPGGIASESLTFTPLEDMIF 503  
Qy 508 LNKKEPLENGIITQYEYSXSSIRSFDPVAVAGPQPTVSNLMNSTHVFHMLHPGTTYQ 567  
Db 504 LKWEPEVPEGLIITQYEISYQSISSDPANVPGPRTVSKLRNETHVPSNLHPGTTYL 563  
Qy 568 FFIRASTVKGPGPATAINVTNISAPSLDPYEGVDASINETAATTITVLLRPAQAKGAPIS 627  
Db 564 FSVRAARTKGFGQALTAEITTNISAPTF-DYGDMPSPGLGESESTITVLLRPAQGRGAPIS 622  
Qy 628 AYQIVVQLHPHRTKRAGAMECYOVPTVYONALSGGAPYVFAALPPGNLPPEPAPTVG 687  
Db 623 TYQIVVEDPKRIKRELGGQCEFPVLPFDDAMSGSVHVFAGELPASSLUTEAKPTVG 682  
Qy 688 DNRTYKGFNPPLAPRGYNIYFOAMSVEKETKTQCVRIATKAAATEEPEVDPAPKQT 747  
Db 683 DNQYSGVNPPLPKKAYLIYFOAMSLNKGELTRLCIRIARKAACKESKPL-EVSQHS 741  
Qy 748 DRVVKIAGISA-GILVFIILLVIVVVKSKLAKKRDAMGNTRQETHMNVNMDRSYA 806  
Db 742 EEMGLILGICAGGLVLLIILGAIIVIRKGPVNMTK-ATINVRHEKTHMMSAIDRSFT 800  
Qy 807 DQSTLHAEDPLSLTFMDQHNFSPLPNDPLVPTAVLDENHSATAESRLL-DVPRYLCEG 865  
Db 801 DQSTLQEDERLGLSFMDSHNSR-----GDORSVNVNESSLLGSPRQGR 849  
Qy 866 TESPYQTGQLHPARVADLLQHLNMTSDSYGPKBEYESPFQSGASWDVAKKQDNRAK 925  
Db 850 KGSPIYHTGQLHPARVADLLQHLNMQMTAEGYGFQBEYESPFEG----WDASKK-KDKTK 904  
Qy 926 NRYGNIITAYDHSRILQVDEDDPSDYINANYIDILYRQYORPSHYIATQGPVHETVY 985  
Db 905 GRODHVSTYDRHVKLHPLLDGPNDSYINANYI-----DGYHRSNHFIATQGPQEMVY 958  
Qy 986 DFWRMVMQESACIWMVNLVVEURVKCYKWPDDTEVYDGFKTCVMEPELAEYVVRTF 1045  
Db 959 DFWRMVMQECSSIVMTIKLVEGRVKCSKWPDDSEMYGDIKITLVKSEKLAEYAVRTF 1018  
Qy 1046 TLERRGYNREVKQFHTGWPDRGVPYHATGLLSFTIRRVKLSNPPSGAPVIVHCSAGAG 1105  
Db 1019 ALERGYSARHEVVKQFHTSWPEGVPHATGLLAFIRRVKASTPPDAGPVIHCSAGTG 1078  
Qy 1106 RTGCVIIVIDIMLMAEREGVVDIYCNVKALSRSRINMVQTESEQYIFIHDAILEACLCGET 1165  
Db 1079 RTGCVIIVLDMVMAECEGVVDIYCNVKTLCSRRINMQTEEQYIFIHDAILEACLCGET 1138  
Qy 1166 AIPVCEKAAFYDMIRDSQTNLSHLKDFOTLNSVTFRLQAECDSCACLPRNHDKRFM 1225  
Db 1139 SIPASEFPKPTYKEMVRIEPOSNSQLREEFOTLNSVTFPHLDVERCSIALLPNRNRNRM 1198

Qy 1226 DMLPPDRCLPLITIDGESSNYINAAWMDSYRQPAAFIVTQYPLPNTVKDFWRLVYDYG 1285  
Db 1199 DVLPPDRCLPLISVDGDSNNYINAAWTDSTYKSAAFIVTLHLPLQNTTDFWRLVYDYG 1258  
Qy 1286 TSIVMLNEVDLSQ--CPOYWPBEGMLRVPQIOVEKSCSMDCDVINRIPRICNLTRPO 1342  
Db 1259 TSIVMLNQLNOSANPCLQVPEPGLQHYGPEVEYVSGAEDIVSRLEFRVQNTRLQ 1318  
Qy 1343 EGYLMVQOQFYLWASHREVPVSGSKRSLKLITQVEKQKECEEGEGRTIIHCLNGGGRSG 1402  
Db 1319 EGHLMVRFQYLRWSAYDTPDSKSLHLHLLAQQVERWQK--ESDGRVTVHCLNGGGRSG 1376  
Qy 1403 MFCAIGIVEMVKRQNVVDVHFAVTKLURNKPNMVEAPEQYRPFYCDVALEYLE 1456  
Db 1377 TYCASTMILEMIKHNADIFYAAKTLRNKPNMVELEQVHFYCDYALEYLE 1430  
  
RESULT 10  
O00197 PRELIMINARY; PRT; 1436 AA.  
AC O00197;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Receptor protein tyrosine phosphatase hPTP-J precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal muscle;  
RX MEDLINE=9723402; PubMed=9070223; DOI=10.1006/bbrc.1997.6004;  
RA Wang B., Kishihara K., Zhang D., Hara H., Nomoto K.;  
RT "Molecular cloning and characterization of a novel human receptor  
protein tyrosine phosphatase gene, hPTP-J: down-regulation of gene  
expression by PMA and calcium ionophore in Jurkat T lymphoma cells.";  
RL Biochem. Biophys. Res. Commun. 231:77-81(1997).  
DR EMBL; J73727; AB51343.1; -;  
DR PIR; JC5290; JCS290.  
DR HSP; P28827; IRPM.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR003962; FNIII\_subd.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR InterPro; IPR003599; Ig-like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR000998; MAM.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00041; fn3\_3.  
DR Pfam; PF00629; MAM; 1.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PRO0014; FNTYPEIIL.  
DR PRINTS; PRO0020; MAMDOMAIN.  
DR PRINTS; PRO0700; PRTPHPTASE.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00137; MAM; 1.  
DR SMART; SM00194; PTEC; 2.  
DR PROSITE; PS00853; FN3; 3.  
DR PROSITE; PS00740; MAM; 1; 1.  
DR PROSITE; PS00060; MAM; 2; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
KW Glycoprotein; Hydrolase; Receptor; Signal.



SQ SEQUENCE 1436 AA; 161108 MW; 8F15DC340958A809 CRC64;

Query Match 59.0%; Score 4610; DB 2; Length 1436;  
Best Local Similarity 60.3%; Pred. No. 6.4e-303;  
Matches 865; Conservative 202; Mismatches 331; Indels 36; Gaps 12;

QY 32 AGGCTFD---DGPACDYHQDLYDDFEWVHVSQAQEPHYLPPEMQSGVMVDDSNHPDGE 88  
DB 24 AAGCTFEASDPAPVCEYSQAQYDDFQWEQVRIHPGTRAPADLPHGSLYLVNTSCHAPGQ 83  
QY 89 KARLQPTMKENDTHCIDFYSLLYSQKGLNPGTLLNVLNVNKGPLANIPNVVTFGTGRDW 148  
DB 84 RAHVIFQSLSENDTHCQVFSFLYSRDGHSGPTLCVYRVNNGPLGSAVNMNTHSGHQW 143  
QY 149 LRAELAVSTFWPNFYQVIFEAEVSGRSGYTAIDDIQVLSYPCDKSPHFLRLGDEVEYNAG 208  
DB 144 HQAELAVSTFWPNFYQVIFEALISPDRRGYMGLDDILLSPYCAPKAPHSRLGDEVEYNAG 203  
QY 209 QNATFQCIATGRDAVHNKLMLORENDEDI PVAQTKNINHRPFAASFLQEVTKTDQDLYR 268  
DB 204 QNASFOCMAAGRAAEAEERFLQROSGALVPAAGVRHISHRRFLATFTFLAAVSRAEQDLYR 263  
QY 269 CVTOSERGSGVNSFAQLIVRPPPIAPPOLLGVGPTVLLIQLNANSLIGDGPILLKEVE 328  
DB 264 CVSQAPRGAGVNSFAELIVKEPPTPIAPPOLLRAGPTVLLIQLNANSLIGDGPILVRKEIE 323  
QY 329 YRMTSGSWTETHAVNPTYKLMHLDPDOTEVEIRVLLTRPGEGGTGLPGPPLITRTKCAEP 388  
DB 324 YRMARGPWAHVAVSLQTYKLMHLDPDOTEVEISVLLTRPGDGGTGRPGPPLISRTKCAEP 383  
QY 389 MRPXTKLIKABIQARRIADWESLGYNITRCHTNVTICVHYFRG--HNESRADCLMDMP 446  
DB 384 MRAPKGLAFABIAQRLTLOWEPLGYNVTRCHTYVSLCYHYTLGSSHNQITRECVKTEQ 443  
QY 447 KAPOHVNHLPYTNVSLKMLTNPGRKSESEETIIOTDEEDVPVFPVKSLOQTSFENKI 506  
DB 444 GVGRYITKNLLPYRNHVRLVLTNPGRKSGEVTFTQDEEDVPSGIAAESLTFPLEDMI 503  
QY 507 FLNWKLEPNNGIITQYEVSYSSIRSPDPAVPVAGPPTQVSNLWSTHVFHMLHPGTTY 566  
DB 504 FLKWEEOEENGLITQYEISQSISSDPAVNVPGPRTTISKLRNETHYFVSNLHPGTTY 563  
QY 567 OFFIRASTVKGFGPATAINVTNIIISAPSLPDYEGVDASLNETAITITVLLRPAQAGAPI 626  
DB 564 LFSVRARTGKFGQALTEITTNISAPSF-DYADMPSPGLGSESENTITVLLRPAQGRGAPI 622  
QY 627 SAYQIVVEQLHPHRTKEAGMECYQVPTVYQNNALSGAPYFAAEIIPGNLPEPAPFTV 686  
DB 623 SVYQVIVEERARRLRREPQGCPCFPVLTFAALARGLVHYFGAELAAASLPEAMPFTV 682  
QY 687 GDNRTYKGFNPPPLAPRKGYNIYFOAMSSVEKETKTQCVRIATKAAATEPEVLPDPAQ 746  
DB 683 GDNQTYGFWNPPLEPKAVLIYFOASHLKGTRFLNCIRIARNAACKESKRPL-EVSQR 741  
QY 747 TDRVVKIAGISA-GILVFIILLVIVIVKSKLAKRCKDAMGNTRQEMTHVMNAMDRSY 805  
DB 742 SEEMGLILGICAGLAVLILLGAILIIRKGPVNTK-ATVNYRQEKTHMSAVDRSP 800  
QY 806 ADQSTLHABDPLSTFMDQNFSPRLNDPLVPTAVLDENHSATAESSRL-LDVPRVLCE 864  
DB 801 TDQSTLQEDRLGSLFMDTHGYSTR-----GDQRSGGVTEASSLLGGSPRRPCG 849  
QY 865 GTPSPYOTGOLHPAIRVADLLOHNLNMTSDSYGFKEEYSFPEGQASWDVAKQDNRA 924  
DB 850 RKGSPIYTGQHPAVRVADLLOHINQMTAEGYFKQEYSFPEG----WDATKKDKVK 905  
QY 925 KNRYGNIAYDHSRVILQPVDEDDPSDIYINANYIDILWLRDGYQRPSPHYIATQPVHETV 984  
DB 906 GSROEPMPAYDRHVKLHPMLGDNADYINANYI-----DGYHRSNHFATQGPKEMV 959  
QY 985 YDFWRMWWQSGACINVMVNLVEGRVKCYKYPDDTDEVYDGFVKTCVEMEPALAEYVRT 1044  
DB 960 YDFWRMWWQHCSSIVMITKLVEGRVKCSYWPEDSDTYGDIKIMLVKTETLAEYVRT 1019

QY 1045 FTLERRGYNEIREYKQFHTGWPDPHGVPYTHATGLLSFIRRVKLSNPPSAGPIVVHCSAGA 1104  
DB 1020 FALERRCYSARHEVRQFHTAWPEHGVYTHATGLLAFIRRVKASTPPDAGPIVHCSAGT 1079  
QY 1105 GRTCYIVIDIMLDMAREGVVDIYNCVKALRSRRINNVQTEEQYIFIHDAILEACLCGE 1164  
DB 1080 GRTCYIVLDMVDMAREGVVDIYNCVKALRSRRINNVQTEEQYIFIHDAILEACLCGE 1139  
QY 1165 TAIPTVCFAKAYPMIRIDISTNSSHLKDFOTLNSVTPRLOAEDCSIACLPRNHDKNRF 1224  
DB 1140 TTPVSEFKATYEMIRIDPQSNSSQLRREBFOTLNSVTPPLDVEECISIALPRNRDKRS 1199  
QY 1225 MDMLPPDRCLPFLITIDGESSNYINAALMDSYRQAAAFIVTQYPLNTPVKDFWLVVDYG 1284  
DB 1200 MDVLPADRCPLPFLISTDGSNNYINAALTDSTYRSAAFIVTLHPLQSTTPDFWLVVDYG 1259  
QY 1285 CTSIVMLNEVDLSQG----CQYWPBEGMLRYGPTQVECMSCMDCVINRIFRICNLTRP 1341  
DB 1260 CTSIVMLNQLNQSANSAPWPCQLQYWPBEGMLRYGPTQVECMSCMDCVINRIFRICNLTRP 1319  
QY 1342 QEGYLMVQQOYLQWASHREVPGRSKRSFLKLIQVQEKWQEBCEGEGRTIHCILNGGGRS 1401  
DB 1320 QEGHLLVRHFQLRWSAYRDTDPKKAFLHLAEVDKQW--AESGDGRTIVHCLNGGGRS 1377  
QY 1402 GMFCAIGVVMVKRQNVVDVFAVKTLRNKNMVEAPEQYRQYCFYDVALEYLE 1455  
DB 1378 GTFCACATVLEMIRCHNLVDVFFAAKTLRNYKNMVMETQYHFCYDVALEYLE 1431

RESULT 12

P78399 PRELIMINARY; PRT; 1439 AA.

AC P78399;  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Protein tyrosine phosphatase receptor omicron.  
GN Name=PTPRO;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=38094249; PubMed=9434160; DOI=10.1016/S0378-1119(97)00420-4;  
RA Avraham S., London R., Tulloch G.A., Ellis M., Fu Y., Jiang S.,  
RA White R.A., Painter C., Steinberger A.A., Avraham H.;  
RT "Characterization and chromosomal localization of PTPRO, a novel  
RT receptor protein tyrosine phosphatase, expressed in hematopoietic stem  
RT cells";  
RL Gene 204:5-16(1997).  
DR ENBL; U71075; AAC51938.1; -.  
DR HSPG; P28827; IRPM.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR003962; FNIII subd.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR000998; MAM.  
DR InterPro; IPR000387; TYR phosphatase.  
DR InterPro; IPR00242; Tyr\_Pp.  
DR Pfam; PF00041; fn3; 3.  
DR Pfam; PF00629; MAM; 1.  
DR Pfam; PF00102; Y phosphatase; 2.  
DR PRINTS; PR00014; FNTYPEIII.



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DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00014; FNTYPEI1.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPc; 2.
DR PROSITE; PS00853; FN3; 3.
DR PROSITE; PS00660; MAM 2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Hydrolyase.
SQ SEQUENCE 1436 AA; 161157 MW; 8D406DE4948643FF CRC64;

Query Match      58.98; Score 4597; DB 2; Length 1436;
Best Local Similarity 60.08; Pred. No. 4.9e-302;
Matches 861; Conservative 208; Mismatches 330; Indels 36; Gaps 12;

QY 32 AGGCTFDGPG--ACDYHODLYDDFEWVHVSQAQEPHYLPPEMQSGVMVYDSSNHPDGE 88
DB 24 AGCTFEASDPVPCFESQAQYDDFQEQVRHPGTRTPEDLPHGAYLWNASQAPGQ 83
QY 89 KARLQPTMKENDTHCIDFSYLLYSQKGLNPGLTILNLRVKNKGLPLANPVNVTGFGTDW 148
DB 84 RAHIIQFTLSNDTHCVQFSYFLYSRDGHSGPTLGVVYRVNNGPLGSAVNMWMTGSHGQW 143
QY 149 LRAELAVSTWPNQYQVIFEAVSQSGSGVIAIDDIQVLSYPCDKSPHFRLGLDVEYNAG 208
DB 144 HQAELAVSTWPNQYQVIFEAISPDHKGITGLDILLFSPYCAKAPHFSLRGLDVEYNAG 203
QY 209 QNATFOCIATGRDAVHKNLWLRNGEDIPVAOTPKNINHRFAASPRLEQVTKDQDLYR 268
DB 204 QNASFCQMAAGRAAEHFFLQROSGVLVPAAGVRHISHRRFLATFFPLASVGRSEQDLYR 263
QY 269 CVTQSERGSGVNSPAQLIVREPPRIAPPOLLGVGPTLYLLIQLNANSIIGDGPILKEVE 328
DB 264 CVSQAPRGAGVNSFAELIVKEPTPIAPPOLLRAGPTLYLLIQLNANSIIGDGPVIRKEIE 323
QY 329 YRMTSGSWTETHAVNATPYKLMHLDPTQTEYRVLTRPGEQGLPGPPLITRTKCAEP 388
DB 324 YRMARGPWAEBVAVNLQTKLWHLDPDTEYRISVLLTRPGDGGTRPGPPLISRTKCAEP 383
QY 389 MRPKTLKIAEQARRTAVDWESIGYNTSCHFNVTICVHYFRG--HNESRADCLMDP 446
DB 384 TRAPKGLAFIEIQARQLTQWEPYGVNTRCHTVAVSLCYRYTLGGSHNQTIRECVMER 443
QY 447 KAPQHVNVHLPPYTNVSKMLTNPEGRKSEETIIQTDDEDVPGVPVVKSLQGTSEFNKI 506
DB 444 GASRYTIKNLLPFRNIHVRLLTNPEGRKEGKVEVTFQTDDEDVPGVIAESLTTFPLEDMI 503
QY 507 FLNWKPEPLNGIITQEVSYSSIRSPDPAVAVAGPQPTVSNLWNSHTHVFMHLHPGTTY 566
DB 504 FLKWEPEQEPNGLIITQEVISQSISSDPAVAVAGPQPTVSNLWNSHTHVFMHLHPGTTY 563
QY 567 QFFIRASTVKGCPATAVNTNLSAPSLPDYEGVDASINETATITIVLIRPAQAKAPI 626
DB 564 LFSVRAKTSFGQQAALTEITNLSAPSF--DYADMPSPLGESNTIITVLLRPAQGRAPI 622
QY 627 SAYQIVVQELHPHRTKREAGAMECYQVPVTVYQNALSGAPYFAAELPPGNLPEPAPFTV 686
DB 623 SVYQVVEERPRRLRREPQAGDCFSVPLTFETALRGLVHYFGAELAAASLLEAMPFTV 682
QY 687 GDNRTYKGFVNPPPLAPRKGYNIYFQAMSSVEKTKTQCVRATKAAATEBPEVIPDPAKQ 746

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DB 683 GDMQTYRGFWNPPLPRKAYLIYFQAASHLKGTELNCIRIARAKACKESKRPL-EVSQR 741
QY 747 TDRVVVKIAGISA-GILVFIILLVIVIVKSKLAKRKKDAMGNTRQEMTHMNVAMDRSY 805
DB 742 SEEMGLJLGICAGGLAVLILLGAIIVIRKGPVNMWK-ATVNYRQEKTHMSAVDRSP 800
QY 806 ADQSTLHAEDPLSLTFMDQHNFPRLPNDPLVPTAVLDENHSATAESRLL-DVPRYLCE 864
DB 801 TDQSTLQEDERLGLSLFDAPGYSR-----GDQRSGGVTEASSLLGGSPRRPCG 849
QY 865 GTPSPYOTGOLHPAIRVADLLOHNLNMTSDSYGFKEEYSEFFEGQSGASDVAQDNRA 924
DB 850 RKGSYHTGOLHPAVRVADLLOHNLNMTAGYGFQKOEYSEFFEG---WDATKKOKLK 905
QY 925 KNRYGNIAYDHSRVLQPVEDDPSSDIYANITIDILWLYRDGYQRPSPSHYIATQCPVHETV 984
DB 906 GGRQEPVSAVDRHHVKLHMLADPDADYISANYI-----DGYHRSNHFATQCPKEMI 959
QY 985 YDFWRMVWQESQACIVMVTNLVGRVKCYKYPDDTEVYGDPKVTCVMEPLAEYVVRT 1044
DB 960 YDFWRMVWQESQACIVMITKLVEGRVKCSRYNPEDSDMYGDIKITLVKTETLAEYVVRT 1019
QY 1045 FTLERGYNEIRVKQPHFTGMPDHGVPYHATGLLSFIRVKLSNPSAGPIVHVCSGA 1104
DB 1020 FALERRGYSARHEVRQPHFTAWPEHGVPYHATGLLAFIRVKASTPPDAGPIVHCSAGT 1079
QY 1105 GRTGCVIIVIMLDMAREGVWDIYNCVKALRRRRINNVOTEEOYIFIHDAILEACLCGE 1164
DB 1080 GRTGCVIIVLMDMAECEGVWDIYNCVKTLCSRRVNMVITEBOYIFIHDAILEACLCGE 1139
QY 1165 TAIPECFKAAAYDMIRIDISQTNSSHLKDFQTLNSVTPRLQADCSIACLPRNHDKNRF 1224
DB 1140 TTIPEVNEFKATYEMIRIDISQTNSSQLREBFQTLNSVTPPLDVECSIALPRNRDKNRS 1199
QY 1225 MDMLPDRCLPFLITIDGESSNYINALMDSYQPAFIVTYQVPLPNTVKDFWLVVDYG 1284
DB 1200 MDVLPDRCLPFLISSDGPNNYINAAITDSYTRSAAFIVTLPLQSTTDFWLVVDYG 1259
QY 1285 CTISVMLNEVDLSQG--CPQYWPPEGMLRYGPIQVECMSCMDCVINRIFRICNLTRP 1341
DB 1260 CTISVMLNLQNQNSAWPCLOYPFEPGRQYGLMEVFEVSGTANEDLVSRVFRVQNSRL 1319
QY 1342 QEGYLMVQOQYQLGWASHREVPGSKSFLKILIQVEKWQEBCEGEGRTIICHLNGGGRS 1401
DB 1320 QEGHLLVRHFQFLRWSAYRDTSDSKAFHLHLAEVDKMQ--AESGDGRTVVHCLNGGGRS 1377
QY 1402 GMFCALGIVVWVKRQNVVDVFAVKTILRSKNMVEAPEQYRFCYDVALEYLES 1456
DB 1378 GTFCACATVLEMRCHSLVDVFFAAKTLRNYKPNMVTMDQYHFCYDVALEYLEA 1432

RESULT 14
P70125 PRELIMINARY; PRT; 1436 AA.
AC P70125;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Receptor protein tyrosine phosphatase-lambda.
GN Name=Ptpu; Synonyms=ptp-lambda;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Cheng J., Armanini M., Phillips H., Dowbenko D., Daimaru L.,
RA Lasky L.A.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U55057; AAB17895.1; -.
DR HSSP; P28827; 1RPM.

```

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DR MGD; MGI:1321151; Ptpnu.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF00102; y_phosphatase; 2.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00853; FN3; 3.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Hydrolase; Receptor.
SQ SEQUENCE 1436 AA; 161199 MW; EFFAAE52C6903F02 CRC64;

Query Match 58.8%; Score 4591; DB 2; Length 1436;
Best Local Similarity 59.9%; Pred. No. 1.2e-330;
Matches 859; Conservative 210; Mismatches 330; Indels 36; Gaps 12;

QY 32 AGGCTFDDGPG--ACDTHQDLYDDFWVHVSQAQPHYLPPMPGSGYMYVDSSNHDPEG 88
DB 24 AAGCTFEASDPVCEFSQAQYDDFQWEQVRIHFGTTPEDLPHGAYLWNASQHTFGQ 83

QY 89 KARLQPTMKENDTHCIDFSYLLYSQKGLNPOTLNLVKNKGPANPIWVNTGFTGRDW 148
DB 84 RAHIIFQTLSENDTHCVQFSYFLYSRQDHSPTLGVVYVNGGPLGSAVNMNTHGSHGQW 143

QY 149 LBAELAVSTFWNEQVIFEAUSGGRGYTAIDDIQVLSYPCDSKSPFLRLGDVEVNAQ 208
DB 144 HQAELAVSTFWNEQVIFEAUSGGRGYTAIDDIQVLSYPCDSKSPFLRLGDVEVNAQ 203

QY 209 QNATFQCIATGRDAVHNKMLWLRQNGEDIPVAQTKNINHRFAASFRLEQVTKDQDLYR 268
DB 204 QNASFQCHWAGRAAEAEHFFLQSQGLVPAAGVGRHSHRRFLATFPLASVGRSQDLYR 263

QY 269 CVTQSGRSGVSNFAQLIVREPRPIAPQLLGVGPTLYLLIQLNANSIIGDGPILKVE 328
DB 264 CVSQAPRGAGVSNFAELIVKEPPTPIAPQLLRAGPTLYLLIQLNANSIIGDGPVIRKE 323

QY 329 YMTSGSWTETHAVNAPTKLWHLDDPTEYERVLTRPGEGGTGLPGPPLITRCKAEP 388
DB 324 YRMARGPMAEVAHVNLQTYKLWHLDDPTEYERVLTRPGEGGTGLPGPPLISRTCKAEP 383

QY 389 METPKTLTAETQARRIAVDWESLGVNITRCHTFENVITCYHYFRG--HNESRACLDMDP 446
DB 384 TRAPKGLAPAEIQAQQLTLQWEPLGVNTRCHTYAVSLCYRTLGGSHQITRECVKMER 443

QY 447 KAPQVHNLPPYTNVSLKMLTNPEGRKESETIIGTDEDVPGVPVVKSLQGTSPENKI 506
DB 444 GASRYTIKNLLFPRIHVLRLTNPEGRKEGEVTFQTDDEVPVGGIAAESLFTPLEDMI 503

QY 507 FLNWKPELPLENGLIITQYEYSYSIRSFDPAVPAGPQTVNLWNSTHVFHLLHPTTY 566
DB 504 FLKWEPEPQENGLITQYEYSYSQSISSDPVAVNPGPRTISKLNETYHVFNLHPTTY 563

QY 567 QFFIRASTVKGFGPATAINVTNINISAPSLPDYEGVDASLNATATTITVLLRPAQAKGAPI 626
DB 564 LFSVARTSKGRGQAALTEITNINISAPSF-DYADMPSPLGSENTITVLLRPAQGRGAPI 622

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QY 627 SAYQIVVEQLHPHRTKEAGAMECYQVPTVYQNALSGAPVYFAAEPLPGNLPBPAPPTV 686
DB 623 SVYQVVEERPRRLRREPQAGQCFSVPLTFETALARGLVHYFGAEAAASLLAMPPTV 682

QY 687 GDNRTYKGFNPPPLAPKGYNIYFOAMSSVEKETKTQCVRIATKAAATEEPEVDPFAKQ 746
DB 683 GDNQTYRGFNPPPLAPKGYNIYFOAMSSVEKETKTQCVRIATKAAATEEPEVDPFAKQ 741

QY 747 TDRVVKIAGISA-GILVFIILLVIVVVKSKLAKRKKOMAGNTRQEMTHVWAMDES 805
DB 742 SEEMGLILGICAGGLAVLILLGAILIIRKKGPNMTK-ATVNYROEKTHMSAVDRSF 800

QY 806 ADQSTLHAEDPLSLTFMDQHNFSRPLNDPLVPTAVLDENHSATAESRLL-DVPRYLCE 864
DB 801 TDOSTLOEDERLGLSFMDAPGYSR-----GDQRSGGVTEASSLLGGSPRRPCG 849

QY 865 GTESPYQTQLHPAIRVADLLQHLINLMKTSYSGFKEYESFFEGQSASNDVAKKQNR 924
DB 850 RKGSPYHTGQLHPAVRVADLLQHLINLMKTAEGYGFKEYESFFEG---WDATKKDKLK 905

QY 925 KRYGNTIADHSRVILQPVDEDDSSDIYINANYIDIMLYRDGYORPSPHYIATQGVHET 984
DB 906 GGRQEPVSAYDRHHVHLHPMLADPDADYISANYI-----DGYHRSNHFIIATQGPKEMI 959

QY 985 YDFRWVWQBSACIVMVTNLVEGRVKCYKYPDDTEVYGDGVKTCVEMEPLEAYVVRT 1044
DB 960 YDFRWVWQBSACIVMVTNLVEGRVKCYKYPDDTEVYGDGVKTCVEMEPLEAYVVRT 1019

QY 1045 FTLERRGYNEIREVKQFHTGWPDPHGVPIYHATGLLSFTRRVKLSNPPSAGPIVHCSAGA 1104
DB 1020 FALERGYSAHREVRQFHTAWPEHGVPIYHATGLLSFTRRVKLSNPPSAGPIVHCSAGT 1079

QY 1105 GRTCYIVDMLDMAEREGVVDIYNCVKALRSRRINNVQTEQYIFIHDAILEACLCGE 1164
DB 1080 GRTCYIVDMLDMAEREGVVDIYNCVKALRSRRINNVQTEQYIFIHDAILEACLCGE 1139

QY 1165 TAIPVCEFAAYPMIRIDSQTNSSHLKDEPOTLNSVTPRLOAEDCSACIPLHDKNRF 1224
DB 1140 TTIPVNEFRATYREMRIDPQSSNSQUREEFTLNSVTPRLOAEDCSACIPLHDKNRS 1199

QY 1225 MDMLPPRCPLPFLITIDGESSNYINAAIMDSYROPAAFIQYPLPNTVKDFWRLVYDYG 1284
DB 1200 MDVLPDRCLPFLISSDGPNNYINAAITDSYTSAAFIQYPLPNTVKDFWRLVYDYG 1259

QY 1285 CTSIVMLNEVDLSQ---CPQYWPBEGMLRYGPIQVECMSCMCDVINRIPRINLRTP 1341
DB 1260 CTSIVMLNQLNQSNAWPCLYWPBEGMLRYGPIQVECMSCMCDVINRIPRINLRTP 1319

QY 1342 QEGYLMVQFOYLGWASHREVPGSKRSFLKILLQVEKQWQEECEGEERTIHLCLNGGGRS 1401
DB 1320 QEGHLLVRHFQFLWMSAYRDTFDSRKAFHLHLAEVDKQW---AESGDGRTVVHCLNGGGRS 1377

QY 1402 GMFCAIGIVBWKQNVVDVFAVKTLRNPKNNVEAPEQYRCFYCDVALEYLES 1456
DB 1378 GTFCACATVLEIRCHSLVDVFFAAKTLRNYKPNVETMDQVHFCDVALEYLEA 1432

RESULT 15
PTPT_MOUSE
ID PTPT_MOUSE STANDARD; PRT: 1454 AA
AC Q99M80; Q99M81; Q99M82; Q9JIZ1; Q9JIZ2; Q9JUC2; Q9JLPO;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Receptor-type protein-tyrosine phosphatase T precursor (EC 3.1.3.48)
DE (R-PTP-T) (RPTPrho) (mRPTPrho) (RPTmam4).
GN Name=PtpT;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 5), AND ALTERNATIVE SPLICING.  
 RC STRAIN=CS/BL/6J;  
 RX MEDLINE=22730707; PubMed=11423001;  
 RA Besco J.A., Frostholt A., Popesco M.C., Burghes A.H.M., Rotter A.;  
 RT "Genomic organization and alternative splicing of the human and mouse  
 RL RPTPrho genes."; BMC Genomics 2:1-1(2001).  
 RN [2]  
 RP ERRATUM.  
 RX MEDLINE=22730717; PubMed=11814386;  
 RA Besco J.A., Frostholt A., Popesco M.C., Burghes A.H.M., Rotter A.;  
 RL BMC Genomics 2:5-5(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).  
 RA Buchli A.D., Zimmermann D.R., Pfister F., Vaughan L.;  
 RT "RPTPrho: a fourth member of the MAM family of receptor protein  
 RL tyrosine phosphatases expressed in adult brain."; Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).  
 RA Mizuta M., Bergman B., Miki T., Hutton J.C.;  
 RT "Molecular cloning and functional characterization on mouse receptor-  
 RL like protein tyrosine phosphatase, mRPTPrho, which mediates cell-cell  
 RT adhesion of pancreatic beta cells."; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP TISSUE SPECIFICITY.  
 RA MEDLINE=98146229; PubMed=9486824;  
 RX DOI=10.1002/(SICI)1096-9861(19980822)391:4<444::AID-CNE3>3.0.CO;2-0;  
 RA McAndrew P.E., Frostholt A., Evans J.E., Zolotar D., Goldowitz D.,  
 RA Chiu I.-M., Burghes A.H.M., Rotter A.;  
 RT "Novel receptor protein tyrosine phosphatase (RPTPrho) and acidic  
 RL fibroblast growth factor (FGF-1) transcripts delineate a rostrocaudal  
 RT boundary in the granule cell layer of the murine cerebellar cortex."; J. Comp. Neurol. 391:444-455(1998).  
 CC -I- FUNCTION: May be involved in both signal transduction and cellular  
 CC adhesion in the CNS. May have specific signaling roles in the  
 CC tyrosine phosphorylation/dephosphorylation pathway in the anterior  
 CC compartment of the adult cerebellar cortex.  
 CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -I- ALTERNATIVE PRODUCTS:  
 CC Name=1; Event=Alternative splicing; Named isoforms=5;  
 CC Name=2; IsoId=Q99M80-1; Sequence=Displayed;  
 CC Name=3; IsoId=Q99M80-2; Sequence=VSP\_007803, VSP\_007806;  
 CC Name=4; Synonyms=RPTPrho2; IsoId=Q99M80-3; Sequence=VSP\_007803, VSP\_007804;  
 CC Name=5; Synonyms=RPTPrho1; IsoId=Q99M80-4; Sequence=VSP\_007803;  
 CC Name=5; IsoId=Q99M80-5; Sequence=VSP\_007803, VSP\_007805;  
 CC -I- TISSUE SPECIFICITY: Expression is restricted to the CNS.  
 CC Distributed throughout the brain and spinal cord.  
 CC -I- DEVELOPMENTAL STAGE: Exceptionally high levels found in the cortex  
 CC and olfactory bulbs during perinatal development and are down-  
 CC regulated during postnatal week 2. Expression in the cerebellar  
 CC cortex is restricted to the granule cell layer of lobules 1-6.  
 CC Anterior and posterior compartments become discernible only during  
 CC postnatal weeks 2 and 6.  
 CC -I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
 CC Receptor class 2B subfamily.  
 CC -I- SIMILARITY: Contains 4 fibronectin type III domains.  
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -I- SIMILARITY: Contains 1 MAM domain.  
 CC -I- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 CC -----  
 DR EMBL; AF152556; AAD34158.4; -  
 DR EMBL; AY026861; AAK18741.1; -  
 DR EMBL; AY026862; AAK18742.1; -  
 DR EMBL; AY026863; AAK18743.1; -  
 DR EMBL; AF244125; AAF44712.1; -  
 DR EMBL; AF162856; AAF82400.2; -  
 DR EMBL; AF162857; AAF82401.1; -  
 DR HSP; P10586; ILAR  
 DR MGD; MGI:1321152; Pcppt.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR000998; MAM.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.  
 DR Pfam; PF00041; fn3; 3.  
 DR Pfam; PF00629; MAM; 1.  
 DR Pfam; PF0102; Y\_phosphatase; 2.  
 DR PRINTS; PR00020; MAMDOMAIN.  
 DR PRINTS; PR00700; PRTYPHPHTASE.  
 DR SMART; SM00060; FN3; 3.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00137; MAM; 1.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00853; FN3; 4.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00740; MAM\_1; 1.  
 DR PROSITE; PS00060; MAM\_2; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Alternative splicing; Glycoprotein; Hydrolase; Immunoglobulin domain;  
 KW Protein phosphatase; Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 29 Potential.  
 FT CHAIN 30 1454 Receptor-type protein-tyrosine  
 FT DOMAIN 30 770 Phosphatase T.  
 FT TRANSMEM 771 791 Extracellular (Potential).  
 FT DOMAIN 792 1454 Cytoplasmic (Potential).  
 FT DOMAIN 34 195 MAM.  
 FT DOMAIN 197 288 IG-like C2-type.  
 FT DOMAIN 292 383 Fibronectin type-III 1.  
 FT DOMAIN 390 484 Fibronectin type-III 2.  
 FT DOMAIN 485 588 Fibronectin type-III 3.  
 FT DOMAIN 670 767 Fibronectin type-III 4.  
 FT DOMAIN 902 1156 Protein-tyrosine phosphatase 1.  
 FT DOMAIN 1188 1450 Protein-tyrosine phosphatase 2.  
 FT ACT\_SITE 1097 1097 Phosphocysteine intermediate (By  
 FT similarity).  
 FT ACT\_SITE 1391 1391 Phosphocysteine intermediate (By  
 FT similarity).  
 FT DISULFID 217 271 Potential.  
 FT CARBOHYD 82 82 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 425 425 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 514 514 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 551 551 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 605 605 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 658 658 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 688 688 N-linked (GlcNAc...) (Potential).  
 FT VARSPLIC 731 749 Missing (in isoform 2, isoform 3, isoform  
 FT 4 and isoform 5).  
 FT FTId=VSP\_007803.  
 FT R -> RNNAYSYSYLL (in isoform 3).  
 FT FTId=VSP\_007804.  
 FT R -> RNNAYSYSYLSQR (in isoform 5).  
 FT VARSPLIC 794 794  
 FT VARSPLIC 794 794

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FT VARSPLIC 1007 1007 /FTid=VSP 007805.
FT R -> RHPAETHVGTATIGRAASPCM (in isoform
FT 2).
FT CONFLICT 13 16 /FTid=VSP 007806.
FT CONFLICT 21 21 Missing (in Ref. 1).
FT CONFLICT 34 37 R -> P (in Ref. 1).
FT CONFLICT 87 87 GCSC -> RGVP (in Ref. 1).
FT CONFLICT 254 254 A -> T (in Ref. 4; AAF82401).
FT CONFLICT 266 266 A -> S (in Ref. 4; AAF82401).
FT CONFLICT 602 602 I -> V (in Ref. 4; AAF82401).
FT CONFLICT 822 822 T -> S (in Ref. 4; AAF82401).
FT CONFLICT 825 825 G -> T (in Ref. 4; AAF82401).
FT CONFLICT 844 845 G -> S (in Ref. 4; AAF82401).
FT CONFLICT 1016 1016 TD -> N (in Ref. 4; AAF82401).
FT CONFLICT 1049 1049 D -> A (in Ref. 4; AAF82401).
FT CONFLICT 1050 1050 Y -> H (in Ref. 1).
FT CONFLICT 1076 1076 H -> N (in Ref. 4; AAF82401).
FT CONFLICT 1103 1103 L -> V (in Ref. 4; AAF82401).
FT CONFLICT 1259 1259 R -> K (in Ref. 1).
FT CONFLICT 1266 1266 F -> L (in Ref. 4; AAF82401).
FT CONFLICT 1269 1269 L -> I (in Ref. 4; AAF82401).
FT CONFLICT 1269 1269 T -> S (in Ref. 4; AAF82401).
SQ SEQUENCE 1454 AA; 163012 MW; C60464F7B423F8A8 CRC64;

Query Match 58.6%; Score 4579; DB 1; Length 1454;
Best Local Similarity 57.8%; Pred. No. 8.3e-301; Mismatches 333; Indels 42; Gaps 8;
Matches 841; Conservative 239;

QY 21 PLLGALQFAGGCTFDGACDYHQDL-YDDPEWVHVSAQEPHYLPPEMPOGGSYVWV 79
DB 22 PPLPAGAGQAAGGCSFDEHVSNCYSVALCTNGFTWEQINTWEKPMPLDPAVPTGSPMVV 81

QY 80 DSSNHPGKARLQLPWKENDTHCIDFSYLLYSQKLNPGTLNLVRNKGPLANPTWN 139
DB 82 NSSGRASGOKAHLPLTKENDTHCIDFHYFSSDRSGALNVYVKGNGPQGNPVNM 141

QY 140 VTGFTGRDMLRAELAVSTFWPEYQVIEAEVSGSGSYIAIDDDIQLVSYCDKSPHLR 199
DB 142 VSGVTEGWKAEIAISTFWPHFYQVIFESVSLKGHPGVIADVEVRVLAHPCRKAPHFLR 201

QY 200 LGDEVNAGONATFOCIATGRDAVHKNLWLRNGEDIPVAQTKNHNRRHRAASPRLOEV 259
DB 202 LQNEVNVGONATFOCIAGGKWSQDKLWQWNGRDTALMVRVNVNRRFSATVSADT 261

QY 260 TKTDQDLRCVTSRSGSVSNFAQLIVREPPRIAPQLLGVGPTYLLIQLNANSIIGD 319
DB 262 SQRISKVCVIRSDGSGSVSNYAEILVKEPPTIAPPELLAVGATYLWIKPNANSIIGD 321

QY 320 GPIILKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYRVLVTRPGEQGTGLPGPPL 379
DB 322 GPIILKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYRVLVTRPGEQGTGLPGPPL 381

QY 380 ITRTKCABPMRPTKTLKAEIQARRIADVWESLGNITRCHTFENVITCVHYFRGHNESRA 439
DB 382 ITRTKCABPMRPTKTLKAEIQARRIADVWESLGNITRCHTFENVITCVHYFRGHNESRA 439

QY 440 DCLDMDPKAQHVNHLPPTYTVNSUKMLITNPGRKESEETIIQDEDPVGPVPVKSQ 499
DB 440 EAEVEIQTSSHTVLRGLRPFMTIRLRLLSNPEGRMESEELVVQTEEDVPVAVPLESIQ 499

QY 500 TSPENKIFLNWKEPLEPNGIITQYEVSYSSIRSPDPVAVPGPPTQVSNLWNSTHVPMH 559
DB 500 GFPEEKIYQWKPNETNGVITLYEINYKAVGSLDPSADLSSQSGKVFKLNETHFLFVG 559

QY 560 LHPGTYTOFFIRASTVKGPGPATAINVTNIGAPSLPDYEGVDASINETATTITVLLRPA 619
DB 560 LHPGTYTOFFIRASTVKGPGPATAINVTNIGAPSLPDYEGVDASINETATTITVLLRPA 619

QY 620 QAKGAPIISAYQIVBQLPHRTRKRBAGAMECYQVPVTVYONALSGGAPYVFAAELPPGNLP 679
DB 619 QSRGAPSVYQLVWKEERLQSRRAADIIECPVSVSYRNASNLDSLHYFAAELKPSNLP 678
DB 680 EPAPFTVGNRTYKGFNWPPLAPRKGYNLYFOAMSSVEKETKTQCVRATKAAATEEPV 739
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Search completed: June 1, 2005, 13:55:00  
Job time : 177.044 secs

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Db 679 VTQFTVGDKNKYNGYWNPPSLPKSYISIFQALSKANGETKINCVRLATKAGPMGSAQV 738
QY 740 IP-----DPAKQTRVVKIAGISAGILVFILLLLVVIVVVKSKLAK 781
Db 739 TPGTPCLLLTASTQNSNTVEPEKQVDNTVMAGVIAGLLMFIILLGVMLTKRKLAK 798
QY 782 KRKDMGNTROEMTHMNMADRSDADQSTLHAEDPLSLTFMDQHNFSRPLENDPLVPTAV 841
Db 799 KQKETQSGAQRREM-GPVASTDKPTAKLGTNRNDEGFSSSQDVNGFTDGSRGELSQPTLT 857
QY 842 LDENHSATABESSRLLDVPRYLCEGTESPYQTGQLHPAIRVADLLQHLNMLKTSYSYGE 901
Db 858 I-QTH-----PYRTCDPVMSYPRDQQAIRVADLLQHTQMKRGQGYGKE 904
QY 902 EYESFFEQSASWDVAKQONRAKNRYNIIAYDHSRVILQFVEDDPSDDSYINANYIDW 961
Db 905 EYEALPEGQTASWDATAKEDENRNKNRYNIIISYDHSRVLLVLDGDPHSDSYINANYI--- 961
QY 962 LYRDGYORPSHYIATQGPVHETVYDFWRMWOBSACIVMTNLVEVGRVKCYKWPDDT 1021
Db 962 ---DGYHRPHRYIATQGPVHETVYDFWRMWOBSACIVMTNLVEVGRVKCYKWPDDT 1018
QY 1022 BVYGDVKVTCVEMEPLAEBYVVRTFTLERRGYNEIREVKOPHTGWPDRHGVPHATGLLSF 1081
Db 1019 EYVGIKVTIETPLAEBYVIRFTVQKKGHYEIRLRLFTSWPDHGVPCYATGLLGF 1078
QY 1082 IRRYKLNPPSPAGPIVHCSAGAGRTGCIYIVIDIMDMAEREGVVDIYNCVKALRSRIN 1141
Db 1079 VRQVKFLNPPBAGPIVHCSAGAGRTGCFIADTMDMAENEGVVDIENCVCRELRAQRVN 1138
QY 1142 MVQTEBOYIFHDAILEACLCGETAIPVCEPKAAYPDMIRIDQTSNSSLKDEPOTLNSV 1201
Db 1139 LVQTEBOYVFDHDAILEACLCGETAIPVCEPKAAYPDMIRIDQTSNSSLKDEPOTLNSV 1198
QY 1202 TPLQAEDCSITACLPNRHDKNRFMDLPPDRCLPFLITIDGESSNYINAAIMDSVRQPA 1261
Db 1199 TPRVRPDCSITGLLPNRHDKNRFMDLPPDRCLPFLITIDGESSNYINAAIMDSVRQPA 1258
QY 1262 FIVTQYPLNPTVKDFWRLVVDYDGTCTSIYMLNEVDLSQGCPOYWPBEGMLRYGPIQV 1321
Db 1259 FVVTQYPLNPTVKDFWRLVVDYDGTCTSIYMLNEVDLSQGCPOYWPBEGMLRYGPIQV 1318
QY 1322 CSMDCDVINRIFRICNTRPOEGYLMVQOFOYLGWASHREVPVPGSKRSLKILQVEKQ 1381
Db 1319 ADIDEDIIHFRICNTRPOEGYLMVQOFOYLGWASHREVPVPGSKRSLKILQVEKQ 1378
QY 1382 BCEBEGRTIITHCLNGGSGMFCAGIGIVVBMVQRNVVDVFAVKTLLRNKSPNVEAPE 1441
Db 1379 QYDREGRTVHCLNGGSGMFCAGIGIVVBMVQRNVVDVFAVKTLLRNKSPNVEAPE 1438
QY 1442 QYRFDYDVALEYLES 1456
Db 1439 QYKFYVVALEYLES 1453
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:31:52 ; Search time 145.589 Seconds  
(without alignments)  
3822.724 Million cell updates/sec

Title: US-09-887-669-2  
Perfect score: 7709  
Sequence: 1 MDITAAALPAFVALLLSP.....EAPQYRCYDVALLYLESS 1439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7692	99.8	1439	2	AAR63632 Human rec
2	7688	99.7	1439	7	ADJ68478 Human hea
3	7656.5	99.3	1440	2	AAY29591 Human pro
4	7656.5	99.3	1440	8	ADI23886 Human PTP
5	7571	98.2	1457	5	ABB57308 Mouse isc
6	7524	97.6	1457	2	AAR63633 Murine re
7	7174	93.1	1407	2	AAR63631 Murine re
8	4818	62.5	1452	4	AAW79159 Human pro
9	4807	62.4	1452	8	ADI80761 Human pro
10	4806	62.3	1452	6	ABR58629 Human can
11	4784	62.1	1452	7	ADJ68277 Human hea
12	4777.5	62.0	1455	4	AAW80143 Human pro
13	4602.5	59.7	1436	7	ADB79775 Rat putat
14	4586.5	59.5	1436	2	AAW41361 Receptor
15	4577.5	59.4	1462	5	ABB97521 Novel hum
16	4564	59.2	1463	6	ABJ37035 Human bre
17	4564	59.2	1463	7	ADB75519 Prostate
18	4564	59.2	1520	5	ABJ05584 Breast ca
19	4555	59.1	1499	4	AAW25768 Human pro
20	4374.5	56.7	1442	7	ADJ68999 Human hea
21	4287	55.6	1430	2	AAW49907 Human pan
22	2493.5	32.3	623	4	AAW25675 Human pro
23	2210.5	28.7	815	4	AAW25875 Human pro
24	1529.5	19.8	1501	2	AAW72858 Rat recep
25	1513	19.6	1254	8	ADN02662 Liver dis

26	1512	19.6	1796	6	AAE37971 Human kin
27	1509	19.6	1897	3	AAY81785 Human pro
28	1509	19.6	1897	3	AAY56100 LAR tyros
29	1509	19.6	1897	3	AAB19712 Human pro
30	1509	19.6	1897	7	ADD18740 Human dis
31	1509	19.6	1897	8	ADJ33670 Human leu
32	1509	19.6	1907	8	ADP18674 Human pro
33	1506.5	19.5	1266	8	ADQ66041 Novel hum
34	1506	19.5	1948	7	ADD18742 Human dis
35	1505.5	19.5	1907	4	AAU14143 Human nov
36	1505.5	19.5	1912	8	ADR40183 Human pro
37	1505	19.5	1949	7	ADE57117 Human pro
38	1505	19.5	1949	7	ADE57121 Human pro
39	1505	19.5	1949	7	ADD47019 Human pro
40	1505	19.5	1949	7	ADD47015 Human pro
41	1493	19.4	1291	2	AAR75201 Tyrosine
42	1491	19.3	1495	5	ABB57380 Rat mucoc
43	1491	19.3	1496	7	ADE57115 Rat Prote
44	1491	19.3	1496	7	ADE57119 Rat Prote
45	1491	19.3	1496	7	ADD47013 Rat Prote

## ALIGNMENTS

RESULT 1  
AAR63632  
ID AAR63632 standard; protein; 1439 AA.

XX AAR63632;  
AC AAR63632;  
XX  
DT 21-OCT-2004 (revised)  
DT 25-MAR-2003 (revised)  
DT 26-OCT-1995 (first entry)  
XX  
DE Human receptor-type protein tyrosine phosphatase (RPTP) kappa.

XX Receptor-type protein tyrosine phosphatase protein; cellular signal;  
KW RPTPase-kappa; PTPase.

XX Homo sapiens.  
OS Unidentified.

XX Key Location/Qualifiers  
FT Domain 207..277  
FT Domain /label = Ig-like domain  
FT Domain 755..774  
FT Domain /label = alpha helical transmembrane domain

XX WO9424161-A1.

XX 27-OCT-1994.

XX 20-APR-1994; 94WO-US004377.

XX 21-APR-1993; 93US-00049384.

XX 01-JUL-1993; 93US-00087244.

XX (UNY-) UNIV NEW YORK MEDICAL CENT.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Schlessinger J, Sap JM, Ullrich A, Vogel W, Fuchs M;

XX WPI; 1994-341769/42.

XX N-PSDB; AAQ72913.

XX Mammalian receptor-type protein tyrosine phosphatase-kappa (RPTP-k) protein and DNA - useful to identify cpds. which bind to RPTP-k and modulate enzymatic activity. Also inhibition of type II RPTP homo.philic binding (Eng).

XX Claim 4; Fig 15; 144pp; English.

XX

CC The novel receptor-type protein tyrosine phosphatase protein or  
 CC glycoprotein is termed RPTP kappa (also known as Rptase-kappa). Human  
 CC breast cancer cell line SK-BR-3 was examined by PCR using primers  
 CC corresp. to conserved sequences within the PTP catalytic domain shared  
 CC by all identified PTPases. Several known PTPases were revealed together  
 CC with some novel members of the PTPase family. One of the novel sequences,  
 CC designated MCP7 (Mammary carcinoma-derived PTPase clone 7) was highly  
 CC represented in all 121 clones examined. The MCP7 PCR fragment was used to  
 CC screen a SK-BR-3 cDNA library. The results are AAQ72913 and its deduced  
 CC AA sequence AAR63632. The AA sequence displays the structural  
 CC organisation of a type II transmembrane PTPase. The N-terminal  
 CC hydrophobic stretch of 20-26 AAs is typical of signal peptides. A second  
 CC region consisting of hydrophobic residues (see FT) is predicted to be a  
 CC single alpha-helical transmembrane domain. It is followed by a short  
 CC region of mainly basic residues characteristic of a transfer stop  
 CC sequence. The amino-terminal portion of the putative extracellular domain  
 CC contains a sequence motif, a so-called WAM domain, spanning a region of  
 CC about 170 residues. This motif is followed by one possible Ig-like domain  
 CC (see FT). (Updated on 25-MAR-2003 to correct FN field.)

Revised record issued on 21-OCT-2004 : Correction to feature table key

Sequence 1439 AA;

Query Match 99.8%; Score 7692; DB 2; Length 1439;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1437; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDTTAAALPAFVALLLSPPLGSAQGSAGGCTFDDGPGADYHQDLYDFEWHV 60  
 DB 1 MDTTAAALPAFVALLLSPPLGSAQGSAGGCTFDDGPGADYHQDLYDFEWHV 60  
 QY 61 SAQEPHYLPPEMPOGSGYIMVDSDDHDPGEKARLQPTMKENDTHCIDFSYLLSQKGLNP 120  
 DB 61 SAQEPHYLPPEMPOGSGYIMVDSDDHDPGEKARLQPTMKENDTHCIDFSYLLSQKGLNP 120  
 QY 121 GTLNTLVRNKGPLANPIVNWVGTGROWLRAELAVSTFWPNEYQVIFEAESVSGRSGYI 180  
 DB 121 GTLNTLVRNKGPLANPIVNWVGTGROWLRAELAVSTFWPNEYQVIFEAESVSGRSGYI 180  
 QY 181 AIDDIQVLSYPCDKSPHFLRLGDVFNAGONATFOCIATGRDAVINKLWLRNGEDIPV 240  
 DB 181 AIDDIQVLSYPCDKSPHFLRLGDVFNAGONATFOCIATGRDAVINKLWLRNGEDIPV 240  
 QY 241 AQTKNINHRFAASFRLQEVTKTDQDLYRCVTSERGSVSNFAQLIVREPPRTIAPPQL 300  
 DB 241 AQTKNINHRFAASFRLQEVTKTDQDLYRCVTSERGSVSNFAQLIVREPPRTIAPPQL 300  
 QY 301 LGVGPYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYE 360  
 DB 301 LGVGPYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYE 360  
 QY 361 IRVLLTRPGEGETGLPGPLITRTKCAEPMRTPKTKIAEIOARRIADVWESLGYNITRC 420  
 DB 361 IRVLLTRPGEGETGLPGPLITRTKCAEPMRTPKTKIAEIOARRIADVWESLGYNITRC 420  
 QY 421 HTFNVTICVHYFRGHNESKADCLMDPKAPQHVHNLPPYTNVSLKMLITNPEGRKESEE 480  
 DB 421 HTFNVTICVHYFRGHNESKADCLMDPKAPQHVHNLPPYTNVSLKMLITNPEGRKESEE 480  
 QY 481 TTIQTDVEDVPGVPVKSLQGTSTFENKIFLNWKEPLDPNGIITQYEISYSSIRSFDPAPV 540  
 DB 481 TTIQTDVEDVPGVPVKSLQGTSTFENKIFLNWKEPLDPNGIITQYEISYSSIRSFDPAPV 540  
 QY 541 AGPPTQVSNLWNSTHHVFHMLHPGTYQFFIRASTVKGPGATANTVTINISAPTLPDYE 600  
 DB 541 AGPPTQVSNLWNSTHHVFHMLHPGTYQFFIRASTVKGPGATANTVTINISAPTLPDYE 600  
 QY 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELPHRTKREAGAMECYQVPVYQN 660  
 DB 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELPHRTKREAGAMECYQVPVYQN 660  
 QY 661 AMSGGAPYYFAELPPGNLPEPAPFTVGNRTTYQGFNPPPLAPRKGNYIYFQAMSSVEKE 720

DB 661 AMSGGAPYYFAELPPGNLPEPAPFTVGNRTTYQGFNPPPLAPRKGNYIYFQAMSSVEKE 720  
 QY 721 TKTQCVRIATKAAATEEPEVIPPDPKQTRVVKIAGISAGILVFIILLVWILVVKSKLA 780  
 DB 721 TKTQCVRIATKAAATEEPEVIPPDPKQTRVVKIAGISAGILVFIILLVWILVVKSKLA 780  
 QY 781 KKRKDMGNTRQEMTHMVMNMDRSYADOSTLHAEDPLSITFMDQHNFSRPHNSHATAES 840  
 DB 781 KKRKDMGNTRQEMTHMVMNMDRSYADOSTLHAEDPLSITFMDQHNFSRPHNSHATAES 840  
 QY 841 SRLLDVPRYLCEGTSPVQGLHPALRVADLLQHLNLMKTSDSYGFKEEYESFEGQSA 900  
 DB 841 SRLLDVPRYLCEGTSPVQGLHPALRVADLLQHLNLMKTSDSYGFKEEYESFEGQSA 900  
 QY 901 SWDVAKQDNQRAKNRYGNIITAYDHSRVILQVPEDDPSDDYINANYIDGYPQSHYIATQG 960  
 DB 901 SWDVAKQDNQRAKNRYGNIITAYDHSRVILQVPEDDPSDDYINANYIDGYPQSHYIATQG 960  
 QY 961 PVHETVDFRMIWQESACIWMVTNLVEGRVKCYKYWPDDETEYGDGFKTCVMEPLA 1020  
 DB 961 PVHETVDFRMIWQESACIWMVTNLVEGRVKCYKYWPDDETEYGDGFKTCVMEPLA 1020  
 QY 1021 EYVVRTFTLBERGYNEIREVKQPHFTGMPDHGVPHATGLLSFIRRVKLSNPPSAGPIV 1080  
 DB 1021 EYVVRTFTLBERGYNEIREVKQPHFTGMPDHGVPHATGLLSFIRRVKLSNPPSAGPIV 1080  
 QY 1081 HCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRINNMVQTEEQYIFIHDAILE 1140  
 DB 1081 HCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRINNMVQTEEQYIFIHDAILE 1140  
 QY 1141 ACLCGETAIPVCEPKAAYFDMIRIDSTNSHLKDEFTQLNSVTPRLOAEDCSACLPRN 1200  
 DB 1141 ACLCGETAIPVCEPKAAYFDMIRIDSTNSHLKDEFTQLNSVTPRLOAEDCSACLPRN 1200  
 QY 1201 HDKRNFMDLPPDRCLPLITIDGESSNYINAAIMDSYRQPAAFIVTQYPLPNTVKDFWR 1260  
 DB 1201 HDKRNFMDLPPDRCLPLITIDGESSNYINAAIMDSYRQPAAFIVTQYPLPNTVKDFWR 1260  
 QY 1261 LVYDYGCTSIIVMLNEVDLSQSCPOYWPBEGMLRGPQVECMSCMDCDINRIFRICNL 1320  
 DB 1261 LVYDYGCTSIIVMLNEVDLSQSCPOYWPBEGMLRGPQVECMSCMDCDINRIFRICNL 1320  
 QY 1321 TRPEGYLWVQOQFYLGWASHREVPGSKRSLKILQVEKQWKEWKEGEGRTIIHCLNGG 1380  
 DB 1321 TRPEGYLWVQOQFYLGWASHREVPGSKRSLKILQVEKQWKEWKEGEGRTIIHCLNGG 1380  
 QY 1381 GRSGMFCAGIIVEMVKQNVVDVPHAVKTLRNSKPNMVEAPEQYRVCYDVALEYLESS 1439  
 DB 1381 GRSGMFCAGIIVEMVKQNVVDVPHAVKTLRNSKPNMVEAPEQYRVCYDVALEYLESS 1439  
 RESULT 2  
 ADJ68478  
 ID ADJ68478 standard; protein; 1439 AA.  
 XX AC ADJ68478;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Human heat mitochondrial protein as a therapeutic target SeqID284.  
 XX KW mitochondrial; human; screening assay; diabetes mellitus;  
 KW Huntington's disease; osteoarthritis;  
 KW Leber's hereditary optic neuropathy; LHON;  
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
 KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;  
 KW osteopathic; ophthalmological; cytostatic.  
 XX OS Homo sapiens.  
 XX PN WO2003087768-A2.

XX	23-OCT-2003.	QY	421	HTFNVTICVHYFRGHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESSE	480
XX	04-APR-2003; 2003WO-US010870.	DB	421		
XX	12-APR-2002; 2002US-0372843P.	QY	481	TIITQDEDPGPPVKSLOGTSFENKIFLANKKPLDPNGLIITQVEISYSSIRSDPAVPV	540
XX	17-JUN-2002; 2002US-0389987P.	DB	481		
XX	20-SEP-2002; 2002US-0412418P.	QY	541	AGPPQTVSNLWNSTHVFHMLHPGTTTQFFIRASTVKGFGPATVNTVTSAPLDPYE	600
XX	(MITO-) MITOKOR.	DB	541		
XX	(BUCK-) BUCK INST AGE RES.	QY	601	GVDSASNETATTTVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVYQN	660
XX	Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;	DB	601		
XX	Warnock DE;	QY	661	AMSGGAPYFAAELPCNLPBPAPFTVGDNRVTQGFNPNPLAPRKGNVYFQAMSSVEKE	720
XX	WPI; 2003-845369/78.	DB	661		
XX	Identifying a mitochondrial target for drug screening assays and for	QY	721	TKTQCVRIATKAATERPEVIPPDAKOTDRVVKIAGISAGILVFILLVLIIVKSKLA	780
XX	treating diseases associated with altered mitochondrial function,	DB	721		
XX	PT comprises detecting a modified polypeptide in a sample and correlating	QY	781	KRKRDAMGNTRQEMTHMVNAMDRSYADQSTLHAEDPLSITFMQDNHSPRYENHSATAES	840
XX	with the disease.	DB	781		
XX	Claim 1; SEQ ID NO 284; 180pp; English.	QY	841	SRLLDVPRYLCEGTSPYQGLHPAIRVADLLQHNLMKTSDSYGKBEYESFEQSA	900
XX	This invention relates to novel mitochondrial targets that can be used	DB	841		
XX	CC for therapeutic intervention in treating a disease associated with	QY	901	SWDVAKQDNRAKRNVIITAYDHSRVILQVVEDDPSDDYINANYIDGYORPSHYIATQ	960
XX	CC altered mitochondrial function. Specifically, it refers to a method for	DB	901		
XX	CC identifying proteins of the human heart mitochondrial proteome that are	QY	961	PVHETVYDFWRMIWQBSQACIVMVTNLVEVGRVKCYKYPDDTEVYGDVKVTCVMEPLA	1020
XX	CC useful for drug screening assays, as well as therapeutic targets. The	DB	961		
XX	CC present invention describes a method for identifying such proteins that	QY	1021	EYVVRFTLRRGYNEIREVKQFHFTGWPDPHGVPHATGLLSFIRRVKLSNPPSAGPIV	1080
XX	CC can be used in the treatment of various diseases associated with altered	DB	1021		
XX	CC mitochondrial function including diabetes mellitus, Huntington's disease,	QY	1081	HCSSAGAGRTCYIVDIDMLMAEREGVVDIYNCVKALRRRNINMVQTEEOYIFTHDAILE	1140
XX	CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial	DB	1081		
XX	CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy	QY	1141	ACLCGETAIPVCEFAKAYFDMIRIDSQTNSSHLKDEFQTLNSVTPRLQADCSIACLPRN	1200
XX	CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these	DB	1141		
XX	CC compositions have neuroprotective, neurotropic, antidiabetic,	QY	1201	HDKNRPMFMPLPPDRCLPFLITIDGESSNYINAAIMDSYRQPAAFIVTQYPLNTVKDFWR	1260
XX	CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and	DB	1201		
XX	CC cytosolic activities. This polypeptide sequence is a human heart	QY	1261	LVVDYDGTCTSVMLNEVDLSQGCPCQYWPBEGMLRGPIQVECMSCSMDCCDVNIFRICNL	1320
XX	CC mitochondrial protein of the invention.	DB	1261		
XX	Seq Sequence 1439 AA;	QY	1321	TRPQEGYLMVQQPYQLGWASHREVPGSKRSFLKILIQVEKWQBEWKEGEGRTIIHCLNGG	1380
XX	Query Match 99.7%; Score 7688; DB 7; Length 1439;	DB	1321		
XX	Best Local Similarity 99.8%; Pred. No. 0;	QY	1381	GRSGMFCALGIVVEMVKRQNVDFVHAKVTLRNSKPNMVEAPQYRCYDVALEYLESS	1439
XX	Matches 1436; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	DB	1381		
QY	1 MDTTAAALPAFVALLLSLSPPLIGSAQGFSGGCTFDDPGACDHYQDLDDFEWVHV				
DB	1 MDTTAAALPAFVALLLSLSPPLIGSAQGFSGGCTFDDPGACDHYQDLDDFEWVHV				
QY	61 SAQEPHYLPPEMPOGYSYIVDSSDHPDGEKARLQPTMKENDTHCIDFSYLLYSQKGLNP				
DB	61 SAQEPHYLPPEMPOGYSYIVDSSDHPDGEKARLQPTMKENDTHCIDFSYLLYSQKGLNP				
QY	121 GTNLILVRNKGPLANPINWVTGTRDLRAELAVSTFWPNEYQVIFEAESVSGRSGYI				
DB	121 GTNLILVRNKGPLANPINWVTGTRDLRAELAVSTFWPNEYQVIFEAESVSGRSGYI				
QY	181 AIDDIQVLSYPCDKSPHFLRGDVEVNAGQATQCCTATGRDAVHNKWLQRRNGEDIPV				
DB	181 AIDDIQVLSYPCDKSPHFLRGDVEVNAGQATQCCTATGRDAVHNKWLQRRNGEDIPV				
QY	241 AQTKNINHRFAASFRILQEVTKTDQDLRYRCVTSQERGSVSNFAQLIVRPPPIAPPOL				
DB	241 AQTKNINHRFAASFRILQEVTKTDQDLRYRCVTSQERGSVSNFAQLIVRPPPIAPPOL				
QY	301 LGVGPYLLIQLNANSIIGDGPPIILKEVEYEMTSGSWTETHAVNAPTYKLMHLDPDTEYE				
DB	301 LGVGPYLLIQLNANSIIGDGPPIILKEVEYEMTSGSWTETHAVNAPTYKLMHLDPDTEYE				
QY	361 IRVLLTRPGEAGTGLPGPPLITRTKCAEPMTPTKILAEIQARRIADVWESLYNITRC				
DB	361 IRVLLTRPGEAGTGLPGPPLITRTKCAEPMTPTKILAEIQARRIADVWESLYNITRC				

RESULT 3  
AA29591  
ID AA29591 standard; protein; 1440 AA.

XX AAY29591;  
AC 14-OCT-1999 (first entry)  
DT Human protein phosphatase k.  
DE Human; protein phosphatase k; HPTPK.  
KW Homo sapiens.  
OS KR98026246-A.  
PN 15-JUL-1998.  
PD 08-OCT-1996; 96KR-00044614.  
PF 08-OCT-1996; 96KR-00044614.  
PR 08-OCT-1996; 96KR-00044614.  
XX (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.  
PA Hah HJ, Kil MC, Yang Y, Byun GH;  
PI WPI; 1999-33582/28.  
DR N-PSDB; AAZ08539.  
XX Human protein phosphatase, base sequence thereof and amino acid sequence  
PT thereof.  
PT Disclosure; Fig 1a-d; 14pp; Korean.  
PS The present sequence represents human protein phosphatase k (HPTPK)  
XX  
CC  
XX  
SQ Sequence 1440 AA;  
Query Match 99.3%; Score 7656.5; DB 2; Length 1440;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1431; Conservative 3; Mismatches 5; Indels 1; Gaps 1;  
QY 1 MDTTAAALPAPVALLLSPWLLGSAQGSAGGCTFDGPGACDYHQDLYDDFEWVHV 60  
DB 1 MDTTAAALPAPVALLLSPWLLGSAQGSAGGCTFDGPGACDYHQDLYDDFEWVHV 60  
QY 61 SAQEPHYLPPEMPOGYSYIVDSSDHPGKARLQLPWKENDTHCIDFSYLLYSOKGLNP 120  
DB 61 SAQEPHYLPPEMPOGYSYIVDSSDHPGKARLQLPWKENDTHCIDFSYLLYSOKGLNP 120  
QY 121 GTLNLVVRNKGPLANPIWNTGFTGRDWRRAELAVSTFWPNEYQVIFEAESVSGRSYI 180  
DB 121 GTLNLVVRNKGPLANPIWNTGFTGRDWRRAELAVSTFWPNEYQVIFEAESVSGRSYI 180  
QY 181 AIDDIQVLSYPCDKSPHFRLRLGDEVNAGONATFCIATGRDAVHNKWLQRRNGEDIPV 240  
DB 181 AIDDIQVLSYPCDKSPHFRLRLGDEVNAGONATFCIATGRDAVHNKWLQRRNGEDIPV 240  
QY 241 AQTKNINRRFAASFRLOEVTKTDQDLYRCVTSQSGSVNFAQLIVREPRPTAPPQL 300  
DB 241 AQTKNINRRFAASFRLOEVTKTDQDLYRCVTSQSGSVNFAQLIVREPRPTAPPQL 300  
QY 301 LGVGPTYLLIQNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTLYKLWHLDPDTEYE 360  
DB 301 LGVGPTYLLIQNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTLYKLWHLDPDTEYE 360  
QY 361 IRVLLTRFEGGTGLPGPLPILTRTKCABEMRPTKTLKIAEQARRIAVDWESLGYNITRC 420  
DB 361 IRVLLTRFEGGTGLPGPLPILTRTKCABEMRPTKTLKIAEQARRIAVDWESLGYNITRC 420  
QY 421 HFNVTICVHYPRGHNESKADCLMDPKAPQHVNHLPPTYNVSLKMLITNPEGRKESEE 480  
DB 421 HFNVTICVHYPRGHNESKADCLMDPKAPQHVNHLPPTYNVSLKMLITNPEGRKESEE 480  
QY 481 TTIQTDEDVPGVPVKSLQGTSPENKIFLWKEPLDPNGIITQYEISYSSIRSPDPAVPV 540  
DB 481 TTIQTDEDVPGVPVKSLQGTSPENKIFLWKEPLDPNGIITQYEISYSSIRSPDPAVPV 540

DB 481 TTIQTDEDVPGVPVKSLQGTSPENKIFLWKEPLDPNGIITQYEISYSSIRSPDPAVPV 540  
QY 541 AGPPQTVSNLWNSTHHVFMHLHPGCTTYOFFIRASTVKGFGPATAINVTNTNISAPTLDPYE 600  
DB 541 AGPPQTVSNLWNSTHHVFMHLHPGCTTYOFFIRASTVKGFGPATAINVTNTNISAPTLDPYE 600  
QY 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQPVVTYON 660  
DB 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQPVVTYON 660  
QY 661 AMSGAPYFAAELPPGNLPEPAPFTVGDNRITYQGFWNPPPLAPRKGNINYEQAMSSVEKE 720  
DB 661 AMSGAPYFACTPPGNLPEPAPFTVGDNRITYQGFWNPPPLAPRKGNINYEQAMSSVEKE 720  
QY 721 TKTCVRIATK-AATEPEVIPPDAKQTDVVKIAGISAGILVIFILLVILLVIVKSKL 779  
DB 721 TKTCVRIATKAAATEPEVIPPDAKQTDVVKIAGISAGILVIFILLVILLVIVKSKL 780  
QY 780 AKRKDAMGNTRQEMTHVMNAMDRSYADQSTLHAEDPLSITFMDOHNPSPRYENHSATAE 839  
DB 781 AKRKDAMGNTRQEMTHVMNAMDRSYADQSTLHAEDPLSITFMDOHNPSPRYENHSATAE 840  
QY 840 SSRLLDVPYLCGCTESPYQTQLHPAIRVADLLQHINLMKTSYGFKEBYEFFEGQS 899  
DB 841 SSRLLDVPYLCGCTESPYQTQLHPAIRVADLLQHINLMKTSYGFKEBYEFFEGQS 900  
QY 900 ASWDVAKQONRAKRNIGNIIAYDHSRVILQPVDEDDPSSDYINANYIDGQRPQSHYIATQ 959  
DB 901 ASWDVAKQONRAKRNIGNIIAYDHSRVILQPVDEDDPSSDYINANYIDGQRPQSHYIATQ 960  
QY 960 GPVHETVDFWRMIWOSACIWMVTNLVEGRVKYKWPDDTEVVGDFKVCVEMEPL 1019  
DB 961 GPVHETVDFWRMIWOSACIWMVTNLVEGRVKYKWPDDTEVVGDFKVCVEMEPL 1020  
QY 1020 AEYVVRFTLERRGYNEIREVKQPHFTGWPDPHGVPHYATGLLSFIRRVKLSNPPSAGPIV 1079  
DB 1021 AEYVVRFTLERRGYNEIREVKQPHFTGWPDPHGVPHYATGLLSFIRRVKLSNPPSAGPIV 1080  
QY 1080 VHCASAGRTGCTYIVDIMLDMAREGVVDIYNCVKALRSRRINNVQTEEQYIFIHDAI 1139  
DB 1081 VHCASAGRTGCTYIVDIMLDMAREGVVDIYNCVKALRSRRINNVQTEEQYIFIHDAI 1140  
QY 1140 EACLCGETATPVCEFKAAEDMIRIDQTSNSSLKDBFOTLNSVTPRLQADCSACIACLP 1199  
DB 1141 EACLCGETATPVCEFKAAEDMIRIDQTSNSSLKDBFOTLNSVTPRLQADCSACIACLP 1200  
QY 1200 NHDKNRFDMLPPDRCLPFLITIDGESSNYINAALMDSYRQPAAFIVTQYPLPNTVKDFW 1259  
DB 1201 NHDKNRFDMLPPDRCLPFLITIDGESSNYINAALMDSYRQPAAFIVTQYPLPNTVKDFW 1260  
QY 1260 RLVDYDGTCTSIVMNLNEVDLSQGCPOYWPBEGMLRYGPIQVCEMCSMDCDVINRIFRICN 1319  
DB 1261 RLVDYDGTCTSIVMNLNEVDLSQGCPOYWPBEGMLRYGPIQVCEMCSMDCDVINRIFRICN 1320  
QY 1320 LTRPQEGVLMVQOYILGWASHREVPKSRFLKILQVEKWQEBWEGEGRTIHCILNG 1379  
DB 1321 LTRPQEGVLMVQOYILGWASHREVPKSRFLKILQVEKWQEBWEGEGRTIHCILNG 1380  
QY 1380 GGRSGMFCAGIIVVMVKRQNVVDVFAVKTLRNSKPNMVEAPEQYRFCDYVALEYLESS 1439  
DB 1381 GGRSGMFCAGIIVVMVKRQNVVDVFAVKTLRNSKPNMVEAPEQYRFCDYVALEYLESS 1440  
RESULT 4  
AD123886  
ID AD123886 standard; protein; 1440 AA.  
XX  
AC AD123886;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Human PTPRK protein SEQ ID NO:4.  
XX

KW antisense oligonucleotide; human;  
KW protein tyrosine phosphatase receptor type K; PTPRK; cytosolic;  
KW antiinflammatory; antidiabetic; antisense gene therapy; diabetes;  
KW inflammation; hyperproliferative disorder; cancer; chromosome 6.  
XX  
XX Homo sapiens.  
XX WO2004005312-A1.  
XX 15-JAN-2004.  
XX 27-JUN-2003; 2003WO-US016237.  
XX 03-JUL-2002; 2002US-00189429.  
XX (ISIS-) ISIS PHARM INC.  
XX Cowser LM, Freier SM;  
XX WPI; 2004-083493/08.  
XX N-PSDB; AD123748.  
XX  
XX New antisense oligonucleotide, having a sequence targeted to a nucleic  
XX acid encoding PTPRK, useful for preparing a composition for treating  
XX diabetes, inflammation or hyperproliferative disorder, e.g., cancer.  
XX  
XX Example 13; SEQ ID NO 4; 150pp; English.  
XX  
XX The present invention describes an antisense oligonucleotide (I), having  
XX a sequence comprising 8-80 base pairs, targeted to a nucleic acid  
XX encoding protein tyrosine phosphatase receptor type K (PTPRK), that  
XX specifically hybridizes with the nucleic acid encoding PTPRK, and inhibits  
XX expression of PTPRK. Also described: (1) a composition comprising the  
XX compound and a carrier or diluent; (2) a method of inhibiting the  
XX expression of PTPRK in cells or tissues; (3) a method of treating an  
XX animal having or suspected of having a disease or condition associated  
XX with PTPRK; and (4) a method for screening for an antisense compound. (I)  
XX has cytostatic, antiinflammatory and antidiabetic activities, and can be  
XX used in antisense gene therapy. The antisense oligonucleotide (I) can be  
XX used for preparing a composition for treating diabetes, inflammation or  
XX hyperproliferative disorder, e.g., cancer. The present sequence  
XX represents human PTPRK, which is used in an example from the present  
XX invention. The human PTPRK gene is located on chromosome 6, more  
XX specifically to 6q22.2-23.1.  
XX  
XX Sequence 1440 AA;  
Query Match 99.3%; Score 7656.5; DB 8; Length 1440;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1431; Conservative 3; Mismatches 5; Indels 1; Gaps 1;  
QY 1 MDTTAAALPAFVALLLSWPPLGSAQGSAGGCTFDDPGACDYHQDLYDDFEWVHV 60  
DB 1 MDTTAAALPAFVALLLSWPPLGSAQGSAGGCTFDDPGACDYHQDLYDDFEWVHV 60  
QY 61 SAQEPHYLPPEMPOGSGYMI VDDSDHDPGEKARLQPTMKENDTHCIDFSYLLXSQKGLNP 120  
DB 61 SAQEPHYLPPEMPOGSGYMI VDDSDHDPGEKARLQPTMKENDTHCIDFSYLLXSQKGLNP 120  
QY 121 GTLNLVRNKGPLANINWVGTGRDMLRAELAVSTFWPNEVQVIFAEVSGRSGYI 180  
DB 121 GTLNLVRNKGPLANINWVGTGRDMLRAELAVSTFWPNEVQVIFAEVSGRSGYI 180  
QY 181 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQNTFQCIATGRDAVHNLKWLQRRNGEDIPV 240  
DB 181 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQNTFQCIATGRDAVHNLKWLQRRNGEDIPV 240  
QY 241 AQTKNINHRFAAFRIQEVTKTDQDLYRCVTSERGSYVSNFAQLIVREPPRPPIAPPOL 300  
DB 241 AQTKNINHRFAAFRIQEVTKTDQDLYRCVTSERGSYVSNFPQLIVREPPRPPIAPPOL 300  
QY 301 LGVGPYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLVHLDPDTEYE 360

DB 301 LGVGPYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLVHLDPDTEYE 360  
QY 361 IRVLLTRPGGGTCLPGPPLITRTKCAEPMRTPKTKIAIEIQARRIAVDMESGYNITRC 420  
DB 361 IRVLLTRPGGGTCLPGPPLITRTKCAEPMRTPKTKIAIEIQARRIAVDMESGYNITRC 420  
QY 421 HTFNVTICHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLINPEGRKESSE 480  
DB 421 HSFNVTICHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLINPEGRKESSE 480  
QY 481 TIIQTDEDVPGVPVKSLQGTSPENKIFLNKWEPLDNGIITQYEISYSIRSFDPAVPV 540  
DB 481 TIIQTDEDVPGVPVKSLQGTSPENKIFLNKWEPLDNGIITQYEISYSIRSFDPAVPV 540  
QY 541 AGPPQTVSNLWNSHTHVFMHLPGTQYQFFIRASTVKFGPAPATAINVTNISAPTLDPYE 600  
DB 541 AGPPQTVSNLWNSHTHVFMHLPGTQYQFFIRASTVKFGPAPATAINVTNISAPTLDPYE 600  
QY 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVYQN 660  
DB 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVYQN 660  
QY 661 AMSGGAPYYFAAELPCGNLPEPAPFTVGDNRVTQGFNWPPLAPRKGYNIYFOAMSSVEKE 720  
DB 661 AMSGGAPYYFAAELPCGNLPEPAPFTVGDNRVTQGFNWPPLAPRKGYNIYFOAMSSVEKE 720  
QY 721 TKTQCVRATK-AATBEPEVIPDPAKQTDVRVVIAGISAGILVFILLVILVVKSKL 779  
DB 721 TKTQCVRATKAAATEPEVIPPAPKQTDVRVVIAGISAGILVFILLVILVVKSKL 780  
QY 780 AKRKAOMGNTRQEMTHVNMADRSYADQSTLHAEDPLSITFMDQHNFSRYENHSTATAE 839  
DB 781 AKRKAOMGNTRQEMTHVNMADRSYADQSTLHAEDPLSITFMDQHNFSRYENHSTATAE 840  
QY 840 SSRLLDVRVLCGTSPPYQGTGOLHPAIRVADILLOHNLMTKSDSYGKEYESFFEGQS 899  
DB 841 SSRLLDVRVLCGTSPPYQGTGOLHPAIRVADILLOHNLMTKSDSYGKEYESFFEGQS 900  
QY 900 ASMDVAKQONRAKRYGNI IAYDHSRVILOPVEDDPSSDIYINANYIDGQRPSHYIATQ 959  
DB 901 ASMDVAKQONRAKRYGNI IAYDHSRVILOPVEDDPSSDIYINANYIDGQRPSHYIATQ 960  
QY 960 GPVHETVYDFWRMIWQESACI VVWVNLVEVGRVKYKWPDDTEVVGDPKVCVMEPL 1019  
DB 961 GPVHETVYDFWRMIWQESACI VVWVNLVEVGRVKYKWPDDTEVVGDPKVCVMEPL 1020  
QY 1020 AEYVVRTFTLERGYNEIREVKQFHTGWDHGVPHATGCLLSFIRVKLSNPPSAGPIV 1079  
DB 1021 AEYVVRTFTLERGYNEIREVKQFHTGWDHGVPHATGCLLSFIRVKLSNPPSAGPIV 1080  
QY 1080 VHCASAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRINMVQTEBQYIFIHDAIL 1139  
DB 1081 VHCASAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRRINMVQTEBQYIFIHDAIL 1140  
QY 1140 EACLCCGTAIPVCEKAAAYFDMIRIDSQTNSSHLKQEFQTLNSVTPRLQADCSIACLPR 1199  
DB 1141 EACLCCGTAIPVCEKAAAYFDMIRIDSQTNSSHLKQEFQTLNSVTPRLQADCSIACLPR 1200  
QY 1200 NHDKNRFDMLPPDRCLPLITITDGESSNYINAAALMDSYRQPAAFIVQYPLNTVXDFW 1259  
DB 1201 NHDKNRFDMLPPDRCLPLITITDGESSNYINAAALMDSYRQPAAFIVQYPLNTVXDFW 1260  
QY 1260 RLVDYVGCSTSVMLNEVDLSQGCPCQYWPBEGMLRYGPIQVECMSCSDCVINRIFRICN 1319  
DB 1261 RLVDYVGCSTSVMLNEVDLSQGCPCQYWPBEGMLRYGPIQVECMSCSDCVINRIFRICN 1320  
QY 1320 LTRPQEGYLMVQVQFYILGNASHREVFGSKESFLKLILQVEKQWBEKGEGRITIIHCLNG 1379  
DB 1321 LTRPQEGYLMVQVQFYILGNASHREVFGSKESFLKLILQVEKQWBEKGEGRITIIHCLNG 1380  
QY 1380 GGRSGMFCAGIIVEMVKRQNVVDVFAVKTILNSKPNMVEAPEQYRQFCYDVALEYLESS 1439  
DB 1381 GGRSGMFCAGIIVEMVKRQNVVDVFAVKTILNSKPNMVEAPEQYRQFCYDVALEYLESS 1440

RESULT 5  
 ABB57308  
 ID ABB57308 standard; protein; 1457 AA.  
 XX AC ABB57308;  
 XX DT 07-MAR-2002 (first entry)  
 XX DE Mouse ischaemic condition related protein sequence SEQ ID NO:862.  
 XX KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
 XX KW vasospastic ischaemia; ischaemic condition; ischaemic disease.  
 XX OS Mus musculus.  
 XX PN WO200188188-A2.  
 XX PD 22-NOV-2001.  
 XX PF 18-MAY-2001; 2001WO-JP004192.  
 XX PR 18-MAY-2000; 2000JP-00145977.  
 XX PA (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
 XX PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
 XX DR WPI; 2002-034733/04.  
 XX DR N-PSDB; AB199774.  
 XX PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
 PT expression levels of particular genes defined in the specification or by  
 PT determining the expression profile of a gene group comprising these  
 PT genes.  
 XX PS Claim 2; Page 2155-2161; 2690pp; English.  
 XX CC The present invention describes a method for examining ischaemic  
 CC conditions, comprising measuring the expression levels of particular  
 CC genes (I) in a test sample or determining the expression profile of a  
 CC gene group in the sample comprising genes selected from (I). The method  
 CC is useful for examining the ischaemic condition (e.g. compressive  
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
 CC expression levels of particular genes (AB199202 to AB199912, encoding the  
 CC protein sequences in ABB57020 to ABB57374) or by determining the  
 CC expression profile of a gene group comprising these genes. The expression  
 CC levels or expression profiles produced by these genes are used as an  
 CC indicator when screening for ischaemic condition-improving drugs or  
 CC therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR  
 CC primers for a mouse ischaemic condition related sequence, which are used  
 CC in the exemplification of the present invention  
 SQ Sequence 1457 AA;

Query Match 98.2%; Score 7571; DB 5; Length 1457;  
 Best Local Similarity 97.3%; Pred. No. 0;  
 Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

QY 1 MDTTAAALPAFVALLLLSPWLLGSAQGFSGAGGCTFDDGACDYHODLYDDFEWHV 60  
 DB 1 MD-VAAALPAFVALLLLYFWLLGSAQGFSGAGGCTFDDGACDYHODLYDDFEWHV 59  
 QY 61 SAQEPHYLPPEMPQGSYMTVDSDDHDPGEKARLQLPTMKENDTHCIDFSYLLYSQGLNP 120  
 DB 60 SAQEPHYLPPEMPQGSYMWVVDSSNDHPGEKARLQLPTMKENDTHCIDFSYLLYSQGLNP 119  
 QY 121 GTILNLRVKNKGLANPIWNVTGTRDWLRALAVSTFWPNEYQVIFPAEVSGRSGYI 180  
 DB 120 GTILNLRVKNKGLANPIWNVTGTRDWLRALAVSTFWPNEYQVIFPAEVSGRSGYI 179  
 QY 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATFQCIGTATGRDAVHNKMLQRRNGEDIPV 240

DB AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATFQCIGTATGRDAVHNKMLQRRNGEDIPV 239  
 QY AQTKNINHRPAAFRLOEVTKTDODLYRCVTSQSGSVNFAQLIVREPRPIAPPOL 300  
 DB AQTKNINHRPAAFRLOEVTKTDODLYRCVTSQSGSVNFAQLIVREPRPIAPPOL 299  
 QY LGVGPYLLLIQNLANSIIGDGPITLKEVEYMTSGSWTETHAVNAPTIVKWLHLPDPTBE 360  
 DB LGVGPYLLLIQNLANSIIGDGPITLKEVEYMTSGSWTETHAVNAPTIVKWLHLPDPTBE 359  
 QY IRVLLTRPGEGETGLPGPPLITRTKCAEPMRTPTLKTAEIQARRIAVDWSLGYNITRC 420  
 DB IRVLLTRPGEGETGLPGPPLITRTKCAEPMRTPTLKTAEIQARRIAVDWSLGYNITRC 419  
 QY HTFNWTCYHYFRGHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGEKESSE 480  
 DB HTFNWTCYHYFRGHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGEKESSE 479  
 QY TTIQTDDEVPGVPVKSLOQTSFENKIFLNKPELDPNGIITQYEISYSSIRSPDPAPV 540  
 DB TTIQTDDEVPGVPVKSLOQTSFENKIFLNKPELDPNGIITQYEISYSSIRSPDPAPV 539  
 QY AGPPQTVSNLWNSTHVFHMLHPCGTYOFFIRASTVKGFGPATAINVTTNISAPSLDYE 600  
 DB AGPPQTVSNLWNSTHVFHMLHPCGTYOFFIRASTVKGFGPATAINVTTNISAPSLDYE 599  
 QY GVDASLNETATITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTVQN 660  
 DB GVDASLNETATITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTVQN 659  
 QY AMSGAPYFAELPPGGLPEPAPFTVGDNKTQGFNPPPLAPRGYNIYFQAMSSVSK 720  
 DB ALSGAPYFAELPPGGLPEPAPFTVGDNKTQGFNPPPLAPRGYNIYFQAMSSVSK 719  
 QY TKTQCVRIATK-AAATEPEVIPPAPKQTDRTVVKIAGISAGILVFILLVWVIVKSKL 779  
 DB TKTQCVRIATKAAATEPEVIPPAPKQTDRTVVKIAGISAGILVFILLVWVIVKSKL 779  
 QY AKKRDAMGNTRQEMTHMVNAMDSDYADQSTLHAEPLUSITFMDQHNPSRY----- 831  
 DB AKKRDAMGNTRQEMTHMVNAMDSDYADQSTLHAEPLUSITFMDQHNPSRLPNDPLVPT 839  
 QY 832 ----ENHSATAESRLLDVPRYLCGETESPQTGOLHFAIRVADLQHINLMKTSYGF 887  
 DB AVLDEHNSATAESRLLDVPRYLCGETESPQTGOLHFAIRVADLQHINLMKTSYGF 899  
 QY KEEVESFFEGQSASWDVAKQDNRAKNRYGNI IAYDHSRVILQPVEDDPSSDIYANAYI- 946  
 DB KEEVESFFEGQSASWDVAKQDNRAKNRYGNI IAYDHSRVILQPVEDDPSSDIYANAYI 959  
 QY 947 ----DGVRPSHYIATQGPVHETVYDFWRMIWQSQSACIWMVTNLVEGRVKCYWPD 1001  
 DB IWLVRDGYQRPESHYIATQGPVHETVYDFWRMIWQSQSACIWMVTNLVEGRVKCYWPD 1019  
 QY 1002 DTEVVGDFKVTCEMEPLAEYVVRFTLLERGYNEIREVKOPHETGWDHGVPHYATGL 1061  
 DB 1020 DTEVVGDFKVTCEMEPLAEYVVRFTLLERGYNEIREVKOPHETGWDHGVPHYATGL 1079  
 QY 1062 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCYIVIDIMLDMAREGVDIYNCVKALRSR 1121  
 DB 1080 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCYIVIDIMLDMAREGVDIYNCVKALRSR 1139  
 QY 1122 INMVQTEQYIFIHDAILEACLCGETAIPVCEFFKAAFYDMIRIDISQTNSSHLKDFOTLN 1181  
 DB 1140 INMVQTEQYIFIHDAILEACLCGETAIPVCEFFKAAFYDMIRIDISQTNSSHLKDFOTLN 1199  
 QY 1182 SVTPQLQEDCSIACLPRNHDKNRPMWMLPPDRCLPELITIDGSSNYINAAIMDSYROP 1241  
 DB 1200 SVTPQLQEDCSIACLPRNHDKNRPMWMLPPDRCLPELITIDGSSNYINAAIMDSYROP 1259  
 QY 1242 AAFIVTQPLPNTVDFWRLVYDYCTSIWMLNEVDLSQGCQFYWPEBGLRYGPIQVBC 1301

Db	1360	A A F V T Q Y P L N T W K D F R W L V D Y G C T S I V M L N E V D L S Q G C P Q W P B E G M L R Y G P I Q V E C	1319
Qy	1302	M S C S M D C D V I N R I F R I C N L T R P Q E G Y L M W Q O F Y L G W H A S H R E V P G S X R S F L K I L Q V E K W	1361
Dd	1320	M S C S M D C D V I N R I F R I C N L T R P Q E G Y L M W Q O F Y L G W H A S H R E V P G S X R S F L K I L Q V E K W	1379
Qy	1362	Q E E W K E G E G R T I I H C L N G G R S G M F C A I G I V E M V K R Q N V D V F H A V K T L R N S K P N M V E A	1421
Dd	1380	Q E E C E G E G R T I I H C L N G G R S G M F C A I G I V E M V K E Q N V D V F H A V K T L R N S K P N M V E A	1439
Qy	1422	P E Q Y R F C Y D V A L E Y L E S S	1439
Dd	1440	P E Q Y R F C Y D V A L E Y L E S S	1457

RESULT 6  
AAR63633  
ID AAR63633 standard; protein; 1457 AA.

AC AAR63633;

DT	21-OCT-2004	(revised)
DT	25-MAR-2003	(revised)
DT	08-JUN-1995	(first en

DE Murine receptor-type protein tyrosine phosphatase precursor protein.

Receptor-type protein tyrosine phosphatase protein; cellular signal;  
KW  
RPTPase-kappa; enzyme.  
KW

XX	
OS	Mus musculus.
OS	Unidentified.

Key	Location/Qualifiers
Peptide	1. .25
FT	/label = signal
FT	
FT	
Region	33. .189
FT	/label = A5 surface protein homology
FT	
Domain	733. .774
FT	
FT	/label = Transmembrane
Domain	926. .1158
FT	/label = PTase I
FT	
Domain	1218. .1455
FT	/label = PTase II
FT	
FT	

XX  
PN  
WO9424161-A1.

XX  
PD 27-OCT-1994.

20-APR-1994: 94WO-US004377.

XX  
PR 21-APR-1993: 93US-00049384.

PK	21-APR-1993;	93US-00049384.
PR	01-JUL-1993;	93US-00087244.

PA (UUNY-) UNIV NEW YORK MEDICAL CENT.  
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Schlessinger J, Sap JM, Ullrich A, Vogel W, Fuchs M;

WPI; 1994-341769/42.

DR N-PSDB; AAQ72914.

xx Mammalian receptor-type protein tyrosine phosphatase-kappa (RPTP-k)  
PT protein and DNA - useful to identify cpds. which bind to RPTP-k and  
PT modulate enzymatic activity. Also inhibition of type II RPTP homo:philiic  
PT binding (Eng).

PS Claim 2; Fig 1; 144pp; English.

The novel receptor-type protein tyrosine phosphatase protein or glycoprotein is termed RPTP kappa (also known as RPTase-kappa). The first approx. 170AAs of RPTP kappa show similarity (26% overall identity) to a region in the xenopus cell surface protein A5 with features of Ig-like

domains. There are four putative fibronectin type III-like repeats (residues 296-681). The tandem repeat of two PTPase homologues is typical for most RPTases. A feature of RPTP kappa is the extended distance between its transmembrane domain and the start of the first phosphatase homology domain. The RPTP kappa cDNA sequence comprises a 5' UTR of 1072 bps and a 3' UTR of 388 bps. The translational initiation codon is identified by a std. environment for initiation of translation (Kozak) and by the existence of an upstream in-frame stop codon, and is followed by a hydrophobic region that may serve as a signal peptide. (Updated on 25-MAR-2003 to correct PN field.)

CC Revised record issued on 21-OCT-2004 : Correction to feature table key  
XX  
SQ Sequence 1457 AA;

Query Match	97.6%	Score 7524;	DB 2;	Length 1457;
Best Local Similarity	96.8%	Pred. No. 0;		
Matches 141;	Conservative 15;	Mismatches 12;	Indels 20	

Qy	1	MDTTAAALPAFVALLLLSPWLLGSSAQGFSAAGCTFDDGPGACDYHQLYDDFEWVHV	60
Db	1	MD - VAAALPAFVALWLLYWPWLLGSSALGQFSAAGCTFDDGPGACDYHQLYDDFEWVHV	59
Qy	61	SAQEPHYLPPEMFGSSWMIWVDSDDHDPGEKARQLPTMKENDTHCIDFSYLLYSQKGLNP	120
Db	60	SAQEPHYLPPEMFGSSWVWVDSNHDHDPGEKARQLPTMKENDTHCIDFSYLLYSQKGLNP	119
Qy	121	GTLLNILVRNKGPLANPIWNVGTGFTGRDWLRAELAVSTFWPNEYQVILFEAEVSGRSGYI	180
Db	120	GTLLNILVRNKGPLANPIWNVGTGFTGRDWLRAELAVSTFWPNEYQVILFEAEVSGRSGYI	179
Qy	181	AIDDIQVLSYPCDKSPHFRLGDEVNAGONATFQCIATGRDAVHNKMLQRRNGEDIPV	240
Db	180	AIDDIQVLSYPCDKSPHFRLGDEVNAGONATFQCIATGRDAVHNKMLQRRNGEDIPV	239
Qy	241	AQTKNINHRFPAAASFRLOEVTKTDDLYRCVTOSERGSGVSNFAQLIVRBPPIAPQOL	300
Db	240	AQTKNINHRFPAAASFRLOEVTKTDDLYRCVTOSERPSPGVSNFAQLIVRBPPIAPQOL	299
Qy	301	LGVGPTVLLILQLNANSIIGDGPILILKEVEYRMTSGSWTETHAVNAPYKLUHLWLDPDTEYE	360
Db	300	LGVGPTVLLILQLNANSIIGDGPILILKEVEYRMTSGSWTETHAVNAPYKLUHLWLDPDTEYE	359
Qy	361	IRVLLTRPGGGTCLPGPPLITRTKCAEPMRTPKTLKIAEIQARRIAVDWESLGYNITRC	420
Db	360	IRVLLTRPGGGTCLPGPPLITRTKCAEPMRTPKTLKIAEIQARRIAVDWESLGYNITRC	419
Qy	421	HTFNVTICYHYFRGHNESKADCLDMDPKAQHVVNHLPPYTNVSLKMLITNPEGRKESEE	480
Db	420	HTFNVTICYHYFRGHNESRADCLDMDPKAQHVVNHLPPYTNVSLKMLITNPEGRKESEE	479
Qy	481	TIQTDEDVPGVPVKSLOGTSFENKIFLNWKEPLDPNGHIIIOYEVSYSSIRSFDPAPVP	540
Db	480	TIQTDEDVPGVPVKSLOGTSFENKIFLNWKEPLDPNGHIIIOYEVSYSSIRSFDPAPVP	539
Qy	541	AGPQTVSNLWNTHVFMHLHGTTYYQFFIRASTVKFGFPATAINVTNTISAPTLPDYE	600
Db	540	AGPQTVSNLWNTHVFMHLHGTTYYQFFIRASTVKFGFPATAINVTNTISAPTLPDYE	599
Qy	601	GVDSASLNETAATTIVLLRPAQAKGAPISAYQIYVEELHPHRTKREAGAMECYQVPVTYQN	660
Db	600	EVDASLNETAATTIVLLRPAQAKGAPISAYQIYVEQLHPHRTKREAGAMECYQVPVTYQN	659
Qy	661	AMSGGAPYFAAELPGNLPPEPAFTVGDNRITVQGFWNPPPLAPRKGNIFYQAMSSVEKE	720
Db	660	ALSGGAPYFAAELPGNLPPEPAFTVGDNRITVKGFWNPPLAPRKGNIFYQAMSSVEKE	719
Qy	721	TKTQCVRIATK - AATSEPEVIPPAAQOTORVVKIAGISAGILVFILLILVILVVKSKL	779
Db	720	TKTQCVRIATKAATSEPEVIPPAAQOTDKVKIAGISAGILVFILLILVILVVKSKL	779
Qy	780	AKRKDAMGNTRQEMTHVNMAMDRSYADOSTLHAEDPLSITFMDDQHNFSPRY - - - - -	831



Db 360 IRVLLTRPGGGTGLPGPPLITRTKCAEPHRTPTKTKIAIBIQARRIAVDWESLGYNITRC 419  
Qy 421 HTFNVTTCYHYFRGHNSKADCLMDPKAPQHVNNHLPPTYNVSLKMLTNPEGRKESEE 480  
Db 420 HTFNVTTCYHYFRGHNSRADCLMDPKAPQ----- 450  
Qy 481 TITQDEVDVGPVPVKSQGTSPENKIFLNWKEPLDPNGIITQVEISYSSIRSPDPAVPV 540  
Db 451 -----SFEHKIFLNWKEPLEPNGIITQVEISYSSIRSPDPAVPV 489  
Qy 541 AGPPQTVSNLWNSHHVFMHLHPCTTYQFFIRASTVKGFGPATAINVTTNISAPTLDPYE 600  
Db 490 AGPPQTVSNLWNSHHVFMHLHPCTTYQFFIRASTVKGFGPATAINVTTNISAPSLDPYE 549  
Qy 601 GVDASLNEMATTITVLLRPAQAAGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTYQN 660  
Db 550 GVDASLNEMATTITVLLRPAQAAGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTYQN 609  
Qy 661 AMSGGAPYYFAAELPPGNLPEPAPFTVGDNRITVQGFNPPPLAPRKGNYYFOAMSSVEKE 720  
Db 610 ALSGGAPYYFAAELPPGNLPEPAPFTVGDNRITVQGFNPPPLAPRKGNYYFOAMSSVEKE 669  
Qy 721 TKTCQVRIATK-AATEPEVIPPAPKOTDRVVKTAGISAGILVFILLLVILVIVKSKL 779  
Db 670 TKTCQVRIATKAAATEPEVIPPAPKOTDRVVKTAGISAGILVFILLLVILVIVKSKL 729  
Qy 780 AKRKKDAMGNTRQEMTHMNMADRSYADQSTLHAEDPLSITFMDQHNFSRY----- 831  
Db 730 AKRKKDAMGNTRQEMTHMNMADRSYADQSTLHAEDPLSITFMDQHNFSRPLNDPLVPT 789  
Qy 832 -----ENHSATAESRLLDVPRYLCEGTSPYQTLHPAIRVADLLQHLINLMKTSYGF 887  
Db 790 AVLDEHNSATAESRLLDVPRYLCEGTSPYQTLHPAIRVADLLQHLINLMKTSYGF 849  
Qy 888 KEYESFFEGQSASWDVAKKQDNRAKRNRYNIIAYDHSRVILQVDEDDPSDDVINYI- 946  
Db 850 KEYESFFEGQSASWDVAKKQDNRAKRNRYNIIAYDHSRVILQVDEDDPSDDVINYI 909  
Qy 947 -----DGYQRPSPHYIATQGPVHETVDFWRMIWQESACIWMVTLNVEGRVKCYKWP 1001  
Db 910 IWLRYDGYQRPSPHYIATQGPVHETVDFWRMIWQESACIWMVTLNVEGRVKCYKWP 969  
Qy 1002 DTEVYGDVKTCVEMEPALBYVVRFTFLRRGNYEIREVKQFHTGPHDGVPHATGLL 1061  
Db 970 DTEVYGDVKTCVEMEPALBYVVRFTFLRRGNYEIREVKQFHTGPHDGVPHATGLL 1029  
Qy 1062 SFTRRVKLSNPPSAGPIVHCSAGAGRTGCIYVIDIMLDAEREGVVDIYNCVKALRSR 1121  
Db 1030 SFTRRVKLSNPPSAGPIVHCSAGAGRTGCIYVIDIMLDAEREGVVDIYNCVKALRSR 1089  
Qy 1122 INNVQTEEQYIFHDAILEACLCGETAIPVCEPKAAAFDMIRIDQSNSSHLKDFOTLN 1181  
Db 1090 INNVQTEEQYIFHDAILEACLCGETAIPVCEPKAAAFDMIRIDQSNSSHLKDFOTLN 1149  
Qy 1182 SVTPRLQAECDSCIAPRNHDKNRMFLPDRCLPELITIDGESSNYINAALMDSYROP 1241  
Db 1150 SVTPRLQAECDSCIAPRNHDKNRMFLPDRCLPELITIDGESSNYINAALMDSYROP 1209  
Qy 1242 AAFIVTQYPLPNTVKDFWRLVYDGTSTIYMLNEVDLSQCPQVWPEGLRMYGPTQVE 1301  
Db 1210 AAFIVTQYPLPNTVKDFWRLVYDGTSTIYMLNEVDLSQCPQVWPEGLRMYGPTQVE 1269  
Qy 1302 MSCMDCDVINRIFRICNLTRPOEGLYMWQOQFYLWASHREVPGRKSLKILQVEKW 1361  
Db 1270 MSCMDCDVINRIFRICNLTRPOEGLYMWQOQFYLWASHREVPGRKSLKILQVEKW 1329  
Qy 1362 QEBWKEGEGRTIICHLNGGGRSGMFCAGIIGVWENVKRQNVVDVFAVKTILRNSKPNVEA 1421  
Db 1330 QEBWKEGEGRTIICHLNGGGRSGMFCAGIIGVWENVKRQNVVDVFAVKTILRNSKPNVEA 1389  
Qy 1422 PEQYRFCYDVALEYLESS 1439  
Db 1390 PEQYRFCYDVALEYLESS 1407

## RESULT 8

AAM79159

ID AAM79159 standard; protein; 1452 AA.

XX

AC AAM79159;

XX DT 06-NOV-2001 (first entry)

XX Human protein SEQ ID NO 1821.

XX

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
XX tissue growth factor; immunomodulatory; cancer; leukaemia;  
XX nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

XX

XX WO200157190-A2.

XX

XX 09-AUG-2001.

XX

XX 05-FEB-2001; 2001WO-US004098.

XX

XX 03-FEB-2000; 2000US-00496914.

XX

XX 27-APR-2000; 2000US-00560875.

XX

XX 20-JUN-2000; 2000US-00598075.

XX

XX 19-JUL-2000; 2000US-00620325.

XX

XX 01-SEP-2000; 2000US-00654936.

XX

XX 15-SEP-2000; 2000US-00663561.

XX

XX 20-OCT-2000; 2000US-00693325.

XX

XX 30-NOV-2000; 2000US-00728422.

XX

(HYSE-) HYSEQ INC.

XX

Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

Xue AJ, Yang Y, Wejhrman T, Goodrich R;

WPI; 2001-476283/51.

DR

N-PSDB; AAK52292.

XX

Nucleic acids encoding polypeptides with cytokine-like activities, useful

in diagnosis and gene therapy.

XX

Claim 20; Page 4196-4199; 6221pp; English.

XX

The invention relates to polynucleotides (AAK51456-AAK53435) and the  
encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to  
cytokine, cell proliferation or cell differentiation or which may induce  
production of other cytokines in other cell populations. The  
polynucleotides and polypeptides are useful in gene therapy, vaccines or  
peptide therapy. The polypeptides have various cytokine-like activities,  
e.g. stem cell growth factor activity, haematopoiesis regulating  
activity, tissue growth factor activity, immunomodulatory activity and  
activin/inhibin activity and may be useful in the diagnosis and/or  
treatment of cancer, leukaemia, nervous system disorders, arthritis and  
inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
(AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the  
sequence listing were missing at the time of publication

XX

SQ Sequence 1452 AA;

XX

Query Match 62.5%; Score 4818; DB 4; Length 1452;

Best Local Similarity 60.8%; Pred. No. 0;

Matches 890; Conservative 207; Mismatches 324; Indels 42; Gaps 8;

Qy

4 TAAALPAFVALLLLSPWPLGSAQGFSGAGCTDDGPGACDYHODLYDDFEWVHYSAQ 63

Db

3 TLGTCLATLALLL-----TAAGETFGGCLFDEPYSTCGYSQSGDDFNWQNTL 54

Qy

64 EPHYLPPEPQGSYMTIVDSHDHPGKARLQLPTMKENDTHCIDFSYLLYSQKLNPGTL 123

Db 55 TKPTSDPMPGSGFWLVNASRPEQORAHLLLPOLKENDTHCIDPHFVSSKSNPGLL 114  
Qy 124 NILVRVNGKPIANPIVNWVGTFTGRDMLDABELAVSTFWPNEYQVIFAEVSGRSGYTAID 183  
Db 115 NVYKVNNGPLGNPIWNISGDPTRTNRAELAISTFWENFYQVIFEV-ITSCHQGYLAD 173  
Qy 184 DIOVLSYPCDKSPHFLRLGDVENVAGONATQCTATGRDAVHKLWLQRRNGEDI PVAQT 243  
Db 174 EVKVLGHECTTTPHFLRIQNVENVAGOPATFQCSAIGRTVAGDRMLWQGDIVROAPLKEI 233  
Qy 244 KNIHRRFAAFLQEVTKTDQDLYRCVTOESRSGVSNFAQLIVREPPRIAPPPQLGV 303  
Db 234 KVTSSRRFIASFVNVNTTKRAGKRCMRITGGVGSINYAELVKKEPPVPIAPPQLASV 293  
Qy 304 GPTYLLIQNLANSIIGDGPPIILKEVEYRMTSGSWTETHAVNAPTYKLMHLPDPTYEYIRV 363  
Db 294 GATYLLIQNLANSINGDGPFI VAREVEYCTASGSMNDROPVDSTSYKIGHLPDPTYEYISV 353  
Qy 364 LLTRPGEGETGLPGPPLITRTKCAPMRTPTKLTAEIQARRIADVMSLGYNITRCHTF 423  
Db 354 LLTRPGEGETGSPGALTRTKCADPMRGPKLEVEVKSQOITIRWEPFGYNNVTRCHSY 413  
Qy 424 NVTCYHYFRGHNESKAD--CLDMDPKAPQVNVNHLPPYTNVSLKMLNTNPEGRKESSEET 481  
Db 414 NLTVHYCYQVGOEQVREVSNDTENSHPQHTITNLSPTVSVKLIILMNPGRKESQEL 473  
Qy 482 IIQTDEDVPGVPVKSLOQTSFENKI FLNWKPELDPNGIITQYEISYSIRSFPDPAVPA 541  
Db 474 IVQTDDELPGAVPTESI QGSTFEKIFLOWREPTQYGVITLYEITYKAVSSPDPEIDL 533  
Qy 542 GPQTVSNLWNSHTVFMHLHPGTYQFFIRASTVKGFGPATINVTINISAPLTPDYEG 601  
Db 534 NQSGRVSKLGNETHFLFGLYPGTYSTFTIRASTAKGFGPATNQFTTKISAPSNPAYE- 592  
Qy 602 VDASINETAATTITVLLRPAQAGAPISAVQIVBELHPHRTKREAGAMECYQVPVYQNA 661  
Db 593 LETPLNQDNTVTVMLKPAHSGAPSVQIVVEEERPRRTKTEILKCPVPIHFQNA 652  
Qy 662 MSGGAPYIFAALPLPGNLPEPAPFTVGNRTYQGFNPPPLAPRKGNYIFYQAMSVKET 721  
Db 653 SLLNSQYFAAEFFADSLQAQPFITGDKNTYGVWNTPLLPYKSYRIYFQAASRANGET 712  
Qy 722 KTCQVRIATKAATEPEVIPPDAKOTDRVVKIAGISAGILFILLVILLVILVKSKLAK 781  
Db 713 KIDCQVATKGAA--TPKVPPEPEKQDHTVKIAGIAGILLFVITFLGWLVLMKRRKLAK 771  
Qy 782 KRKDAWNTROBMTMNVAMDRSYAQDSTLHAEDPLSITFMDOHNFSPRY----- 831  
Db 772 KRKETMSSTRQEMTVVNSMDKSYAEQGTNCDE---AFSMDTHNLNGRSVSSPSFTWK 828  
Qy 832 -----ENHSATAESSRLDLVPYR-LCEGTESPYQTQQLHPAIRVADLLQH 875  
Db 829 TNLSTSVNSYYPDETHMTASDTSLSVQSHYTKKREPADVQYQQLHPAIRVADLLQH 888  
Qy 876 INLMKTSDSYGKEEYESFPEGQASWDVAKQDQRAKNRYGNIITAYDHSRVILQVDEDD 935  
Db 889 ITQMKCAEYGFKEEYESFPEGQASAPWDSAKDENMKRNYGNIITAYDHSRVRLQTIQED 948  
Qy 936 PSSDYINANYIDGYORPSHYIATQCPVHETVDFWEMTWEOQACIVMVTNLVEYGRVKC 995  
Db 949 TNSDYINGNIIDGYHRPNHYIATQCPMQETIYDFWRMWHENTASLIIMVTNLVEYGRVKC 1008  
Qy 996 KYKVPDDTVEYDFKVKTCVMEPLAEYVVRVTRFTLERRGYNEIREVKQFHTGPDHGVY 1055  
Db 1009 KYKVPDDTEIYDKVLTLETALLAEYVIRTAFAVEKRGVHEIREIRQFHTGPDHGVY 1068  
Qy 1056 HATGLLSFTRRVKLNPPSAGPIVHCSAGAGRTCYIVIDIMLMAEREGVVDIYNVCK 1115  
Db 1069 HATGLLGFVRQVKSPPSPSAGPLVHCSAGAGRTCFIVIDIMLMAEREGVVDIYNVCR 1128  
Qy 1116 ALRSRRINNVQTEEQYIFTHDAILEACLGETAIPVCEPKAAYPFMDIRDSQTNSSHLKD 1175

Db 1129 ELRSRRVNVQTEBEQYVFIHDAILEACLGDTSVPASQVRSRSLYYDMNKLDPQTNSSQIKE 1188  
Qy 1176 EFQTLASVTRLOAECDSCIACLRNHDKNRPMWLPPDRCLPFLITIDGSSSNVINAALM 1235  
Db 1189 EFTLANVPTFLRVEDCDSCIALPRNHEKRCMDILPPDRCLPFLITIDGSSSNVINAALM 1248  
Qy 1236 DSVRQPAAFIVTOVPLPNTVKDFWRLVYDYGCTSI VMLNEVDLSQGCPCQYWPBEGMLRYG 1295  
Db 1249 DSYQSPSAFIVTQHPLENTVKDFWRLVLDYHCTSVMLNDVDPAQLCPQYWPBENGVRHG 1308  
Qy 1296 PIQVECMSCMDCVNIIRIICNLTRPQBYLMVQOFOYLGWASHREVPGSKRSPFLKLI 1355  
Db 1309 PIQVEFVSADLEEDIISRIYNAARPDQGYRMVQOQFLGWPMYRDTVPVSKRSFLKLI 1368  
Qy 1356 LOYKWOEENKEGEGRTIIHCLNGGSGRSGMFCAGIUVVMKQNVVDVHFAVKTLRNSK 1415  
Db 1369 RQVDKWOEEYNGEGRTVTHCLNGGSGRSGTFCALISVCEMLRHQRTVDVHFAVKTLRNKK 1428  
Qy 1416 PNVVEAPEQYRVCYDVALEYLES 1438  
Db 1429 PNWDLLDQYKFCYEVALEYLNS 1451  
RESULT 9  
ADI80761  
ID ADI80761 standard; protein; 1452 AA.  
XX AC ADI80761;  
XX DT 15-APR-2004 (first entry)  
XX DE Human protein tyrosine phosphatase receptor type mu protein sequence.  
KW protein tyrosine phosphatase receptor type mu; PTPRM; cytostatic;  
KW antidiabetic; gene therapy; expression pattern;  
KW hyperproliferative disorder; cancer; metabolic disorder; diabetes;  
XX infection; inflammation; tumour formation; human.  
OS Homo sapiens.  
XX OS Unidentified.  
XX PN US2004014699-A1.  
XX PD 22-JAN-2004.  
XX PF 18-JUL-2002; 2002US-00200293.  
XX PR 18-JUL-2002; 2002US-00200293.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Cowser LM, Dobie KW;  
XX DR WPI; 2004-121596/12.  
XX DR N-PSDB; ADI80645.  
XX PT New antisense compound targeted to a nucleic acid molecule encoding  
PT protein tyrosine phosphatase receptor type mu, useful for treating cancer  
PT or diabetes or modulating expression of protein tyrosine phosphatase  
PT receptor type mu.  
PS Example 13; Page 33-38; 56pp; English.  
XX CC This invention relates to a novel compound with an oligonucleotide 8-80  
CC nucleotides in length targeted to a nucleic acid molecule encoding  
CC protein tyrosine phosphatase receptor type mu (PTPRM) which specifically  
CC hybridises with the nucleic acid molecule encoding PTPRM and inhibits the  
CC expression of PTPRM or specifically hybridises with at least 8-nucleotide  
CC portion of a preferred target region on a nucleic acid molecule encoding  
CC PTPRM. The invention may be useful for the production of compositions  
CC with a cytostatic or antidiabetic activity. In addition, the disclosed  
CC sequences may be useful for gene therapy. The compound, particularly the  
CC antisense oligonucleotide is useful in modulating the function of nucleic





XX AC ADJ68277; DB  
XX DT 06-MAY-2004 (first entry) QY  
XX DE Human heat mitochondrial protein as a therapeutic target SeqID83.  
XX KW Mitochondrial; human; screening assay; diabetes mellitus;  
KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
KW osteopathic; ophthalmological; cytostatic.  
XX OS Homo sapiens.  
XX PN WO2003087768-A2.  
XX PD 23-OCT-2003.  
XX PF 04-APR-2003; 2003WO-US010870.  
XX PR 12-APR-2002; 2002US-0372843P.  
XX PR 17-JUN-2002; 2002US-0389987P.  
XX PR 20-SEP-2002; 2002US-0412418P.  
XX PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM,  
PI Warnock DE;  
XX DR WPI; 2003-845369/78.  
XX PT Identifying a mitochondrial target for drug screening assays and for  
PT treating diseases associated with altered mitochondrial function,  
PT comprises detecting a modified polypeptide in a sample and correlating  
PT with the disease.  
XX XX Claim 1; SEQ ID NO 83; 180pp; English.  
CC This invention relates to novel mitochondrial targets that can be used  
for therapeutic intervention in treating a disease associated with  
altered mitochondrial function. Specifically, it refers to a method for  
identifying proteins of the human heart mitochondrial proteome that are  
useful for drug screening assays, as well as therapeutic targets. The  
present invention describes a method for identifying such proteins that  
can be used in the treatment of various diseases associated with altered  
mitochondrial function including diabetes mellitus, Huntington's disease,  
osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
compositions have neuroprotective, nootropic, antidiabetic, these  
anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
cytostatic activities. This polypeptide sequence is a human heart  
mitochondrial protein of the invention.

Query Match 62.1%; Score 4784; DB 7; Length 1452;  
Best Local Similarity 60.5%; Pred. No. 0;  
Matches 885; Conservative 208; Mismatches 328; Indels 42; Gaps 8;

QY 4 TAAALPAFVALLLLSPWLLGSAQQFSAGCGCTFDGPGACDHYQDIYDDFEWHVSAQ 63  
DB 3 TLGTCLATLAGLLL-----TAAGTSGGCLFDEPYSTCGYSQSSEGGDFNWEQNVL 54  
QY 64 EPHYLPEPMQGSYIMVDSGDHPGEKARLOLPWKENDTHCIDPSLYLSQKGLNPCTL 123  
DB 55 TKFTSDPWNSGLMLVNASGRPEGORAHLLPLQKENDTHCIDPHYFVSXSNPPGLL 114  
QY 124 NILVRNVKGPLANIPWNVTGFTGRDWLRRAELAVSTFWPNFYQVIPEAEVSGRSYGTAID 183

Db	1189	EFTLNMVPTTLRV	VEDCSIALLP	RNHEKRCMDILPP	DRCLPFLITIDGSSNY	1248
Qy	1236	DSYRQPAAFIVTQV	PLNTVKDFWRLV	VDYGYCTSI	VMLNEVDLSQGC	PQYWPPEGMLRYG 1295
Db	1249	DSYKQPSAFIVTQ	PLNTVKDFWRLV	DLTCTSVMLNDV	DPALQCPQYWPENGVRHG	1308
Qy	1296	PIQVECMSCMDC	VINRIFRICNL	TRPQEGYLMVQ	QOYLGWASHRE	VFGSKRSFLKLI 1355
Db	1309	PIQVEFVSADLE	EDIISKIFRIY	NAARPDGHRM	VQOQFGLGWP	MYRDTFVSKSALLLI 1368
Qy	1356	LOVEKWOEEWKE	GEGRTHIICL	NGGGRSGMFC	AIIGIVEMVK	QNVVDVFHAVKTLRNSK 1415
Db	1369	RQVDKWOEEYNG	EGEPTFVHCL	NGGGRSGTFC	AI	SIVCMLRHQRTVDVDFHAVKTLRNNK 1428
Qy	1416	PNMVEAPEQYR	FCYDVALE	YLES	1438	
Db	1429	PNMVDLDDQY	KFCYEALE	YDLS	1451	
RESULT 12						
AA080143						
ID	AA080143	standard; protein; 1455	AA.			
XX	AA080143;					
AC						
XX						
DT	06-NOV-2001	(first entry)				
XX						
DE	Human protein	SEQ ID NO 3789.				
XX						
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;					
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;					
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;					
KW	nervous system disorder; arthritis; inflammation.					
XX						
OS	Homo sapiens.					
XX						
PN	WO200157190-A2.					
XX						
PD	09-AUG-2001.					
XX						
XX	05-FEB-2001; 2001WO-US004098.					
XX						
PR	03-FEB-2000; 2000US-00496914.					
PR	27-APR-2000; 2000US-00560875.					
PR	20-JUN-2000; 2000US-00598075.					
PR	19-JUL-2000; 2000US-00620325.					
PR	01-SEP-2000; 2000US-00654936.					
PR	15-SEP-2000; 2000US-00663561.					
PR	20-OCT-2000; 2000US-00693325.					
PR	30-NOV-2000; 2000US-00728422.					
XX	(HYSE-) HYSEQ INC.					
PA						
XX						
PI	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;					
PI	Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;					
PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R;					
XX						
XX	WPI; 2001-476283/51.					
DR	N-PSDB; AAK53276.					

CC	activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAKS52581), 2111 (AAKS52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
XX	Sequence 1455 AA;
SQL	Query Match 62.0%; Score 4777.5; DB 4; Length 1455; Best Local Similarity 60.4%; Pred. No. 0; Matches 885; Conservative 207; Mismatches 330; Indels 43; Gaps 9;
QY	4 TAAALPAFVALLLGFMPWLLGSAQGFSGAGCTFDDGPGACDYHQLYDDFEWVHVSAQ 63
DB	3 TLGTCLATLAGLL-----TAAGTFSGGLFDEPYSTCGYSQSEGDFNWEQVNTL 54
QY	64 EPHYLPBEMQGSYMIVDSSDHPDGEKARLQLPTMKENDTHCDFSLLYSQKGLRPGTL 123
DB	55 TKPTSDPMPWPGSGFMLVNASRGPGRARHLLLPOLKENDTHCIDFHYFVSSKNSPPGLL 114
QY	124 NILVRVNGKPLANPIWNVTGTCGRDWLRABELVSTFWPNPEYQVIFAEVSGGRSGYIAID 183
DB	115 NVVVKVNGPLGNPIWNIISGDPTRTNRAELALSTFWPNFYQVIFEV-ITSGHQLYLAID 173
QY	184 DIQVLSYPCDKSPHFRLRLGSDVENVAGNATFOCIATGRDAVHNKMLQRRNGSDIPVAQT 243
DB	174 EVKVLGHFCTRTPHFLRIQNVENVAGQFATFQCISAIGRTVAGDRMLQGLDVRADAPLKEI 233
QY	244 KVINHRFPAAFLQOEVTKDQDLYRCVTOSERGSGVSNFAQLIVREPPPIAPPOLLGV 303
DB	234 KVTSSRRFIASFNVVNTTKRDAGKYRIMRTGGVGVISNYABLVKVEPPVPIAPPOLASV 293
QY	304 GPTYLLQLNANSIIGDGPILLKEVEYRMTSGSWTETHVANPTYKLWLHLDPPTEYBIRV 363
DB	294 GATVLTQLNANSINGDPIVAREVEYCTASGWNDRQPVDSISYKIGHLDPPTEYBISV 353
QY	364 LLTRPGEGGTGLPGPPLITRTKCAEPMRTPTKLIKIAIQARRIADVWESLGYNITRCHTF 423
DB	354 LLTRPGEGGTSGPAPALRTTKCADPMRGPRLKEVVEVKSQGITIRWEPFGYNVTRCHSY 413
QY	424 NVTICVHYFQHNEKAD--CLMDMPKAPORHVNHLPPYTNVSLKMLTNPBGRKESSEET 481
DB	414 NLTVHYCYQVGGQEQVREEVSWDTENSHPQHTITNLSPYTNVSVKJLMLNPEGRKESQEL 473
QY	482 ILOTDEDVPGVPVKSLQGSFSENKIFLNWKEPLDPNGIITQVEISYSSIRSDDPAPVPA 541
DB	474 IVQDEDLPGAVPTSESQGSFTEKIFLQWREPTQYGVITLVEITTKAVSSDPDEIDL 533
QY	542 GPPQTVNLWNSTHVMHMLHPGTYTQFFIRASTVKGFGPATAINVTTNISAPTLDPYEG 601
DB	534 NOSGRVSKLGNETHFLFGLYPGITYFTIRASTAKGFGPATNQFTTKISAPMPAYE- 592
QY	602 VDAISNETATTITVLLRPAQAKAPISAYQIVVEELHPHRTKREAGAMECYQVPVTYQNA 661
DB	593 LETPLNOTDNTVTMLKPAHSRGAPAVSYQIVVEEERPRRTKKTTEILKCYVPVPIHFQNA 652
QY	662 MSGGAPYYEAEULPPGNLPEPAPPTVGDNTYQCGFWMNPLAPRKGYNIYFOAMSSVEKET 721
DB	653 SLNLSQYIFYFAEFPADSLQAAPPTIGDNKTYNGVWNTPLLPYKSYRIYFOAASRANGET 712
QY	722 KTCQVRIATKAATEPEPEVIPPDAKQTDVRVKIAGISAGILVFILLLLWILIVKSKKLAK 781
DB	713 KIDCVQVATKGA--TPKVPVPEPEQTDHTVKIAGVIAGILFVIFLGVVLVWKRRKLAK 771
QY	782 KRKDAMGNTRQEMTHVMNAMD--RSYADQSTLHAEDPLSTFMDQHNFSPRY----- 831
DB	772 KRKETMSSTRQEIIDLWIGELNGPRSYAEQGTKLATRAFS--FMDTHNLNGRSVSSPSFT 829
QY	832 -----ENHSATAESRLLDVPEY-LCEGTESPYQTGLHPALRVADLL 873
DB	830 MKTNTLSTSVNPSVYYPDETHMTASDTSLSVQSHYTKKREPADVPYQTGLHPALRVADLL 889
QY	874 QHINLMKTSIDSYGFKEEYESFFEQGSASWDVAKQDNRAKNRYGNIITAYDHSRVILQVPE 933

Db 890 QHITQMKCAGYGFKEEYVESFEQSAFWDGSAKDDENMKRYGNIITAYDSRVRLOTIE 949  
 Qy 934 DPDSYINAIIDYQRPSHYIATQGFVHEVTVDFWRMIWQEQSACIWMVYNLVEVGRV 993  
 Db 950 GDTNSDYINGNYIDGHRPNHYIATQGFMOETIYDFWRWVWHEHTASIIWYNLVEVGRV 1009  
 Qy 994 KCYKWPDDTBYGDKVTCVEMPELAYVVRITLERRGNEIREVKQHFHTGWPDHGV 1053  
 Db 1010 KCKYWPDDTBYIKDKIVLTETELAEYVIRTFAVEKRGVHEIREIRQHFHTGWPDHGV 1069  
 Qy 1054 PYHATGLLSFRRRVKLSNPPSAGPIVHCSAGAGTCGYIIVIDIMLMAERGVVDIYNC 1113  
 Db 1070 PYHATGLLGFVRQVKSPPSAGPLVHCSAGAGTCGFIIVIDIMLMAERGVVDIYNC 1129  
 Qy 1114 VKALRSRRNNVQTEQYIFIHDAILEACLCGETAIPVCEPKAAYFDMIRIDSQTNSSHL 1173  
 Db 1130 VRELRSRRNNVQTEQYVFTHDAILEACLCGDTSVPASQVRSYLYDMNKLDPTQNSSQI 1189  
 Qy 1174 KDEQTLNSVTPRLOAEDCSIACLPRNHDKVRFDMLPPDRCLPFLITIDGESSNYINAA 1233  
 Db 1190 KBEFTLNMVTPTRVEDCSIALPRNHEKRCMDILPPDRCLPFLITIDGESSNYINAA 1249  
 Qy 1234 LMDSYROPAAFIYQYPLPNTVDFWRLVVDYDYGCTSIWMLNEVDLSQCPQYWEPEGMLR 1293  
 Db 1250 LMDSYKQPSAFIVTQHLPNTVDFWRLVLDYHCTSVVMLNDVDPALCPQYWPENGVHR 1309  
 Qy 1294 YGPIQVCMSCMDCDVINRIFRICNLTRPOEGLMWQOFOYLGWASHREVPVSGKRSFLK 1353  
 Db 1310 HGPIQVEFVSADLEDIISRFIRYNAARPDQGYRMVQOQFLGWPMYRDTFVSKRSFLK 1369  
 Qy 1354 LIQVKEQWKEWKEGEGRTIHCINGGGRSGMFCAGIGVEMVKRQNVDFVHAKVTLRN 1413  
 Db 1370 LIQVQWKEBYNGEGRTVHCLINGGGRSGTFCASIVCEMLRHQRTVDVHAKVTLRN 1429  
 Qy 1414 SKPMVEAPEQYRCYDVALEYLES 1438  
 Db 1430 NKPMNVLDLQYKFCYEALEYLNS 1454

## RESULT 13

ADB79775  
 ID ADB79775 standard; protein; 1436 AA.

XX ADB79775;

XX 04-DEC-2003 (first entry)

DE Rat putative receptor tyrosine phosphatase, SEQ ID 15.

XX Analgesic; pain; streptozocin-induced diabetes; rat.

XX Rattus norvegicus.

XX EPI279744-A2.

XX 29-JAN-2003.

XX 26-JUL-2002; 2002EP-00255249.

XX 27-JUL-2001; 2001GB-00018354.

XX 07-FEB-2002; 2002GB-00002910.

XX (WARN ) WARNER LAMBERT CO.

XX Brookebank RA, Dixon AK, Lee K, Pinnock RD;

XX WPI; 2003-395407/38.

XX N-PSDB; ADB79776.

PT Use of isolated gene sequences and encoded polypeptides that are  
 PT upregulated in the spinal cord in response to streptozocin-induced  
 PT diabetes for screening compounds for the treatment of pain, or for

PT diagnosing pain.

PS Claim 1; Page 59-64; 334pp; English.

XX The present invention relates to nucleotide sequences which are useful in  
 CC the screening of compounds for the treatment of pain, or for the  
 CC diagnosis of pain. The nucleotide sequences are up-regulated in the  
 CC spinal cord in response to streptozocin-induced diabetes. The present  
 CC sequence was used to illustrate the invention.

SQ Sequence 1436 AA;

Query Match 59.7%; Score 4602.5; DB 7; Length 1436;  
 Best Local Similarity 60.3%; Pred. No. 0;  
 Matches 855; Conservative 214; Mismatches 329; Indels 19; Gaps 9;

Qy 33 AGGCTFDGPG---ACDYHODLYDDFEWVHVSAQEPHYLPPEMQSGSYMIYDSDHDPGE 89  
 Db 24 AAGCTFEASDPVVPCEFSQAQYDDFQEQVRHPGTRTFEDLPHGAYLMWNASQHTFGQ 83  
 Qy 90 KARLQLPTMKENDTHCIDFSYLSQKGLNPGTILNLRVKNKGLPANIWNVTGFTGRDW 149  
 Db 84 RAHIIFQTLSENDTHCVQFSYFLYSRDGHSPTGLGVVVRVNGPLGSAVNMNTGSHGRQW 143  
 Qy 150 LRABLAVSTFWPNEYQVIFEAESVSGRSYIADDDIOVLSPCDKSPHFLRLGDFEVNAG 209  
 Db 144 HQAELAVSTFWPNEFQVLFREALISPDHKGYIGLDDILLFSPYCAKAPHFSLRGDFEVNAG 203  
 Qy 210 QNATFOCIATGRDAVHNKMLQRNGEDIPVAOTKNINHRREFAASRLOSVTKTDDOLYR 269  
 Db 204 QNASFQCMAGRAAEAEHFLQSGVGLVPAAGVRHISHRRFLATFFPLASVGRSEQDLYR 263  
 Qy 270 CVTQSERGSGVNSPAQLIVREPPIAPPOLLGVGPTYLLIQLNANSIIGDPIILKEVE 329  
 Db 264 CVSQAPGAGVNSFAELIVKEPPTIAPPOLLRAGPTYLLIQLNANSIIGDPIVRKEIE 323  
 Qy 330 YRMTSGSWTTHAVNAPTYKLMHLDPTDEYRVLTRPGEGGTGLPGPLITTKCAEP 389  
 Db 324 YRMARGPWAHVAVNLQTYKLMHLDPTDEYRISVLLTRPDGDTGRGPPLISRTKCAEP 383  
 Qy 390 MRTPKTLKIAEIQARRIADVWESIGYNIIRCHTFNVTICYHYFRG--HNESKADCLMDP 447  
 Db 384 TRAPKGLAFABEIQARQLTLQWEPLGYNVTRCHTYAVSLCYRYTLGGSHNQITRECVKMER 443  
 Qy 448 KAPOHVVNHLPPYTNVSLKMLTNPEGRKESEETIIQTDSDVPVPVPSLQGTSFENKI 507  
 Db 444 GASRYTIKNLLPFNINHVRILTNPEGRKEGKEVTFQTDDEDFGIAAESLTFPLEDMI 503  
 Qy 508 FLWKKEPLDPNGIITOYEISYSSIRSFPDPAVPVAGPQTVSNLWNSHTHVMHLHPGTTY 567  
 Db 504 FLKWEFPQEPNGLITQYEISYQSISSDPVAVNVPGRPTISKLNRNETHYVPSNLHPGTTY 563  
 Qy 568 QPFRASTVKGFPATAINVTNISAPTLDPYEGVDASINETATTIIVLLRPAQAKAPI 627  
 Db 564 LFSVRARTSKFGQAALTEITTNISAPSF--DYADMPSPGSESENTIIVLLRPAQGRGAPI 622  
 Qy 628 SAYQIVVEELHPHRTKREAGAMECYOVPTYQANMSGCAPYPAELPPGPNLPAPFTV 687  
 Db 623 SVYQVVVEERPRLRREPQACQCFSVPLIFETALARGLVHYFGAELAAASLLEAMFTV 682  
 Qy 688 GDNRTYQGFNPPPLAPRKGYNIYFQAMSSVEKETKTQCVRIATKAATEEPEVDPKAKQT 747  
 Db 683 GDNQTYRGFWNPPLPRKAYLIYFQAASHLKGTRLCNIRIARKAACSKSRPLEVQRS 742  
 Qy 748 DRVVKTAGISA-GILVFIILLVILIVKSKLAKKRDAMGNTRQMTWNVNMDRSYA 806  
 Db 743 EEMGLILGICAGGLAVLILLGAIIVIRKGPVNMTK-ATVNYRQEKTHMMSAVDSFT 801  
 Qy 807 DQSTLHAEDPLSITFMDQHNFSPRYNHS--ATAESSRLDDVPYLCETGESPYQTGLH 864  
 Db 802 DQSTLQEDRLGLSFMADAPGYSPRGDQSGVTEASSLLGGSPPRCGRKGPSYHTQLH 861  
 Qy 865 PAIRVADLLQHLNLMKTSDSYGFKEEYESFPEGQSASWDVAKKDQNRKRNRYGNIAYDH 924

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Db 862 PAVRVADLLQHINQMKTAEYGFQKEYSEFEG----WDATKKXDKLKGGRQEPVSADR 917
Qy 925 SRVLQPVDDPSSYINWANYIDGVRQSHYIATQPGVHETVYDFWRMIWQEQSACIWMV 984
Db 918 HHVKLHPMLADPDADYISANVYIDGVRHSHFIATQPKPEMIYDFWRMVWQEQCASIYMI 977
Qy 985 TNLVEGVKCVKYWPDDEYVDFKVCVMEPELAEYVVRTEFLEREGYNEIREVKQFH 1044
Db 978 TKLVEGVKCVKRYWPDSDMYGDIKITLVKTETLAEYVVRTEFLEREGYSARHEVRQFH 1037
Qy 1045 FTGWPDHGVYPYHATGLLSFIRRVKLSNPPSAGPIVHCSAGAGRTGCVIVIDIMLDMAR 1104
Db 1038 FTAMPEHGVYPYHATGLLAFIRRVKASTPPDAGPIVHCSAGTGRGCVIVLDMVMDMAEC 1097
Qy 1105 EGVVDIYNCVKALRSRRINMQTEQYIFIHDAILEALCGETAIPVCFEKAAYPDMIRI 1164
Db 1098 EGVVDIYNCVKTLCSRRVNMIQTEQYIFIHDAILEALCGETTIPVNEFRATYREMIRI 1157
Qy 1165 DSQTNSSHLKDFQTLNSVTPRLOAEDCSIALPRNHDKNRPMDMLPDRCLPELITIDG 1224
Db 1158 DPQSNSSQLREBFQTLNSVTPRDLVECSIALPRNDRKNRSMVLPDRCLPFLISSDG 1217
Qy 1225 ESSNINAAALMDSYRQPAAFIVTOYPLNVTNVDKFWRLVVDYDGTCTSIIVMLNEVDLSQG--- 1281
Db 1218 DPNVYINAAALTDYSTRSAFIVLHPLQSTPDPFWRLVVDYDGTCTSIIVMLNQLNQNSAWP 1277
Qy 1282 CPQYWPEBGMRLYGPQIQCVMSCMDCDVINRIFRICNLTRPQEGYLMVQOQFYVLGMASH 1341
Db 1278 CLQYWPEBGRQYGLMEVEFVSGTANEDLVSRFVRQVNSSRLQEGHLLVRHFQFLRWASAY 1337
Qy 1342 REVPSKRSFLKLILOVEKQWQEWKEGEGRTIIHCLNGGSGRSGMCAIGIVVMVKRQNV 1401
Db 1338 RDTPSRKAFLLHAEVDKQAE--SGDGRTVVHCLNGGSGRSGTFCACATVLEMIRCHSL 1395
Qy 1402 VDVFFAVKTLRNSKPNMVEAPQYRFCYDVDALEYLES 1438
Db 1396 VDVFFAAKTLRNYKPNMVEWTDQYHFCYDVDALEYLEA 1432

RESULT 14
AAW41361
ID AAW41361 standard; protein; 1436 AA.
XX
AC AAW41361;
XX
26-MAY-1998 (first entry)
XX
Receptor protein tyrosine phosphatase lambda polypeptide.
XX
Receptor protein tyrosine phosphatase lambda; mouse; PTP lambda; therapy;
KW cognate ligand; paralytic disease; metastatic spread prevention;
KW epithelial development; neuronal structure development;
neuronal pathfinding.
XX
Mus sp.
XX
Key Location/Qualifiers
FH Misc-difference 158
FT /label= unknown
FT /note= "encoded by TWI"
FT Misc-difference 340
FT /label= unknown
FT /note= "encoded by CAR"
FT Misc-difference 1208
FT /label= unknown
FT /note= "encoded by YGC"
XX
WO9744458-A1.
XX
27-NOV-1997.
XX
22-MAY-1997; 97WO-US009056.
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XX 24-MAY-1996; 96US-00652971.
PR (GETH ) GENENTECH INC.
FA Cheng J, Lasky LA;
PI WPI; 1998-018512/02.
XX N-PSDB, AAV15004.
DR Receptor protein tyrosine phosphatase lambda polypeptide - potentially
PT useful in treating paralytic diseases and preventing metastases.
PT Claim 6; Fig 1; 118pp; English.
XX
CC This sequence represents the mouse receptor protein tyrosine phosphatase
CC (PTP) lambda polypeptide of the invention. PTP lambda is: (i) mainly
CC expressed in adult mammalian brain, lung and kidney; (ii) not expressed
CC in adult liver; and (iii) can dephosphorylate phosphorylated tyrosine
CC (pY) residues. The DNA sequence is used to express recombinant PTP
CC lambda, and also as a source of probes for screening DNA libraries. PTP
CC lambda is used to isolate the receptor's cognate ligand (potentially
CC useful for treating paralytic diseases), and for preventing metastatic
CC spread. PTP lambda is also used as a molecular marker for particular
CC tissues, as a reagent in an assay for identifying PTP (ant)agonists, and
CC as a molecular weight marker in protein gels. The Ab is used in
CC diagnosis, tissue-typing and purification of PTP lambda, also it may
CC crosslink the receptor, resulting in its upregulation. PTP lambda is a
CC mediator of cell adhesion and may be involved in development of
CC epithelial and neuronal structures (neuronal pathfinding)
XX
SQ Sequence 1436 AA;
Query Match 59.5%; Score 4586.5; DB 2; Length 1436;
Best Local Similarity 60.3%; Pred. No. 0;
Matches 854; Conservative 213; Mismatches 331; Indels 19; Gaps 9;
Qy 33 AGGCTFDDGPG---ACDYHQDLYDDFEWVHVYSAQEPHYLPPEMPOGYSYIVDSSDDHDE 89
Db 24 AAGCTFEASDFVVPFCFSQAQYDDFQWEQRIHPGTRTPEDLPHGAYLMVNASQHTPGQ 83
Qy 90 KARLQLPMTKENDTHCIDFSYLLYSQKGLNPGLTILVRNKGPLANIPWNTGTGRDW 149
Db 84 RAHIIFQTLSENDTHCVQFSYFLYSRDGHSGFTLVYRVNGGPGLSAVNMTSGHGRQW 143
Qy 150 LRAELAVSTFWPNEVQVIFEAEVSGRSGYTAIDDIQVLSYPCDKSPHFRLGDEVVNAG 209
Db 144 HQAELAVSTFWPNEQVLFALISPDHKGYICLDDILLFSYPCAKAPHFSRLGDEVVNAG 203
Qy 210 QNATFOCIATGRDAVHNKMLLORNGEDIPIVAQTKNINHRFAASFRLOEYTKTDQDLVR 269
Db 204 QNASFQCNAAAGRAAAEHFFLQSGVLVPAAGVRHHSRRPLATFFPLASVGRSQDLYR 263
Qy 270 CVTOSGRSGVSNFAQLIVREPPIAPPQLLVGPTVLLIQLNANSIIGDGPILKEVE 329
Db 264 CVSQAPRCAGVSNFAELIVKEPPTPIAPPQLLRAGPTVLLIQLNTNSIIGDGPVRKEIE 323
Qy 330 YRMTSGSWTETHAVNAPTYKLWHLDPDTEYIRVLLTRPGSGGTGLPGPLITRTKCAEP 389
Db 324 YRMARGPWAHVAVNLTXYKLWHLDPDTEYISVLLTRPGDGTGRPGPLISRTKCAEP 383
Qy 390 MRPYKTLKIAEIOARRIADVHESLGYNITRCHTFNWTICYHYFRG--HNESKADCLMDP 447
Db 384 TRAPKGLAFABIQARQLTQWEPLGYNVTRCHTVAVSLCYRYTLGSGSHNQITRECVKMER 443
Qy 448 KAPOHVVNHLPPYTNVSLKMLITNPEGRKESEETIIQTDDEDVPGVPVVKSLQGTGFENKI 507
Db 444 GASRYTIKNLLPFRNIHVRLITNPEGRKEGKVEVTFQDDEDVPGGIAAESLTFPLEMI 503
Qy 508 FLNWKPELDPMGIITQYEISYSSIRSFDPVAVPGPOTVSNLWNSTHHVFMHLHPGTTY 567
Db 504 FLKWEPEQENGLITQYEISYQSIESSDPVAVNVPGRRTISKLRNETYHVSFNLHPGTTY 563
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Db 417 CHSYNLTVQYQYV--FNQOQYEAEEVQIOTSSHYTLGLRPFMTIRLRLLLSNPEGRMESE 474  
Qy 480 ETIIQTDEBVPVVKLGQTSFENKIFLNWKBPDPNGIITQYBISYSSIRSFPDPAVP 539  
Db 475 ELVVQTEBDFVGAPELESIOGGPPEEKIYIQWKPNETNGVITLYEINYKAVGLDPSAD 534  
Qy 540 VAGPPTQVSNLWNSTHFMHLHPTTYQPFIRASTVKFGFPATAINVTNISAPTLDPY 599  
Db 535 LSSORGVFKURNETHHUFVGLYPGTTFYSFTIKASTAKGPGPVVTRTATKISAPMPEY 594  
Qy 600 EGVDAASLNETAATTITVLLRPAQAKAPISAYQIVVVEELHPHRTKREAGAMECYQVPVTYQ 659  
Db 595 D-TUTPLNETDTITVMLKPAQSRGAPVSVQLVVKERLQKSRRAADIIECFSPVPVSYR 653  
Qy 660 NAMSGAPYFAAELPPGNLPEPAPFTVGDNRVTQGFNWPPLAPRKGNIIYFOAMSSVEK 719  
Db 654 NASSLDSLHYFAAELKPANLPVTPQFTVGDNKNTNGYWNPLPLKSYIYFOALSANG 713  
Qy 720 ETKQCVRIATKAATEEPEVIP-----DPAKQTDVVKIAGISAGI 760  
Db 714 ETKINCVRLATKAPMSAQVTPGTPCLLTGTASTQNSNTVEPEKQVDNTVMMAGVIAGL 773  
Qy 761 LVFIILLVLIIVKK-----SKLAKKRDAMGNTRQEMTHMYNAMDRSYAD 807  
Db 774 LMFIIILLGVMLTIKRRNAYSYSYLSQRLAKKQKETQSGAQREMGPVASA-DKPTTK 832  
Qy 808 QSTLHAEDPLSITFMQDNHNSPRYNHSATAESRLDV---PRYLCEGTESPYQTGQLH 864  
Db 833 LSASRNDEGFSSSQDVNGF-----NGSRGELSQPTLTITQTHPYRTCDPEVMSYPRDQFQ 887  
Qy 865 PAIRVADLLOHNLNLMKTSYCFKEEYESFEGQSASMDVAKOONRAKNRYGNIIAYDH 924  
Db 888 PAIRVADLLOHNTQMRGGYGFKEEYBALPEGQTASWDTAKEDENRNKNRYGNIIISYDH 947  
Qy 925 SRVILQPVEDDPSYINANYIDGQYRSHYIATQGPVHETVYDFWRMIWQOSACIWMV 984  
Db 948 SRVLLVLDGDPHSDYIINANYIDGYRPHRYIATQGPMEQETVKDFWRMIWQENSASIVMV 1007  
Qy 985 TNLVEVGRVKCYKVPDDTEVYVGVDFKVCVEMEPLAEYVVRFTTLERRGYNEIREVKOPH 1044  
Db 1008 TNLVEVGRVKCVYVPDDTEVYVDIKVLTIEPELAEYVIRFTVQKKGXHEIRELRLFH 1067  
Qy 1045 FTGWDPHGVPHATGLLSFIRVKLSNPPSAGPIVVHCSAGAGRTGCYIVIDIMLMDAER 1104  
Db 1068 FTSPWDPHGVPCYATGLLGFVRQVKFNPPEAGPIVVHCSAGAGRTGCFIADTMDLMAEN 1127  
Qy 1105 EGVVDIYNCVKALRRRINNMVQTEBOYIFIHDAILEACLCEBETAI PVCFKAAAYFDMIRI 1164  
Db 1128 EGVVDIFNCVRELRAQRNMLVQTEQYVVFHDAILEACLCGNTAIPVCFEFRSLYINISRL 1187  
Qy 1165 DSQTNSSHLKDBFQTLNSVTPRLQADDCSIACLPRNHDKNRPMMLPPDRCLPFLITIDG 1224  
Db 1188 DPQTNSSQIKDEFQTLNIVTPRVRPEDCSIGLLPRNHDKNRSMVLPDLRCLPFLISVDG 1247  
Qy 1225 ESSNYINALMDSYQPAAFIYQVPELNTVKDFWRLVYDYGCTSI VMLNEVDLSQGCQ 1284  
Db 1248 ESSNYINALMDSHKQPAAFVVTQHPLENTVADFWRVLDYNCSSVVMLENMDTAQFCMQ 1307  
Qy 1285 YWPEEGMLRYGPIQVECMSCSMDCVINRIFRICNLTRPOEGYLMVQQFOYILGWASHREV 1344  
Db 1308 YWPEKTSYCGYPIQVEFSADIDEDIIHRIFCNMAPQDGYRIVQHLQYIGWPAYRDT 1367  
Qy 1345 PGSKRSFLKILIQVKQOEWEKGEGRTHIICLNGGGRSGMPCFAGIIVVEMVQRNVVDV 1404  
Db 1368 PPSKRSLLKVVRLKQOEYDQREGRTVWHCLNGGGRSGTFCACSVCEMIQQQNIIDV 1427  
Qy 1405 FHAVKTLRNSKNMVEAPEQYFCYDVALEYLES 1438  
Db 1428 FHIVKTLRNNKSNMVTLEQYKFVVEVALEYLSS 1461

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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:41:58 ; Search time 33.7887 Seconds  
(without alignments)  
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Title: US-09-887-669-2  
Perfect score: 7709  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7692	99.8	1439	2	US-08-449-644-2
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3	7571	98.2	1457	2	US-08-652-971-3
4	7571	98.2	1457	2	US-08-449-644-1
5	7571	98.2	1457	2	US-08-087-244A-1
6	7571	98.2	1457	2	US-08-991-258A-3
7	7571	98.2	1457	2	US-08-769-399-3
8	7571	98.2	1457	3	US-08-931-953A-3
9	4807	62.4	1452	2	US-08-449-644-8
10	4807	62.4	1452	2	US-08-087-244A-8
11	4791	62.1	1452	2	US-08-652-971-4
12	4791	62.1	1452	2	US-08-991-258A-4
13	4791	62.1	1452	2	US-08-769-399-4
14	4791	62.1	1452	3	US-08-931-953A-4
15	4586.5	59.5	1436	2	US-08-652-971-2
16	4586.5	59.5	1436	2	US-08-991-258A-2
17	4586.5	59.5	1436	2	US-08-769-399-2
18	4586.5	59.5	1436	3	US-08-931-953A-2
19	4076.5	52.9	777	4	US-09-949-016-7158
20	3725.5	48.3	1075	4	US-09-949-016-8308
21	1529.5	19.8	1501	2	US-08-447-464-3
22	1529.5	19.8	1501	2	US-08-716-679-3
23	1487.5	19.3	1911	1	US-08-348-006B-5
24	1487.5	19.3	1911	1	US-08-800-825A-5
25	1487.5	19.3	1911	3	US-09-158-657-5
26	1487.5	19.3	1911	5	PCT-US94-10166-5
27	1187	15.4	793	1	US-08-015-985-3

28	1187	15.4	793	4	US-09-280-597-3	Sequence 3, Appli
29	1172.5	15.2	802	1	US-08-015-985-1	Sequence 1, Appli
30	1172.5	15.2	802	4	US-09-280-597-1	Sequence 1, Appli
31	1172.5	15.2	807	4	US-09-949-016-7356	Sequence 7356, Ap
32	1168	15.2	538	4	US-09-743-492A-9	Sequence 9, Appli
33	1143	14.8	699	1	US-08-348-006B-7	Sequence 7, Appli
34	1143	14.8	699	2	US-08-800-825A-7	Sequence 7, Appli
35	1143	14.8	699	3	US-09-158-657-7	Sequence 7, Appli
36	1108	14.4	249	2	US-08-685-992-8	Sequence 8, Appli
37	1108	14.4	249	2	US-09-144-925-8	Sequence 8, Appli
38	1085.5	14.1	560	4	US-09-949-016-10786	Sequence 10786, A
39	1023.5	13.3	2314	4	US-09-816-703A-2	Sequence 2, Appli
40	1022.5	13.3	2308	1	US-08-015-973-1	Sequence 1, Appli
41	1022.5	13.3	2308	2	US-08-448-164-1	Sequence 2, Appli
42	1022.5	13.3	2308	3	US-08-081-929-2	Sequence 1, Appli
43	1022.5	13.3	2308	4	US-10-000-954-2	Sequence 2, Appli
44	1017.5	13.2	1442	1	US-08-015-986A-3	Sequence 3, Appli
45	1017.5	13.2	1442	2	US-08-446-363-3	Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
US-08-449-644-2  
; Sequence 2, Application US/08449644  
; Patent No. 5856162  
; GENERAL INFORMATION:  
; APPLICANT: Schlessinger, Joseph  
; APPLICANT: Sap, Jan M.  
; APPLICANT: Ullrich, Axel  
; APPLICANT: Vogel, Wolfgang  
; APPLICANT: Fuchs, Miriam  
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
; TITLE OF INVENTION: PHOSPHATASE-KAPPA  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,644  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/087,244  
; FILING DATE: 01-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7683-042  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1439 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-449-644-2

Query Match 99.8%; Score 7692; DB 2; Length 1439;  
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1437; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDTTAAALPAFVALLILSPPLGSAQOQSAGSCTFDDGACDHYQDLYDDPEWVHV 60  
DB 1 MDTTAAALPAFVALLILSPPLGSAQOQSAGSCTFDDGACDHYQDLYDDPEWVHV 60  
QY 61 SAQEPHYLPPEPQSGSYMIVDSSDHDPEKARLQLPPTMKENDTHCIDFSYLLYSQKGLNP 120  
DB 61 SAQEPHYLPPEPQSGSYMIVDSSDHDPEKARLQLPPTMKENDTHCIDFSYLLYSQKGLNP 120  
QY 121 GTNLNLRVKNKGPLANPIWNTGTFGRDMLRAELAVSTFWPNEYQVIFEAESVSGRSYI 180  
DB 121 GTNLNLRVKNKGPLANPIWNTGTFGRDMLRAELAVSTFWPNEYQVIFEAESVSGRSYI 180  
QY 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFOCIATGRDAVNKLWLRNGEDIPV 240  
DB 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFOCIATGRDAVNKLWLRNGEDIPV 240  
QY 241 AQTKNINRRFAASPRLOEVTKTODLYRCVTSQSGSGSVNFAQLIVREPRPTAPPQL 300  
DB 241 AQTKNINRRFAASPRLOEVTKTODLYRCVTSQSGSGSVNFAQLIVREPRPTAPPQL 300  
QY 301 LGVGPTYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 360  
DB 301 LGVGPTYLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 360  
QY 361 IRVLLTRPGEGETGLPGPPLITRTKCAEPMRTPTKLIAEQARRIAVDWESLGNITRC 420  
DB 361 IRVLLTRPGEGETGLPGPPLITRTKCAEPMRTPTKLIAEQARRIAVDWESLGNITRC 420  
QY 421 HTFNVTICVHPRGHNEKADCLMDPKAPQHVNHLPPTYNVSLKMLTTPGKKESEE 480  
DB 421 HTFNVTICVHPRGHNEKADCLMDPKAPQHVNHLPPTYNVSLKMLTTPGKKESEE 480  
QY 481 TTIOTDEDVPGVPVKSLQGSFENKIFLNWKEPLDNGIITQYBISYSSIRSFPAPVP 540  
DB 481 TTIOTDEDVPGVPVKSLQGSFENKIFLNWKEPLDNGIITQYBISYSSIRSFPAPVP 540  
QY 541 AGPPTQVNLNMTSHVFMHLHPGTYQFFIRASTVKGFGPATAINVTNISAPTLDPYE 600  
DB 541 AGPPTQVNLNMTSHVFMHLHPGTYQFFIRASTVKGFGPATAINVTNISAPTLDPYE 600  
QY 601 GVDASINETATTITVLLRPAQAKGAPISAYQIVBELPHRTKREAGAMECYQVPTVQN 660  
DB 601 GVDASINETATTITVLLRPAQAKGAPISAYQIVBELPHRTKREAGAMECYQVPTVQN 660  
QY 661 AMSGAPYVFAELPGLNLPPEAPFTVGDNRITYQGFNPPPLAPRGYNYIYFOAMSVEKE 720  
DB 661 AMSGAPYVFAELPGLNLPPEAPFTVGDNRITYQGFNPPPLAPRGYNYIYFOAMSVEKE 720  
QY 721 TKTQCVRIATKAATEBEVIPPAPQOTDRVVKIAGISAGILVFILLVILVIVKSKLA 780  
DB 721 TKTQCVRIATKAATEBEVIPPAPQOTDRVVKIAGISAGILVFILLVILVIVKSKLA 780  
QY 781 KKKDKAMGNTRQEMTHVNMNDRSADQSTLHAEDPLSITFMDQHNFPRIYENHSAEAS 840  
DB 781 KKKDKAMGNTRQEMTHVNMNDRSADQSTLHAEDPLSITFMDQHNFPRIYENHSAEAS 840  
QY 841 SRLLDVPRYLCGTSPTQGLHPAIRVADLLQHINLMKTSDSYGFKEEYSPFEGOSA 900  
DB 841 SRLLDVPRYLCGTSPTQGLHPAIRVADLLQHINLMKTSDSYGFKEEYSPFEGOSA 900  
QY 901 SMDVAKQONRAKRNIGNIAYDHSRVILQPVEDDPSSDYINANYIDGQRPESHYIATQG 960  
DB 901 SMDVAKQONRAKRNIGNIAYDHSRVILQPVEDDPSSDYINANYIDGQRPESHYIATQG 960  
QY 961 PVHETVDFWRIWQEOSACIYVMTNLVEGVKCYKYPDDTEYVDFKVCVMEPLA 1020  
DB 961 PVHETVDFWRIWQEOSACIYVMTNLVEGVKCYKYPDDTEYVDFKVCVMEPLA 1020  
QY 1021 EYVVRTFTLERRGYNEIRVKQFHFTGWDHGVPPVHATGLLSFIRRVKLSNPPSAGPIV 1080  
DB 1021 EYVVRTFTLERRGYNEIRVKQFHFTGWDHGVPPVHATGLLSFIRRVKLSNPPSAGPIV 1080

QY 1081 HCSAGAGRTGCIIVIDIMLDMABREGVVDIYNCVKALRRSRINNMVQTEQYIFIHDAILE 1140  
DB 1081 HCSAGAGRTGCIIVIDIMLDMABREGVVDIYNCVKALRRSRINNMVQTEQYIFIHDAILE 1140  
QY 1141 ACLGETAIPVCEPKAAAYFDMIRIDSQTNSSHLKXDEFQTLNSVTPRLQAECDSCIACLPN 1200  
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QY 1201 HDKRFMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFIVTQYPLPNTVKDFWR 1260  
DB 1201 HDKRFMDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFIVTQYPLPNTVKDFWR 1260  
QY 1261 LVYDYGCTSIIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVECMSCMDCDVINRIFRICNL 1320  
DB 1261 LVYDYGCTSIIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVECMSCMDCDVINRIFRICNL 1320  
QY 1321 TRPOEGYLMVQOQFOYLGWASHREVPVGSKRSPFLKILQVEKWQEBWKEGEGRTIIHCLNGG 1380  
DB 1321 TRPOEGYLMVQOQFOYLGWASHREVPVGSKRSPFLKILQVEKWQEBWKEGEGRTIIHCLNGG 1380  
QY 1381 GRSQMFCAIGIVEMVKRQNVVDVHFVAVKTLRNKPMNVPEAQYRFCYDVALEYLESS 1439  
DB 1381 GRSQMFCAIGIVEMVKRQNVVDVHFVAVKTLRNKPMNVPEAQYRFCYDVALEYLESS 1439

## RESULT 2

US-08-087-244A-2  
; Sequence 2, Application US/08087244A  
; Patent No. 5863755  
; GENERAL INFORMATION:  
; APPLICANT: Schlössinger, Joseph  
; APPLICANT: Sap, Jan M.  
; APPLICANT: Ullrich, Axel  
; APPLICANT: Vogel, Wolfgang  
; APPLICANT: Fuchs, Miriam  
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
; TITLE OF INVENTION: PHOSPHATASE-KAPPA  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/087,244A  
; FILING DATE: 01-JUL-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7683-042  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1439 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-087-244A-2

Query Match 99.8%; Score 7692; DB 2; Length 1439;  
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1437; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDTTAAALPAFVALLSPWPLLSAQGSAGGCTFDDGPGACDHYQDLYDDFEWVHV 60  
DB 1 MDTTAAALPAFVALLSPWPLLSAQGSAGGCTFDDGPGACDHYQDLYDDFEWVHV 60

QY 61 SAQEPHYLPPMPGSGYMIYDSSDHPDGEKARLQPTMKENDTHCIDPSYLLYSOKGLNP 120  
DB 61 SAQEPHYLPPMPGSGYMIYDSSDHPDGEKARLQPTMKENDTHCIDPSYLLYSOKGLNP 120

QY 121 GTNLILVRNKGPLANFIMVNTGTRDMLRAELAVSTFWPNEYQVIFEAESVSGRSGYI 180  
DB 121 GTNLILVRNKGPLANFIMVNTGTRDMLRAELAVSTFWPNEYQVIFEAESVSGRSGYI 180

QY 181 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQATPQCIATGRDAVHNKMLQRRNGEDIPV 240  
DB 181 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQATPQCIATGRDAVHNKMLQRRNGEDIPV 240

QY 241 AQTKNINHRFAAFRLQEVTKTDQDLYRCVTQSERGSGVSNFAQLIVRPPPIAPPOL 300  
DB 241 AQTKNINHRFAAFRLQEVTKTDQDLYRCVTQSERGSGVSNFAQLIVRPPPIAPPOL 300

QY 301 LGVGPYLLQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPYKYLWHLDPDTEYE 360  
DB 301 LGVGPYLLQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPYKYLWHLDPDTEYE 360

QY 361 IRVLLTRPBGEGTGLPOPPILITRTKCAEPMTPTKLIABIQARRIAVDWESLGYNITRC 420  
DB 361 IRVLLTRPBGEGTGLPOPPILITRTKCAEPMTPTKLIABIQARRIAVDWESLGYNITRC 420

QY 421 HTFNVTICVYFPGHNSKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGRKESSE 480  
DB 421 HTFNVTICVYFPGHNSKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGRKESSE 480

QY 481 TIIQTDEDVPGPVKSLQTSFENKIFLNKPELDPNGIITQVEISYSSIRGFDPAVPV 540  
DB 481 TIIQTDEDVPGPVKSLQTSFENKIFLNKPELDPNGIITQVEISYSSIRGFDPAVPV 540

QY 541 AGPPQTVSNLWNSHTHVMHLPGTQYFFIRASTVKFGPATAINVTNISAPTLPDYE 600  
DB 541 AGPPQTVSNLWNSHTHVMHLPGTQYFFIRASTVKFGPATAINVTNISAPTLPDYE 600

QY 601 GVDASINETAATITVLLRPAQAGAPISAYQIVVEELHPHRTKREAGAMECYQVPTYQN 660  
DB 601 GVDASINETAATITVLLRPAQAGAPISAYQIVVEELHPHRTKREAGAMECYQVPTYQN 660

QY 661 AMGGAPYYFAELPPGNLPEPAPFTVGDNRQYQGFNNPLAPRKGNYIFQAMSSVEKE 720  
DB 661 AMGGAPYYFAELPPGNLPEPAPFTVGDNRQYQGFNNPLAPRKGNYIFQAMSSVEKE 720

QY 721 TKTCQVRIATKAATEEPEVIPDPAKQTDVVKIAGISAGILVFILLVLLVILVKSCLA 780  
DB 721 TKTCQVRIATKAATEEPEVIPDPAKQTDVVKIAGISAGILVFILLVLLVILVKSCLA 780

QY 781 KKKDAMGNTRQETHMVMNDRSYADQSTLHAEDPLSITFMDQHPSPRYENHSATAES 840  
DB 781 KKKDAMGNTRQETHMVMNDRSYADQSTLHAEDPLSITFMDQHPSPRYENHSATAES 840

QY 841 SRLLDVPRYLCEGTESPYQGLHPALRVADLLOHINLMKTSYSGFKEEYEFEGQSA 900  
DB 841 SRLLDVPRYLCEGTESPYQGLHPALRVADLLOHINLMKTSYSGFKEEYEFEGQSA 900

QY 901 SWDVAKKQDNRAKNRYGNIITAYDHSRVILQVPEDDPSSDIYINANYIDGYORPSHYIATQ 960  
DB 901 SWDVAKKQDNRAKNRYGNIITAYDHSRVILQVPEDDPSSDIYINANYIDGYORPSHYIATQ 960

QY 961 PVHETVYDFWRMIWQEOSACIMVTNLVVEGRVKCYKYPDDTEVYDGFVKTCVMEPELA 1020  
DB 961 PVHETVYDFWRMIWQEOSACIMVTNLVVEGRVKCYKYPDDTEVYDGFVKTCVMEPELA 1020

QY 1021 EYVVRFTLERRGYNEIREVKQHFCTGWPDPGVYHATGLLSFIRRVKLSNPPSAGPIVV 1080  
DB 1021 EYVVRFTLERRGYNEIREVKQHFCTGWPDPGVYHATGLLSFIRRVKLSNPPSAGPIVV 1080

QY 1081 HCSAGAGTCYIVIDIMDMAEREGVVDIYNCVKALRSRRINNVQTEQYIFIHDAILE 1140  
DB 1081 HCSAGAGTCYIVIDIMDMAEREGVVDIYNCVKALRSRRINNVQTEQYIFIHDAILE 1140

QY 1141 ACLCGETAIPVCEFKAAYPDMIRIDSTNSHLLKDEFOTLNSVTPRLOAEDCSACIAPRN 1200  
DB 1141 ACLCGETAIPVCEFKAAYPDMIRIDSTNSHLLKDEFOTLNSVTPRLOAEDCSACIAPRN 1200

QY 1201 HDKNRFDMLPPDRCLPFLITIDGESSNYINAAIMDSYRQPAAFIVTQYPLPNTVKDFWR 1260  
DB 1201 HDKNRFDMLPPDRCLPFLITIDGESSNYINAAIMDSYRQPAAFIVTQYPLPNTVKDFWR 1260

QY 1261 LVTDYGTCTSIWMLNEVDLSQGCQYWPBEGMLRYGPIQVECMSCMDCDVINRIFRICNL 1320  
DB 1261 LVTDYGTCTSIWMLNEVDLSQGCQYWPBEGMLRYGPIQVECMSCMDCDVINRIFRICNL 1320

QY 1321 TRPQEGYLMVQQOYQYLGMASHREVPGSKRSFLKILLOVEKWOBEKGEGRTHIHLNGG 1380  
DB 1321 TRPQEGYLMVQQOYQYLGMASHREVPGSKRSFLKILLOVEKWOBEKGEGRTHIHLNGG 1380

QY 1381 GRSGMFCAGIVVEMVKRQNVVDVFAVKTLRNKPNNWEAPEQYRFCYDVALEYLESS 1439  
DB 1381 GRSGMFCAGIVVEMVKRQNVVDVFAVKTLRNKPNNWEAPEQYRFCYDVALEYLESS 1439

## RESULT 3

US-08-652-971-3  
; Sequence 3, Application US/08652971  
; Patent No. 5814507  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd.  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,971  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: P1033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 225-3216  
; TELEFAX: (415) 952-9881  
; TELEX: 910 371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1457 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-652-971-3

Query Match 98.2%; Score 7571; DB 2; Length 1457;  
Best Local Similarity 97.3%; Pred. No. 0;  
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

QY 1 MDTTAAALPAFVALLLSLWPLGSAQOFSAGCTFDDGACDYHQDLYDDPEWHV 60  
Db 1 MD-VAAALPAFVALWLLPLGSAQOFSAGCTFDDGACDYHQDLYDDPEWHV 59  
QY 61 SAQPHYLPPMPQGSYMYVDSDDHDPCKARLQLPMTKENDTHCIDFSYLLYSQKGLNP 120  
Db 60 SAQPHYLPPMPQGSYMYVDSDDHDPCKARLQLPMTKENDTHCIDFSYLLYSQKGLNP 119  
QY 121 GTNLILVRNKGPIANPIWNTGTFRDMLRAELAVSTFWNEQVYIPEAEVSGRSGYI 180  
Db 120 GTNLILVRNKGPIANPIWNTGTFRDMLRAELAVSTFWNEQVYIPEAEVSGRSGYI 179  
QY 181 AIDDIQVLSYPCDKSPHFLRGDVEVNAQONATFQCIATGRDAVHNLKWLORRNGEDIPV 240  
Db 180 AIDDIQVLSYPCDKSPHFLRGDVEVNAQONATFQCIATGRDAVHNLKWLORRNGEDIPV 239  
QY 241 AQTKNINHRRAAASPRLEQVTKTDODLYRCVTSQBSRGSGVSNFAQLIVREPPRIAPPOL 300  
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Db 300 LGVGPYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMHLPDPTYE 359  
QY 361 IRVLLTRREGGTGLPGPLITRTKCAEPMRTPKTLKIAEIOAREIAVDMESLGNITRC 420  
Db 360 IRVLLTRREGGTGLPGPLITRTKCAEPMRTPKTLKIAEIOAREIAVDMESLGNITRC 419  
QY 421 HTFNVTICVHPRGHNSKADCLMDPKAPOHVNHLPYTNVLSKMLITNPEGRKESEE 480  
Db 420 HTFNVTICVHPRGHNSKADCLMDPKAPOHVNHLPYTNVLSKMLITNPEGRKESEE 479  
QY 481 TIIQTDVDPGVVPVKSLOGTSFENKIPLNKKPELDPNGIITQYBISYSSIRSFPDPAVPV 540  
Db 480 TIIQTDVDPGVVPVKSLOGTSFENKIPLNKKPELDPNGIITQYBISYSSIRSFPDPAVPV 539  
QY 541 AGPPQTVSNLWNSHTHVFMHLHPGTYOFFFRASTVKGFGPATAINVTNINSAPLDPYE 600  
Db 540 AGPPQTVSNLWNSHTHVFMHLHPGTYOFFFRASTVKGFGPATAINVTNINSAPLDPYE 599  
QY 601 GVDASLNETAITITVLLRPAQAKGAPISAYQIIVWELPHRTPKRAAGAMECVQVPTVYQN 660  
Db 600 GVDASLNETAITITVLLRPAQAKGAPISAYQIIVWELPHRTPKRAAGAMECVQVPTVYQN 659  
QY 661 AMSGAPYFAAELPPGNLPEPAPFTVGNRTYQGFWMNPPAPLAPRGYNIYFOAMSSVEKE 720  
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QY 721 TKTCQVRIATK-AATEEPEVIPPAAKOTDRVVKIAGISAGILVFTLLLLWVILVKKSKL 779  
Db 720 TKTCQVRIATKAAATEEPEVIPPAAKOTDRVVKIAGISAGILVFTLLLLWVILVKKSKL 779  
QY 780 AKKRKDMGNTQEMTHMNMNDRSYADOSTLHAEDPISITFMDQHNFSRPRY----- 831  
Db 780 AKKRKDMGNTQEMTHMNMNDRSYADOSTLHAEDPISITFMDQHNFSRPLPNDPLVPT 839  
QY 832 ----ENHSATSSRLDDVPRLCEGTESPYQTQLHPAIRVADLLQHINLMKTSDSYGF 887  
Db 840 AVLDEHNSATSSRLDDVPRLCEGTESPYQTQLHPAIRVADLLQHINLMKTSDSYGF 899  
QY 888 KEYESFFBQGSASWDVAKQONRAKNRYGNIAYDHSRVILQPVEDDPSSDIYINANYI- 946  
Db 900 KEYESFFBQGSASWDVAKQONRAKNRYGNIAYDHSRVILQPVEDDPSSDIYINANYID 959  
QY 947 ----DGYORPSHYIATQGPVHETVYDFWMTWQEOSACIMVMTNLVEGRVKCYKYPD 1001  
Db 960 IWLYRDGYORPSHYIATQGPVHETVYDFWMTWQEOSACIMVMTNLVEGRVKCYKYPD 1019  
QY 1002 DTEVYGDVKVTCVMEPLAEYVVRFTFLRRGYNEIREVKQPHFTGWPDPHGVPHYATGLL 1061  
Db 1020 DTEVYGDVKVTCVMEPLAEYVVRFTFLRRGYNEIREVKQPHFTGWPDPHGVPHYATGLL 1079  
QY 1062 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCIYIVIDIMLDMAREGVDIYNCVKALRSRR 1121

Db 1080 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCIYIVIDIMLDMAREGVDIYNCVKALRSRR 1139  
QY 1122 INNVQTEQVIFIHDAILEACLCGETAIPVCEFKAAAFDMIRIDSQTNSSHLKDEFOQLN 1181  
Db 1140 INNVQTEQVIFIHDAILEACLCGETAIPVCEFKAAAFDMIRIDSQTNSSHLKDEFOQLN 1199  
QY 1182 SVTPRLQAECDSTACLPRNHDKNRFDMDLPPDRCLPFLITIDGESSNYINAALMDSYROP 1241  
Db 1200 SVTPRLQAECDSTACLPRNHDKNRFDMDLPPDRCLPFLITIDGESSNYINAALMDSYROP 1259  
QY 1242 AAFIVTQYPLPNTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVEK 1301  
Db 1260 AAFIVTQYPLPNTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVEK 1319  
QY 1302 MSCMDCDVINRIPRINLTPRQBSGYLMVQOQFYLGHASHREVPGSKRSFKLLILOVEKW 1361  
Db 1320 MSCMDCDVINRIPRINLTPRQBSGYLMVQOQFYLGHASHREVPGSKRSFKLLILOVEKW 1379  
QY 1362 QEEWKEGEGRTIHLCLNGGSGRMFCAGIIVEMVKRQNVVDVFAVKTLSRNSKPNMVEA 1421  
Db 1380 QEECEGEGRTIHLCLNGGSGRMFCAGIIVEMVKRQNVVDVFAVKTLSRNSKPNMVEA 1439  
QY 1422 PEQYRFCYDVALEYLESS 1439  
Db 1440 PEQYRFCYDVALEYLESS 1457  
  
RESULT 4  
US-08-449-644-1  
; Sequence 1, Application US/08449644  
; Patent No. 5856162  
; GENERAL INFORMATION:  
; APPLICANT: Schlessinger, Joseph  
; APPLICANT: Sap, Jan M.  
; APPLICANT: Ullrich, Axel  
; APPLICANT: Vogel, Wolfgang  
; APPLICANT: Fuchs, Miriam  
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
; TITLE OF INVENTION: PHOSPHATASE-KAPPA  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,644  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/087,244  
; FILING DATE: 01-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7683-042  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1457 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

MOLECULE TYPE: protein		
us-08-449-644-1		
Query Match 98.2%; Score 7571; DB 2; Length 1457;		
Best Local Similarity 97.3%; Pred. No. 0;		
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;		
QY	1	MDTAAALAFVALLLSWELLGSAQGFAGGCTFDDGPGACDTHQDLYDDFEWVHV 60
DB	1	MD-VAAALAFVALLWLYFWPLLGSALGQFSAGGCTFDDGPGACDTHQDLYDDFEWVHV 59
QY	61	SAOEPHYLPPEMPOGSMYVDSDDHDPGEKARQLPTMKENDTHCIDFSYLLYSQKGLNP 120
DB	60	SAOEPHYLPPEMPOGSMYVDSDDHDPGEKARQLPTMKENDTHCIDFSYLLYSQKGLNP 119
QY	121	GTNLVRVNGKPLANPIMNVGTGRDMLRAELAVSTFWPNEYQVIFEAESVSGRSGYI 180
DB	120	GTNLVRVNGKPLANPIMNVGTGRDMLRAELAVSTFWPNEYQVIFEAESVSGRSGYI 179
QY	181	AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATPQCIATGRDAVHNKLMQRRNGEDIPV 240
DB	180	AIDDIQVLSYPCDKSPHFLRLGDEVNAGQATPQCIATGRDAVHNKLMQRRNGEDIPV 239
QY	241	AQTKNINHRFAAFRLQEVTKTDQDLYRCVTSERSGVSNFAQLIVRPPRIAPPOL 300
DB	240	AQTKNINHRFAAFRLQEVTKTDQDLYRCVTSERSGVSNFAQLIVRPPRIAPPOL 299
QY	301	LGVGPTVLLQLNANSIIGDGPILKEVEYMTSGSWTETHAVNAPTYKLMHLPDPEYE 360
DB	300	LGVGPTVLLQLNANSIIGDGPILKEVEYMTSGSWTETHAVNAPTYKLMHLPDPEYE 359
QY	361	IRVLLTRPBGEGTGLPGPPIITRTKCAEPMRTPKTKIABIQARRIAVDWESLGYNITRC 420
DB	360	IRVLLTRPBGEGTGLPGPPIITRTKCAEPMRTPKTKIABIQARRIAVDWESLGYNITRC 419
QY	421	HTFNVTICVHYFGHNEKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGRKESEE 480
DB	420	HTFNVTICVHYFGHNEKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGRKESEE 479
QY	481	TIQTQEDVGPVVKSLQGTSPENKIFLNKPKPLDPNGIITQVEYSYSSIRSFDPAPV 540
DB	480	TIQTQEDVGPVVKSLQGTSPENKIFLNKPKPLDPNGIITQVEYSYSSIRSFDPAPV 539
QY	541	AGPPQTVSNLWNSHTHVFMLHPGTTTYQFFIRASTVKFGFPATAINVTNISAPLPDYE 600
DB	540	AGPPQTVSNLWNSHTHVFMLHPGTTTYQFFIRASTVKFGFPATAINVTNISAPLPDYE 599
QY	601	GVDAASLNETATITVLLRPAQAGAPISAYQIVVEELHPHRTKREAGAMECYQVPVYQN 660
DB	600	GVDAASLNETATITVLLRPAQAGAPISAYQIVVEELHPHRTKREAGAMECYQVPVYQN 659
QY	661	AMSGGAPYFAAELPGNLPPEPAPFTVGDNRKTYGFWNPLAPRKGNYIFQAMSSVEKE 720
DB	660	AMSGGAPYFAAELPGNLPPEPAPFTVGDNRKTYGFWNPLAPRKGNYIFQAMSSVEKE 719
QY	721	TKTQCVRIATK-AATEPEVIPPAPKOTDRVVKIAGISAGILVFILLVLLVILVKSKL 779
DB	720	TKTQCVRIATKAAATEPEVIPPAPKOTDRVVKIAGISAGILVFILLVLLVILVKSKL 779
QY	780	AKRKQAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSTFMDQHNFSRY ----- 831
DB	780	AKRKQAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSTFMDQHNFSRY ----- 839
QY	832	-----ENHSATAESRLLDVPRYLCEGTSPYQGLHPAIRVADLLOHINLMTSDSYGF 887
DB	840	AVLDENHSATAESRLLDVPRYLCEGTSPYQGLHPAIRVADLLOHINLMTSDSYGF 899
QY	888	KEEYESFFEQSASWDVAKKQONRAKRNRYNIAYDHSRVILQPVEDDPSDDINANYI- 946
DB	900	KEEYESFFEQSASWDVAKKQONRAKRNRYNIAYDHSRVILQPVEDDPSDDINANYI 959
QY	947	-----DGYQRPSPHYIATQGPVHETVDFWFMVWQESACIWMVTNLVEGVRKCYKTPD 1001

RESULT 5  
US-08-087-244A-1  
; Sequence 1, Application US/08087244A  
; Patent No. 5863755  
; GENERAL INFORMATION:  
; APPLICANT: Schlessinger, Joseph  
; APPLICANT: Sap, Jan M.  
; APPLICANT: Ulrich, Axel  
; APPLICANT: Vogel, Wolfgang  
; APPLICANT: Fuchs, Miriam  
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
; TITLE OF INVENTION: PHOSPHATASE-KAPPA  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/087,244A  
; FILING DATE: 01-JUL-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7683-042  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-087-244A-1

Query Match 98.2%; Score 7571; DB 2; Length 1457;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

Qy 1 MDTTAAALPAFVALLSPPLGSAQGSAGGCTDDGPGACDHYHODLYDDFEWVHV 60
Db 1 MD-VAAALPAFVALWLLYPPLGSAQGSAGGCTDDGPGACDHYHODLYDDFEWVHV 59
Qy 61 SAQEPHYLPPEMPQGSYIMVDSDDHPCEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 120
Db 60 SAQEPHYLPPEMPQGSYIMVDSNDHPCEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 119
Qy 121 GTNLILVRNKGPLANPIWNTGFTGRDWLRAELAVSTFWNEYQVIFEAESVSGRSYI 180
Db 120 GTNLILVRNKGPLANPIWNTGFTGRDWLRAELAVSTFWNEYQVIFEAESVSGRSYI 179
Qy 181 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFOCIATGRDAVHNKWLQRRNGEDIPV 240
Db 180 AIDDIQVLSYPCDKSPHFLRLGDEVNAGONATFOCIATGRDAVHNKWLQRRNGEDIPV 239
Qy 241 AQTKNINHRFAASPRLEQVTKTDQDLRYCVTSERGSVSNFAQLIVREPPRIAPPQL 300
Db 240 AQTKNINHRFAASPRLEQVTKTDQDLRYCVTSERGSVSNFAQLIVREPPRIAPPQL 299
Qy 301 LGVGTYLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPTLYKLWHLDDPTEYE 360
Db 300 LGVGTYLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPTLYKLWHLDDPTEYE 359
Qy 361 IRVLLTRPGEGTGLPGPLTRTKCAEPMRTPKTKIAEQARIAVDWESLGVNITRC 420
Db 360 IRVLLTRPGEGTGLPGPLTRTKCAEPMRTPKTKIAEQARIAVDWESLGVNITRC 419
Qy 421 HTFNVTICYHFRGHNESKADCLMDPKAQHVNVNHLPPYTNVSLKMLITNPEGRKESEE 480
Db 420 HTFNVTICYHFRGHNESRADCLMDPKAQHVNVNHLPPYTNVSLKMLITNPEGRKESEE 479
Qy 481 TIIQTDVDPGVVKSLOGTSFENKIFLNKKEPLDNGIITQYBISYSSRSRFPDPAVPV 540
Db 480 TIIQTDVDPGVVKSLOGTSFENKIFLNKKEPLDNGIITQYBISYSSRSRFPDPAVPV 539
Qy 541 AGPPTVSNLWNSHHVFMHLHPGTYOFFIRASTVKGFGPATANVTNINISAPLDPYE 600
Db 540 AGPPTVSNLWNSHHVFMHLHPGTYOFFIRASTVKGFGPATANVTNINISAPLDPYE 599
Qy 601 GVDASLNATATTITVLLRPAQAKGAPISAYQIVVEELPHRPTKREAGAMECYQVPVTYQN 660
Db 600 GVDASLNATATTITVLLRPAQAKGAPISAYQIVVEELPHRPTKREAGAMECYQVPVTYQN 659
Qy 661 AMSGAPYFAELPPGNLPEPAPTVGDNRTYQGFVWNPPLAPRKGYNIYFOAMSSVEKE 720
Db 660 ALSGAPYFAELPPGNLPEPAPTVGDNRTYQGFVWNPPLAPRKGYNIYFOAMSSVEKE 719
Qy 721 TKTCQVRIATK-AAATEEPEVIPPDAKQTDVVKIAGISAGILVFTILLVWILVVKSKL 779
Db 720 TKTCQVRIATKAAATEEPEVIPPDAKQTDVVKIAGISAGILVFTILLVWILVVKSKL 779
Qy 780 AKKRKDMGNTRQEMTHVMNMDRSYADQSTLHAEDPLSLTFMDQHNFSPRY----- 831
Db 780 AKKRKDMGNTRQEMTHVMNMDRSYADQSTLHAEDPLSLTFMDQHNFSPRLPNDPLVPT 839
Qy 832 ----ENHGAATSSKLLDVPVRLCGTSRSPYTGQLHPAIRVADLLQHINLMKTSDSYGF 887
Db 840 AVLNDHSAATSSKLLDVPVRLCGTSRSPYTGQLHPAIRVADLLQHINLMKTSDSYGF 899
Qy 888 KEEYESFFEGQASMDVAKQDNRAKNRYGNI IAYDHSRVILQPVDDPSSDIYNANVI 946
Db 888 KEEYESFFEGQASMDVAKQDNRAKNRYGNI IAYDHSRVILQPVDDPSSDIYNANVI 946

900 KEEYESFFEGQASMDVAKQDNRAKNRYGNI IAYDHSRVILQPVDDPSSDIYNANVI 959
947 -----DGYQRPISHYIATQGPVHETVDFWRMIWQESACIYVMTNLVEVGRVKCYKYPD 1001
960 IWLRYDGYQRPISHYIATQGPVHETVDFWRMIWQESACIYVMTNLVEVGRVKCYKYPD 1019
1002 DTEVYGDPKVTCVMEPLAEVYVTRFTLERGYNEIREVKQFHFTGWDHGVPHYHATGLL 1061
1020 DTEVYGDPKVTCVMEPLAEVYVTRFTLERGYNEIREVKQFHFTGWDHGVPHYHATGLL 1079
1062 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRR 1121
1080 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCYIVIDIMLDMAREGVVDIYNCVKALRSRR 1139
1122 INMVQTBEOYIFIHDAILEACLCGETAIPVCEFAAYFDMIRIDISQTNSSHLKDBFQTLN 1181
1140 INMVQTBEOYIFIHDAILEACLCGETAIPVCEFAAYFDMIRIDISQTNSSHLKDBFQTLN 1199
1182 SVTPRLQAECDSCIACLPRNHDKNRFMDLPPDRCLPFLITIDGESSNYINAAALMDSYROP 1241
1200 SVTPRLQAECDSCIACLPRNHDKNRFMDLPPDRCLPFLITIDGESSNYINAAALMDSYROP 1259
1242 AAFIVTQVPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQGCPOYWPBEGMLRYGPIQVEC 1301
1260 AAFIVTQVPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQGCPOYWPBEGMLRYGPIQVEC 1319
1302 MSCMDCDVINRIFRICNLTRPQSGYLMVQOQFYLGWASHREVPGSKRSFLKLIQVEKW 1361
1320 MSCMDCDVINRIFRICNLTRPQSGYLMVQOQFYLGWASHREVPGSKRSFLKLIQVEKW 1379
1362 QEEWKEGEGRTIICHLNGGSGRMFCAGIIVEMVKQNVVDVHAVKTLRNSKPNMVEA 1421
1380 QEECEGEGRTIICHLNGGSGRMFCAGIIVEMVKQNVVDVHAVKTLRNSKPNMVEA 1439
1422 PEQYRVCYDVALEYLESS 1439
1440 PEQYRVCYDVALEYLESS 1457

RESULT 6
US-08-991-258A-3
; Sequence 3, Application US/08991258A
; Patent No. 5928887
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991.258A
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63478-3/WH/D/MTK
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1457 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-991-258A-3

Query Match 98.28; Score 7571; DB 2; Length 1457;  
Best Local Similarity 97.33; Pred. No. 0;  
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

Qy	1	MDTAAAAALPAFVALLLSWPPLGSAQOQPSAGGCTFDGPGACDYHQDLYDDFEWVHV	60
Db	1	MD-VAAAAALPAFVALWLLYPWLLGSLAQFSAGGCTFDGPGACDYHQDLYDDFEWVHV	59
Qy	61	SAQEPHYLPPEMPOGSMYVDDSDHPGEXKARLQLPMTKENDTHCIDFSYLLYSQKGLNP	120
Db	60	SAQEPHYLPPEMPOGSMYVDDSSNHPGEXKARLQLPMTKENDTHCIDFSYLLYSQKGLNP	119
Qy	121	GTNLILVRVNGKPLANIPWVTGTRDWLRRAELAVSTFWPNEYQVIFPAEVSGRSGYI	180
Db	120	GTNLILVRVNGKPLANIPWVTGTRDWLRRAELAVSTFWPNEYQVIFPAEVSGRSGYI	179
Qy	181	AIDDIQVLSYPCDKSPHFLRLGDVEVNAGONATQCIATGRDAVHNKMLQRRNGEDIPV	240
Db	180	AIDDIQVLSYPCDKSPHFLRLGDVEVNAGONATQCIATGRDAVHNKMLQRRNGEDIPV	239
Qy	241	AQTKNINHRFAASFRLEQVTKDQDLYRCVTOSESGSVNSFAQLIVREPPRPIAPPOL	300
Db	240	AQTKNINHRFAASFRLEQVTKDQDLYRCVTOSESGSVNSFAQLIVREPPRPIAPPOL	299
Qy	301	LGVGPTVLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPYKYLWHLDPDTEYE	360
Db	300	LGVGPTVLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPYKYLWHLDPDTEYE	359
Qy	361	IRVLLTRPGGGTGLPGPPLITRTKCAEPMRTPTKIAIEIQARRIAVDWESLYGNITRC	420
Db	360	IRVLLTRPGGGTGLPGPPLITRTKCAEPMRTPTKIAIEIQARRIAVDWESLYGNITRC	419
Qy	421	HTFNVTICYHYFRGHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESEE	480
Db	420	HTFNVTICYHYFRGHNESRADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESEE	479
Qy	481	TIQTDEDDVPGVPVKSLQGTSPENKIFLNWKEPLDPNGIITQVEISYSSIRGFDPAVPV	540
Db	480	TIQTDEDDVPGVPVKSLQGTSPENKIFLNWKEPLDPNGIITQVEISYSSIRGFDPAVPV	539
Qy	541	AGPPQTVSNLWNSHTHVFHMLHPCGTTQFFIRASTVKFGFPATAINVTNISAPLDPYE	600
Db	540	AGPPQTVSNLWNSHTHVFHMLHPCGTTQFFIRASTVKFGFPATAINVTNISAPLDPYE	599
Qy	601	GVDAASNETATTITVILRPAQAGAPISAYQIVVVEELHPHRTKREAGAMECYQVPVYQN	660
Db	600	GVDAASNETATTITVILRPAQAGAPISAYQIVVVEELHPHRTKREAGAMECYQVPVYQN	659
Qy	661	AMSGGAPYFAAELPPCNLPPEAPFTVGDNRVTQGFNWPPLAPRKGNYIFQAMSSVEKE	720
Db	660	ALSGGAPYFAAELPPCNLPPEAPFTVGDNRVTQGFNWPPLAPRKGNYIFQAMSSVEKE	719
Qy	721	TKTCQVRIATK-AATEPEVIPPAPKOTDRVVKIAGISAGILVFILLLLVILVKKSKL	779
Db	720	TKTCQVRIATKAAATEPEVIPPAPKOTDRVVKIAGISAGILVFILLLLVILVKKSKL	779
Qy	780	AKKRKDMGNTROBMTWNVAMDRSYADQSTLHAEDPLSITFMDQHNFSRY-----	831
Db	780	AKKRKDMGNTROBMTWNVAMDRSYADQSTLHAEDPLSITFMDQHNFSRY-----	830
Qy	832	-----ENHSATAESSRLDDVPRLCEGTSPYQTQGLHPAIRVADLLQHLINLMKTSYGF	887

Db	840	AVLDENHSATAESSRLDDVPRLCEGTSPYQTQGLHPAIRVADLLQHLINLMKTSYGF	899
Qy	888	KEEVESFFEGQSASWDVAKKQDNRAKRYGNIITAYDHSRVILQVEDDPSDDYINANYI-	946
Db	900	KEEVESFFEGQSASWDVAKKQDNRAKRYGNIITAYDHSRVILQVEDDPSDDYINANYID	959
Qy	947	-----DGYPSPHYIATQGPVHETVDFWRMIWQEQSACIWMVTNLVEVGKVKCYKWP	1001
Db	960	IWLRYDGYQRPSPHYIATQGPVHETVDFWRMIWQEQSACIWMVTNLVEVGKVKCYKWP	1019
Qy	1002	DTEVYGDVKVTCVEMBPALAEYVVRTFTLRRGNYEIREVKQFHTGPDGVPVHATGLL	1061
Db	1020	DTEVYGDVKVTCVEMBPALAEYVVRTFTLRRGNYEIREVKQFHTGPDGVPVHATGLL	1079
Qy	1062	SFIRRVKLSNPPSAGPIVHVCSAGAGRTGCIYVIDIMLDMAREGVVDIYNCVKALRSRR	1121
Db	1080	SFIRRVKLSNPPSAGPIVHVCSAGAGRTGCIYVIDIMLDMAREGVVDIYNCVKALRSRR	1139
Qy	1122	INMVQTEEQYIFITHDAILEACLCGETAIPVCEPKAAAYFDMIRIDSQTNSSHLKDEFOTLN	1181
Db	1140	INMVQTEEQYIFITHDAILEACLCGETAIPVCEPKAAAYFDMIRIDSQTNSSHLKDEFOTLN	1199
Qy	1182	SVTPRLOAEDCSIACLPRNHDKNRPFMDLPPDRCLPFLITIDGESSNYINAAALMDSYROP	1241
Db	1200	SVTPRLOAEDCSIACLPRNHDKNRPFMDLPPDRCLPFLITIDGESSNYINAAALMDSYROP	1259
Qy	1242	AAFIIVQYPLPNTVKDFWRLVVDYGCYSIVMLNEVDLSQGCPOYWPBEGMLRYGPIOVEC	1301
Db	1260	AAFIIVQYPLPNTVKDFWRLVVDYGCYSIVMLNEVDLSQGCPOYWPBEGMLRYGPIOVEC	1319
Qy	1302	MSCMDCDVINRIFRINLTPRQEGYLMVQOYQYLGWASHREVPVSGKRSFLKLILQVEKW	1361
Db	1320	MSCMDCDVINRIFRINLTPRQEGYLMVQOYQYLGWASHREVPVSGKRSFLKLILQVEKW	1379
Qy	1362	QEEWKEGEGRTIITCLNGGSGRSMFCAIGIIVEMVKRONVVDVFAVKTILNSKPNMVEA	1421
Db	1380	QEEWKEGEGRTIITCLNGGSGRSMFCAIGIIVEMVKRONVVDVFAVKTILNSKPNMVEA	1439
Qy	1422	PEQYRFDYDVALLEYLESS 1439	
Db	1440	PEQYRFDYDVALLEYLESS 1457	

RESULT 7  
US-08-769-399-3  
Sequence 3, Application US/08769399  
Patent No. 597852  
GENERAL INFORMATION:  
APPLICANT: Cheng, Jill  
APPLICANT: Laeky, Laurence A.  
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd.  
CITY: South San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/769,399  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055

; REFERENCE/DOCKET NUMBER: P1033  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 225-3216  
 ; TELEFAX: (415) 952-9881  
 ; TELEX: 910 371-7168  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1457 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-769-399-3

Query Match 98.2%; Score 7571; DB 2; Length 1457;  
 Best Local Similarity 97.3%; Pred. No. 0;  
 Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

QY	1	MDTTAAARALPAFVALLSPHLLGSAOGQSFAGGCTDDGPGACDHYHODLYDPEWHV	60
DB	1	MD-VAARALPAFVALWLLYPWLLGSLGQFSAGGCTFDGPGACDHYHODLYDPEWHV	59
QY	61	SAQEPHYLPPEMPOGQSYMIVDSSDHPGKARLQLPTMKENDTHCIDFSYLLYSQKGLNP	120
DB	60	SAQEPHYLPPEMPOGQSYMIVDSSDHPGKARLQLPTMKENDTHCIDFSYLLYSQKGLNP	119
QY	121	GTLNLTVRNKGPLANINWVTGFTGRDLWRAELAVSTFWNEVQVIFEAESVSGRSGYI	180
DB	120	GTLNLTVRNKGPLANINWVTGFTGRDLWRAELAVSTFWNEVQVIFEAESVSGRSGYI	179
QY	181	AIDDDQVLSYPCDKSPHFLRGDVEVNAQONATFOCIATGRDAVHKNLWLRNGEDIPV	240
DB	180	AIDDDQVLSYPCDKSPHFLRGDVEVNAQONATFOCIATGRDAVHKNLWLRNGEDIPV	239
QY	241	AQTKNINRRFAASFLQEVTKTDQDLYRCVTSERGSVSNFAQLIVREPPRPIAPPOL	300
DB	240	AQTKNINRRFAASFLQEVTKTDQDLYRCVTSERGSVSNFAQLIVREPPRPIAPPOL	299
QY	301	LGVGPTYLLIQNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYE	360
DB	300	LGVGPTYLLIQNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYE	359
QY	361	IRVLLTRGEGGTGLPGPLTRTKCAEPMRTPKTLKABIOARIVADWESLGNITRC	420
DB	360	IRVLLTRGEGGTGLPGPLTRTKCAEPMRTPKTLKABIOARIVADWESLGNITRC	419
QY	421	HTFNVTICVHYPRGHNEKADCLMDPKAPQHVHNLPPYTNVSLKMLITNPEGRKESEE	480
DB	420	HTFNVTICVHYPRGHNEKADCLMDPKAPQHVHNLPPYTNVSLKMLITNPEGRKESEE	479
QY	481	TTIQTDEDVPGVPVVKSLQGSTFENKIFLNWKEPLDPNGIITQYBISYSSIRSFDPAPVP	540
DB	480	TTIQTDEDVPGVPVVKSLQGSTFENKIFLNWKEPLDPNGIITQYBISYSSIRSFDPAPVP	539
QY	541	AGPPQTVSNLWNSTHHVFHMLHPGTYTQFFIRASTVKGFGPATAINVTTNISAPLDPYE	600
DB	540	AGPPQTVSNLWNSTHHVFHMLHPGTYTQFFIRASTVKGFGPATAINVTTNISAPLDPYE	599
QY	601	GYDASLNETAATITVLLRPAQAKGAPISAYQIIVBELPHRTPKRAGAMECYQVPTVYQN	660
DB	600	GYDASLNETAATITVLLRPAQAKGAPISAYQIIVBELPHRTPKRAGAMECYQVPTVYQN	659
QY	661	AMSGCAPYYFAAELPFGNLPPEPAPPTVGDNRRTYQGFVWNPPLAPRKGYNIFYQAMSSVEKE	720
DB	660	ALSGCAPYYFAAELPFGNLPPEPAPPTVGDNRRTYQGFVWNPPLAPRKGYNIFYQAMSSVEKE	719
QY	721	TKTQCVRIATK-AAATEEPEVIPPDAKQTDVVVKIAGISAGILVFTLLLVILLVILVKKSL	779
DB	720	TKTQCVRIATKAAATEEPEVIPPDAKQTDVVVKIAGISAGILVFTLLLVILVILVKKSL	779
QY	780	AKKRDAMGNTREQMTHVMYNDMSYADQSTLHAEDPLSLITFMDQHNFSPPRY-----	831
DB	780	AKKRDAMGNTREQMTHVMYNDMSYADQSTLHAEDPLSLITFMDQHNFSPPRLPNDPLVPT	839

QY	832	-----ENHSATAESSRLLDVPRYLCEGTESPYQTQOLHPAIRVADLLOHINLMKTSDSYGF	887
DB	840	AVLDENHSATAESSRLLDVPRYLCEGTESPYQTQOLHPAIRVADLLOHINLMKTSDSYGF	899
QY	888	KEEYESFFEGOSASWDVAKQONRAKNRYGNI IAYDHSRVILQPVEDDPSDDYINANYI -	946
DB	900	KEEYESFFEGOSASWDVAKQONRAKNRYGNI IAYDHSRVILQPVEDDPSDDYINANYID	959
QY	947	-----DGYQRPISHYIATQGPVHETVYDFWRMIWQESACIWMVTNLVEVGRVKCYKWPDP	1001
DB	960	IWLRYDGYQRPISHYIATQGPVHETVYDFWRMIWQESACIWMVTNLVEVGRVKCYKWPDP	1019
QY	1002	DTEVYDGFVKVTCVMEPELAEYVVTFTLERRGYNEIREVKQFHTGPDHGVPHATGLL	1061
DB	1020	DTEVYDGFVKVTCVMEPELAEYVVTFTLERRGYNEIREVKQFHTGPDHGVPHATGLL	1079
QY	1062	SPIRRVKLSNPPSAGPIVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNCVKALRSRR	1121
DB	1080	SPIRRVKLSNPPSAGPIVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNCVKALRSRR	1139
QY	1122	INMVQTEQYIFIHDAILEACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEFOFLN	1181
DB	1140	INMVQTEQYIFIHDAILEACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEFOFLN	1199
QY	1182	SVTPRLQAEDCSIACLPNHDKNRPMDLPPDRCLPLITIDGESSNYINAAALMDSYQOP	1241
DB	1200	SVTPRLQAEDCSIACLPNHDKNRPMDLPPDRCLPLITIDGESSNYINAAALMDSYQOP	1259
QY	1242	AAFTVTOVPLPNTVKDFWRLVYDYGCTSI VMLNEVDLSQGCPOYWPBEGMLRYGPIQVEC	1301
DB	1260	AAFTVTOVPLPNTVKDFWRLVYDYGCTSI VMLNEVDLSQGCPOYWPBEGMLRYGPIQVEC	1319
QY	1302	MSCSMDCDVINRIFRICNLTRPQEGYLMVQOQFYLGMASHREVPFGSKSFLKLIQVEKW	1361
DB	1320	MSCSMDCDVINRIFRICNLTRPQEGYLMVQOQFYLGMASHREVPFGSKSFLKLIQVEKW	1379
QY	1362	QEEWKEGEGRTIHLNGLGGRSGMFCALGIIVEMVKQNVVDVHAVKTLRNSKPMVEA	1421
DB	1380	QEEWKEGEGRTIHLNGLGGRSGMFCALGIIVEMVKQNVVDVHAVKTLRNSKPMVEA	1439
QY	1422	PEQYRFCYDVALEYLESS 1439	
DB	1440	PEQYRFCYDVALEYLESS 1457	

RESULT 8  
 US-08-991-953A-3  
 ; Sequence 3, Application US/08991953A  
 ; Patent No. 6083748  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheng, Jill  
 ; APPLICANT: Lasky, Laurence A.  
 ; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
 ; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP  
 ; STREET: 4 Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/991,953A  
 ; FILING DATE: 16-DEC-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63478-3/WH/D/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-991-953A-3

Query Match      98.2%; Score 7571; DB 3; Length 1457;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

QY 1 MDYTAARAALPAFVALLLLSWPLILGSAQGSAGGCTFDDPGACDYHODLYDDFEWVHV 60
DB 1 MD-VAAALPAFVALWLLYWPWLLGSLGALGGSAGGCTFDDPGACDYHODLYDDFEWVHV 59
QY 61 SAQEPHYLPPEMPOGSMYVDDSDHPDGEKARLQPTMKENDTHCIDFSYLLYSOKGLNP 120
DB 60 SAQEPHYLPPEMPOGSMYVDDSDHDPGEKARLQPTMKENDTHCIDFSYLLYSOKGLNP 119
QY 121 GTNLILVRNKGPLANPINVNTGTGRDMLRAELAVSTFWPNEYQVIFEAESVSGRSGYI 180
DB 120 GTNLILVRNKGPLANPINVNTGTGRDMLRAELAVSTFWPNEYQVIFEAESVSGRSGYI 179
QY 181 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQNAFQCIATGRDAVHNKMLQRRNGEDIPV 240
DB 180 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGQNAFQCIATGRDAVHNKMLQRRNGEDIPV 239
QY 241 AQTKNINRRFPASFRLOEVTKTDODLYRCVTOESRSGVSNFAQLIVREPPPIAPPOL 300
DB 240 AQTKNINRRFPASFRLOEVTKTDODLYRCVTOESRSGVSNFAQLIVREPPPIAPPOL 299
QY 301 LGVGPYLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 360
DB 300 LGVGPYLLIQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPTYKLMHLDPDTEYE 359
QY 361 IRVLLTRPGGGTGLPGPPLITRTKCAEPMTPTKTKIAEIQAARRIAVDWESLYNITRC 420
DB 360 IRVLLTRPGGGTGLPGPPLITRTKCAEPMTPTKTKIAEIQAARRIAVDWESLYNITRC 419
QY 421 HTFNVTICYHYFRGHNSKADCLDMDPKAPQHVNVNHLPPYTNVSLKMLTNPRGKESSE 480
DB 420 HTFNVTICYHYFRGHNSRADCLDMDPKAPQHVNVNHLPPYTNVSLKMLTNPRGKESSE 479
QY 481 TIQTDEDDVPGVPVKSLQTSFENKIFLWKEPLDPNGIITQVEISYSSIRSGFDPAPVP 540
DB 480 TIQTDEDDVPGVPVKSLQTSFENKIFLWKEPLENGIITQVEISYSSIRSGFDPAPVP 539
QY 541 AGPQTQVSNLWNTHHVMHLHPGTTQFFIRASTVKGFGPATINVTNISAPTLPDYE 600
DB 540 AGPQTQVSNLWNTHHVMHLHPGTTQFFIRASTVKGFGPATINVTNISAPTLPDYE 599
QY 601 GVDAASLNETATTIVLARPAQAKAPIISAYQIVVEELHPHRTKEAGAMECYQVPTVYQN 660
DB 600 GVDAASLNETATTIVLARPAQAKAPIISAYQIVVEELHPHRTKEAGAMECYQVPTVYQN 659
QY 661 AMSGAPYFAAELPPGNLPEPAPFTVGNRTYQGFWNPPPLAPRKGYNIYFQAMSSVEKE 720
DB 660 ALSGAPYFAAELPPGNLPEPAPFTVGNRTYQGFWNPPPLAPRKGYNIYFQAMSSVEKE 719
QY 721 TKTCQVRIATK-AATEPEPVIPOPAKQTDVRVWIKIAGISAGILVFILLVIVVIVKSKL 779
DB 720 TKTCQVRIATKAAATEPEPVIPOPAKQTDVRVWIKIAGISAGILVFILLVIVVIVKSKL 779
QY 780 AKRDKAMGNTRQEMTHMNVAMDRSYADQSTLHAEDPLSITFMDQHNFSRY----- 831
DB 780 AKRDKAMGNTRQEMTHMNVAMDRSYADQSTLHAEDPLSITFMDQHNFSRPLPNDPLVPT 839
QY 832 ----ENHSATAESSRLLDVPRYLCEGTSPYQGLHPAIRVADLLQHINLMKTSDSYGF 887
DB 840 AVLDENHSATAESSRLLDVPRYLCEGTSPYQGLHPAIRVADLLQHINLMKTSDSYGF 899
QY 888 KEEVESFFEGQSASWDVAKQDNKRNKRYNIIAYDHSRVLQPOVEDDPSDDYINANYI- 946
DB 900 KEEVESFFEGQSASWDVAKQDNKRNKRYNIIAYDHSRVLQPOVEDDPSDDYINANYID 959
QY 947 ----DGQRPSHYIATQGPVHETVDFWRMIWQESACIWMVTNLVEGVRKCYKWPD 1001
DB 960 IWLYRDGYQRPSHYIATQGPVHETVDFWRMVWQESACIWMVTNLVEGVRKCYKWPD 1019
QY 1002 DTEVYGDVKVTCVEMEPALBYVVRTFTLERRGYNIREVKQFHTGPHDGHVPYHATGLL 1061
DB 1020 DTEVYGDVKVTCVEMEPALBYVVRTFTLERRGYNIREVKQFHTGPHDGHVPYHATGLL 1079
QY 1062 SFTRRVKLSNPPSAGPIVHVHCSAGAGTGCYIVIDIMLDMAREGVVDIYNCVKALRSRR 1121
DB 1080 SFTRRVKLSNPPSAGPIVHVHCSAGAGTGCYIVIDIMLDMAREGVVDIYNCVKALRSRR 1139
QY 1122 INNVQTEEQYIFIHDAILEACLCGETAIPVCEFAAYFDMIRIDSTQNSSHLKDEFOTLN 1181
DB 1140 INNVQTEEQYIFIHDAILEACLCGETAIPVCEFAAYFDMIRIDSTQNSSHLKDEFOTLN 1199
QY 1182 SVTPRLOAEDCSIACLPRNHDKNRFMDMLPPDRCLPLITIDGESSNYINAAALMDSYROP 1241
DB 1200 SVTPRLOAEDCSIACLPRNHDKNRFMDMLPPDRCLPLITIDGESSNYINAAALMDSYROP 1259
QY 1242 AAFIVTQYPLPNTVKDFWRLVVDYDGTCTIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVE 1301
DB 1260 AAFIVTQYPLPNTVKDFWRLVVDYDGTCTIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVE 1319
QY 1302 MSCMDCDVNIRIFRINLTPRQEGYLMVQOFOYLGWASHREVPKSRFLKILQVEKW 1361
DB 1320 MSCMDCDVNIRIFRINLTPRQEGYLMVQOFOYLGWASHREVPKSRFLKILQVEKW 1379
QY 1362 QEEWKEGEGRTIIHCLNGGGRSGMFCAGIIVEMVKRQNVVDVPHAVKTLRNSKPNMVEA 1421
DB 1380 QEEWKEGEGRTIIHCLNGGGRSGMFCAGIIVEMVKRQNVVDVPHAVKTLRNSKPNMVEA 1439
QY 1422 PEQYRCYDVALEYLESS 1439
DB 1440 PEQYRCYDVALEYLESS 1457

RESULT 9
US-08-449-644-8
; Sequence 8, Application US/08449644
; Patent No. 5856162
; GENERAL INFORMATION:
; APPLICANT: Schlesinger, Joseph
; APPLICANT: Sap, Jan M.
; APPLICANT: Ullrich, Axel
; APPLICANT: Vogel, Wolfgang
; APPLICANT: Fuchs, Miriam
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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1	COMPUTER: IBM PC compatible	593	LETPLNQTDNTVTVMLEPAHSGRGPVSVYQIVVEEPRRRTKTKTEILKCYVPPIHFQNA	652
2	OPERATING SYSTEM: PC-DOS/MS-DOS	662	MSGGAPYYFAAEPLPGNLPPEPAPFTVGDNRRTYQGFWMNPLAPRKGNYIYFQAMSSVEKET	721
3	SOFTWARE: Patent In Release #1.0, Version #1.25	653	SILNSQYYFAAEFPADSLQAAQPTTIGDNKTYNGWNTTLLPKYSYRIYFQAASRANGET	712
4	CURRENT APPLICATION DATA:	722	KTCQVRIATKAATBEPEVIPPAPAKQTRVVKIAGISAGILVFIILLVILVILVVKSKLAK	781
5	APPLICATION NUMBER: US/08/449,644	713	KIDCVQVATKGAA-TPKVPPEPEKQTOHTVKIAGVIGILLFVIFIGVVLVVMKKRKLAK	771
6	FILING DATE: 24-MAY-1995	782	KKDAMGNTRQEMTHMNMNDRSYADQSTLHAEDPLSLITMDQHNFPSPRY-----	831
7	CLASSIFICATION: 514	772	KRKETMSSTROEMTVMNMSMDKSYABQGTNCDE---AFSFMDDTHNLNGRSVSSPSSMTM	828
8	PRIOR APPLICATION DATA:	832	-----ENHSATAESSRLLDVPRY-LCEGTSPYQGTQLHPAIRVADLLQH	875
9	APPLICATION NUMBER: US 08/087,244	829	TNLTSTSPNSVYPDETHMTASDTSLSLVQSHYKKEPADVPYQGTQLHPAIRVADLLQH	888
10	FILING DATE: 01-JUL-1993	876	INLMKTSDSYGFKEEYESFFEGQASQSDVAKQONRAKNRYGNIAYDHSRVLQPVVDD	935
11	ATTORNEY/AGENT INFORMATION:	889	ITQMKCAEGYGFKEEYESFFEGQASQSDVAKQONRAKNRYGNIAYDHSRVLQPVVDD	948
12	NAME: Coruzzi, Laura A.	936	PSSDYINANYIDGYORPSHYATQGPVHETVYDFPWRMTWQBSACIYVMTNLEVGRVKC	995
13	REGISTRATION NUMBER: 30,742	949	TNSDYINGNYIDGHRPNHYIATQGPQOETIYDFPWRMVHHEHTASIIIMVTNLEVGRVKC	1008
14	REFERENCE/DOCKET NUMBER: 7683-042	996	YKWPDDTEVYGDFFKVTCEMEPLAEYVVRTFTLERRGYNEIREVKQFHFTGPDHGVVPY	1055
15	TELEPHONE: 212-790-9090	1009	CKYWPDDTEIYKDIKVTIETELAEYVIRITFAVEKGVHEIREIRIQFHFTGPDHGVVPY	1068
16	TELEFAX: 212-869-8864/9741	1056	HATGLLSFIRRYKLSNPPSAGPIVVHCSAGAGRTGCVIVIDIMLDMABEGVVDIYNCVK	1115
17	TELEX: 66141 PENNIE	1069	HATGLLGFVRQVKSKSPSAGPLVHCSAGAGRTGCVIVIDIMLDMABEGVVDIYNCVR	1128
18	INFORMATION FOR SEQ ID NO: 8:	1116	ALRSRINMVQTEEQYIFIHDAIIEACLCGETATPVCEFAAAYFDMTRIDTSQTNSSHLKD	1175
19	SEQUENCE CHARACTERISTICS:	1129	EURSRVNMVQTEEQYIFIHDAIIEACLCGETATPVCEFAAAYFDMTRIDTSQTNSSHLKD	1188
20	LENGTH: 1452 amino acids	1176	BEOTLNSVTPRLQABDCSIAICLRNHDKNRPMWMLPPDRCLPFLITIDGESSNYINAALM	1235
21	TYPE: amino acid	1189	EPRTLNMVTPTRLURVEDCSIALPRNHEKRNCRMDILPPDRCLPFLITIDGESSNYINAALM	1248
22	STRANDEDNESS: single	1236	DSYQPAAFIVTQYPLPNTVKDFWRLVVDYDGTCTSIVMLENDLSQGPCQYWPBEGMLRYG	1295
23	TOPOLOGY: unknown	1249	DSYQKPSAFIVTQYPLPNTVKDFWRLVVDYDGTCTSIVMLENDLSQGPCQYWPBEGMLRYG	1308
24	MOLECULE TYPE: protein	1296	PIQVECMSCMDVQINRIFRICNLTRPQEGYLMVQOYIOLGASHREVPGSKESFLKLI	1355
25	US-08-449-644-8	1309	PIQVEFVSADLEEDIISIRIFRIYNAARPDQGYRMVQOYFQFGLGWPYMDTTPVSKESFLKLI	1368
26	Query Match 62.4%; Score 4807; DB 2; Length 1452;	1356	LOVEKMQEWEKGEGRITIIHCLNGGRCSCMFCAIGIVVEMVKRQNVVDVFAVHTKLRNSK	1415
27	Best Local Similarity 60.8%; Pred. No. 0;	1369	RQVDMQEEYNGEGEPTVVHCLNGGRCSCMFCAIGIVVEMVKRQNVVDVFAVHTKLRNSK	1428
28	Matches 889; Conservative 206; Mismatches 326; Indels 42; Gaps 8;	1416	PNMVEAPEQYRCFYDVALEYLS 1438	
29		1429	PNMVDLLDQYKFCYEALEYLS 1451	
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ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/087,244A  
FILING DATE: 01-JUL-1993

## CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-042  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1452 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein

US-08-087-244A-8

Query Match 62.4%; Score 4807; DB 2; Length 1452;  
Best Local Similarity 60.8%; Pred. No. 0;  
Matches 889; Conservative 206; Mismatches 326; Indels 42; Gaps 8;

QY 4 TAAALPAFVALLLLSPWLLGSAQGFSGAGCTFDDGPGACDYHQDLYDDFEWVHSAQ 63  
DB 3 TLGTCLATLGLL-----TAAGTFSGCLFDFPSTYSGSQSEGGDFNWEQNTL 54  
QY 64 BPHVLPPEMGGSMIVDSDHDGPKARLQLPMTKENDTHCIDFSYLLYSQKLNPGTL 123  
DB 55 TKPTSDPMWSSGSLMVLNAGRPGRQRAHLLLPOLKENDTHCIDFHYFVSKSNSPGLL 114  
QY 124 NILVRNKGPLANIMVNTGFTGRDLRAELAVSTFWPNEYQVTFEAEVSGSGSYIAID 183  
DB 115 NVVKNVNGPLNGPIWNISGDPFTWRAELAISTFWPNEFQVIFEV-ITSGHQYLAI 173  
QY 184 DIQVLSYPCDKSPHFLKLDGVENVAGNATFQCTATGRDAVHNKLMLORNGEDIPVAQT 243  
DB 174 EVKVLGHPCRTTHFLRIQNVENVAGQFATFQCSAIGRTVAGDRLWLGIDVDRAPLKEI 233  
QY 244 KNINHRFAASFRLOEVTKTDOLYRCVTOSESGSYNFAQLIVREPPPIAPPQLLV 303  
DB 234 KVTSSRRFIASFVNVTTKRDAGKYRCMIRTEGGVGISNVAELVVKPEPPIAPPQLASV 293  
QY 304 GPTVLLQLNANSIIGDPIILKEVVRMTSGSWTETHVNAPTYKLWHLDPDTEYEIRV 363  
DB 294 GATVLTQLNANSINGOPIVAREVEYCTASGWNDRQPDVSTYKIGHLDPDTEYEISV 353  
QY 364 LLTRPGEGGTGLPGPPIITRTKCAEMRTPTKLKIAIBIARRIAVDWESLGYNITRCHTF 423  
DB 354 LLTRPGEGGTGSPGALTRTKCADPMRGRKLEVEVSKRQITIRWEPPGYNVTRCHSY 413  
QY 424 NVTCIHYFRGNESKAD--CLMDPKAPQHVNVHLPPYTNVSLKMLLTPBGRKSEET 481  
DB 414 NLTVHYCYQVGGQVQREVEVSWDTEHNPQHTITNLSPYTNVSKLILMNPBGRKSEQL 473  
QY 482 LIOTDEDPGVPVVKSLQGSFENKIFLNWKEPLDPNGILITQYEISYSSIRSDPAPVA 541  
DB 474 IVQDDEDPGAVPSTEQSGSTFEKIFLQWREPTQTYGVITLVEITYKAVSSDFPEIDL 533  
QY 542 GPPQTVSNLWNSTHVFHMLHPGTTQOFFRASTVKGFGPATAINVTNISAPTLPDYG 601

## RESULT 11

US-08-652-971-4

; Sequence 4, Application US/08652971

; Patent No. 5814507

; GENERAL INFORMATION:

; APPLICANT: Cheng, Jill

; APPLICANT: Lasky, Laurence A.

; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE

; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA

DB 534 NQGRVSKLGNETHFLFFGLYPGTYSTFTRASTAKGFGPPATNQFTTKISAPSMPAYE- 592  
QY 602 VDAISNETATTITVLLRPAOKAGAPISAYQVIVVEELPHRTKREAGAMECYQVPTVYQNA 661  
DB 593 LETPLNQTDNTVTVMLKPAHSGAPSVYQVIVVEERPRRTKKTTELKCYVPVIFQNA 652  
QY 662 MSGGAPYFAAELPPGNLPEPAPTVDGNTQYQGFNPPPLAPRGYNYIYFOAMSSVBKET 721  
DB 653 SLLNSQYFAAEPADSLQAAQPTIGDNKTYNGYNTPLLPYKSYRYIYFOAASRANGET 712  
QY 722 KTCVRIATKAATEEPEVIPPDAKQDTRVKIAGISAGILFILLVILLVILVVKSKLAK 781  
DB 713 KIDCVQVATGAA--TPKPVPEPEKQTDHTVKIAGIAGILLFVIFLGVVLVKKRKLAK 771  
QY 782 KRKDMGNTREQEMTHVMNMDRSYADQSTLHAEPLSITFMDQHNFSPPY----- 831  
DB 772 KRKETSSITREQEMTHVMNMDKSYAEQGTNCDE---AFSPMDTHNLNGRSVSSPSTPMK 828  
QY 832 -----ENHSATASSRLLDVPY-LCEGTSPYQTQQLHPAIRVADLLQH 875  
DB 829 TNLSTSVNPSYYPDETHTWASDTSLSVQSHYTKKREPADVPTQGLHPAIRVADLLQH 888  
QY 876 INLMKTSDSYGFKEEYESPFEGQSASWDVAKDONRAKNRYGNIIAYDHSRVILQPVEDD 935  
DB 889 ITQMKCAEGYGFKEEYESPFEGQSAPWDSAKDENRMKNRYGNIIAYDHSRVILQVIEGD 948  
QY 936 PSSDIYNANYIDGQRPVSHYATQGPVHETVYDFWRMIWQOSACIWMVNLNVEGVKVC 995  
DB 949 TNSDIYNGNIYDGHYRPNHYIATQGPQETIYDFWRMVWHENTASIIWMVNLNVEGVKVC 1008  
QY 996 KYWPDDETEYIGDFKVTCEMEPLAEYVVRFTFLERRGYNEIREVKQFHFTGWDHGVY 1055  
DB 1009 CKYWPDDTEYIKDVKTLIETELLAEVIRTFAVEKGVHEIREIRQFHFTGWDHGVY 1068  
QY 1056 HATGLLSFIRVKLSNPPSAGPIVHCSAGAGRTGCVIVIDIMLDMAREGVVDIYNCKV 1115  
DB 1069 HATGLLGFVRQVKSQSPSAGPLVHCSAGAGRTGCFIVIDIMLDMAREGVVDIYNCRV 1128  
QY 1116 ALASRRINMVQTEQYIFIHDAILEACLGCETAIPVCEPKAAVDFMIRIDSQTNSSHLD 1175  
DB 1129 ELASRRNMVQTEQYIFIHDAILEACLGCSTSVASQVRSLYYDMKMLDQPTNSSQIKE 1188  
QY 1176 EFOTLSNVTPLQAEDCSIACLPRNHDKNRFDMLPPDRCLPFLITIDGESSNYINAALM 1235  
DB 1189 EFTLANVTPTLAVEDCSIALPRNHEKNRCDILPPDRCLPFLITIDGESSNYINAALM 1248  
QY 1236 DSYRQPAAFIVTQYPLPNTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCQYWPBEGMLRYG 1295  
DB 1249 DSYKQPSAFIVTQYPLPNTVKDFWRLVLDYHCTSVVMLNDVDPAQLCPQYWPENGVRHG 1308  
QY 1296 PIVOECMSCMDCDVINRIENLTPQSGYLMVQOFOYLGWASHREVPSKESFTKLI 1355  
DB 1309 PIVOEFVSADLEEDISIRIFRIYNAARPDQGYRMVQOQFGLGMPWRDTPVSKRSFKLI 1368  
QY 1356 LQVEKQWEEKKEGERTIIHCLNGGSGRMFCAIGIIVEMVXQNVVDVFAVATLRNSK 1415  
DB 1369 RQVDKQWEEVNGEGPTVHCLNGGSGRTFCAISIVCEMLRQRTVDVFAVATLRNSK 1428  
QY 1416 PNWVEAPEQYFCYDVALEYLS 1438  
DB 1429 PNWDLDDQYKFCYVALEYLS 1451

## RESULT 11

US-08-652-971-4

; Sequence 4, Application US/08652971

; Patent No. 5814507

; GENERAL INFORMATION:

; APPLICANT: Cheng, Jill

; APPLICANT: Lasky, Laurence A.

; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE

; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA



; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
 ; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT, LLP  
 ; STREET: 4 Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/991,258A  
 ; FILING DATE: 17-DEC-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/652,971  
 ; FILING DATE: 24-MAY-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dreger, Walter H.  
 ; REGISTRATION NUMBER: 24,190  
 ; REFERENCE/DOCKET NUMBER: A-63478-3/WH/D/MTK  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEFAX: (415) 398-3249  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1452 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-991-258A-4

Query Match 62.1%; Score 4791; DB 2; Length 1452;  
 Best Local Similarity 61.3%; Pred. No. 0;  
 Matches 885; Conservative 205; Mismatches 320; Indels 34; Gaps 7;

Qy	23	LLGSAQGFAGGCTFDGPGACDHYQDLVDFWVHVSQAEPHYLPMPQSGYMIQVDS	82
Db	14	LLLAAGETFGGCLFDEPYSTCGYSQADEDFWQVNTLTKPTSDPMPGSGFMLVNT	73
Qy	83	SDHDPGEKARLQPTMKENDTHCIDFSYLLYSQGLNPGLTILVRVKNKGLPIANVNT	142
Db	74	SGKEGORAHLLLPOLKENDTHCIDFHYFVSSKSNAAFGLLNVYKVNNGPLGNPNWIS	133
Qy	143	GFTGRDLRAELAVSTWPNFYQVIFRAEVSGRSGVIAIDDIQVLSYPCDKSPHFLRLG	202
Db	134	GDPTRTWRAELALSTWPNFYQVIFEV-VTSGHQYLALDEVKVLGHPCRTTTPHFRLIQ	192
Qy	203	DVEVAGNATFOCIATGRDAVHNKMLQRLRNGSDIIPVAOTKTNHRRFAASFLQEVTK	262
Db	193	NVEVAGQFATFCQSAIGRTVAGDRMLQGDVDRDAPLKEIKVTSRRFIASFVNVTK	252
Qy	263	TDQDLYRCVTSRGSGVSNPAQLIVRPPPIAPPOLLGVGPYLLIQLNANSIIGDGP	322
Db	253	RDAGKYRCMICEGGVGISNVAELVWKEPPVPIAPPQLASVATYLIQLNANSINGDGP	312
Qy	323	IILKEVEYRMTSGSWTETHAVNAPTYKLHLDPDTEYRVLTRPGEGTGLPGPLIT	382
Db	313	IVAREVEYCTASGWNDRQPVDSYSYKIGHLDPDTEYRISVLLTRPGEGTGSFGPALRT	372
Qy	383	RTKCAEPMWPTKLIKIAEIQARRIADVWESLGVNITRCHTFNVITCYHYFRGHNESKAD	441
Db	373	RTKCADPMRGPRLKLEVVEVKSRLQITRPPGVNVTCHSNLTVHGYQVGGEQVREE	432
Qy	442	-CLDMDPKAPOHVNHLPPYNTVSLKMLTNPEGRKESBETIIQTDEDFGPPVVKSLQG	500

Db	433	VSWDTNSHPQHTITNLSPTYNVSVKILMNPBGRKESQELTVQTDDELPGAVPTESIQQ	492
Qy	501	TSFENKIFLNWKEPLDPNGIITQYEISYSSIRSDPAPVAGPQPTVSNLWNSTHVMH	560
Db	493	SAFEKIFLOWREPTQYVITLIEYIKAVSSFDPEIDLSNQSGRVSKLNEHTFLPFG	552
Qy	561	LHPGTTTQFFIRASTVKGFGPATVNTTNSATPLPDYEGVDASLNETATITVLLRPA	620
Db	553	LYPGTTYSFTIRASTAKGFGPATNQFTTKISAPSPAYE-FETPLNQDNTVTVMKPA	611
Qy	621	QAKGAPISAYQIVVEELHPHRTKREAGAMECYQPVTVYQAMSGGAPVFAELPPGNLP	680
Db	612	QSRGAPSVYQIVVEERPRTKTKTILKCYPIPIHFQNASIINQSYFAETPADLSLQ	671
Qy	681	EPAPFTVGDNRITYQGFNPNPLAPRGYNIYFQAMSSVEKETKTCQVRIATKAAATEEPEVI	740
Db	672	AAQFTTIGDNKTYGYNWNTPLPHKSYRIYQAASTRANGETKIDCVRVATKGAV-TPKPV	730
Qy	741	PDPAKQTRVVKIAGISAGILVFIILLVILVVKSLAKGRKDANGTRQETHMVNA	800
Db	731	PEPEKQTDHTVKIAGVIAGILLFVILFGLVVLVMMKRLAKRKETMSSTQETVMVNS	790
Qy	801	MDSYADQSTLHAEDPLSITFMDHNFSPRY-----ENHS	835
Db	791	MDKSYAEQGNCD----AFSPMGTHNLNGRSVSSPSTMTKNTLTSTSVNSYYPDETH	847
Qy	836	ATAESSRLDVPY-LCEGTESPYQTQLHPAIRVADLLQHLINLMKTSDSYGFKEEYESF	894
Db	848	MASDTSLAQPHYTKKREADVQYQQLHPAIRVADLLQHLITQMKCAEGYGFKEEYESF	907
Qy	895	FEQOSASNDVAKQDNRAKRYGNI IAYDHSRVILQPVEDDPSDDYINANVIDYQRP	954
Db	908	FEQOSAPWDSAKKDENEKRYGNI IAYDHSRVRLQMLEGDNNSDYINGYDHYRPNH	967
Qy	955	YIATQGPVHETVDFWEMIQEOSACIVMTNLVEGVKCYKYMPDDTVYGFKTCV	1014
Db	968	YIATQGPVHETVDFWEMIQEOSACIVMTNLVEGVKCYKYMPDDTVYGFKTCV	1027
Qy	1015	EMBLAEYVVRTFTLERRGYNEIREVKQFHTGPHDGVPHATGLLSFRRVKLSNPPS	1074
Db	1028	DTELLAAYVTRTFAVEKRGHEIREIRQFHTGPHDGVPHATGLLGFRVQVKSPPN	1087
Qy	1075	AGPIVHCSAGAGRTGCIYVIDIMLMAEREGVVDIYNCVRLSRVRVNMVQTEEQYFI	1134
Db	1088	AGPLVHCSAGAGRTGCIYVIDIMLMAEREGVVDIYNCVRLSRVRVNMVQTEEQYFI	1147
Qy	1135	HDAILACLGETAI PVCEFAAYFDMIRDSQTNSSHLKDEPOTLNSVTPRQAECS	1194
Db	1148	HDAILACLGETSIPASQVRSYLYDMNKLDPQTNSSQIKKEEFRTLMNVTPLREDCS	1207
Qy	1195	ACLPRNHDKRFRMDLPPDRCLPLITIDGESSNY INAAALMDSYRQPAAFIVTQYPLPNT	1254
Db	1208	ALLPRNHDKRFRMDLPPDRCLPLITIDGESSNY INAAALMDSYRQPAAFIVTQYPLPNT	1267
Qy	1255	VKDFWRLVYDYGCTSI VMLNEVDLSQGCPOQWPEEGMLRGPIQVECMSCMDCDVNRI	1314
Db	1268	VKDFWRLVLDYHCTSVMLNDVDPALQCPQWPEENGVRHGPQVEFVSADLEEDISRI	1327
Qy	1315	FRICNLTRPQEGKLMVQFOYLGNASHREVPGSKRSPKLILQVEKQWBEKWBEGGTII	1374
Db	1328	FRIYNASRPDQGHMVRQQFQFLGMPMYRDTFVSKRSPKLIRQVDKQWBEYNGEGTIV	1387
Qy	1375	HCLNGGGRSCMFCAGIVVEMKRVQNVVDVFAVKTLSNKPNNVPEAPEQYRFCYDALE	1434
Db	1388	HCLNGGGRSGTFCAGISIVCEMLRHQRTVDVFAVKTLSNKPNNVPEAPEQYRFCYDALE	1447
Qy	1435	YLES 1438	
Db	1448	YLSN 1451	

RESULT 13  
 US-08-769-399-4

; Sequence 4, Application US/08769399  
; Patent No. 5976852  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Jill  
; APPLICANT: Lasky, Laurence A.  
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd.  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/769,399  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dregler, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: P1033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 225-3216  
; TELEFAX: (415) 952-9881  
; TELEX: 910 371-7168  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1452 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-769-399-4

Query Match 62.1%; Score 4791; DB 2; Length 1452;  
Best Local Similarity 61.3%; Pred. No. 0;  
Matches 885; Conservative 205; Mismatches 320; Indels 34; Gaps 7;  
QY 23 LIGSAQGFAGGCTFDGPGACDYHQDLYDDFEWVHYSAQBPHYLPPMPQGSYMYDS 82  
DB 14 LLLTAAGTFSGCLFDBEPYSTCGYSQAQEDDFNWEQVNTLTKTSDPMPSPGSMVNT 73  
QY 83 SHDPGEKARLQPTWKENDTHCIDPSYLLYSQKGLNPGTLNLRVNGKPLANPWNVT 142  
DB 74 SGKPEGORAHLLLPQKENDTHCIDPHYFVSSKSNAAFGLLNVYVKVNGNPLGNPNWIS 133  
QY 143 GFTGDLWLAELAVSTFWNEYQVIFAEVSGRSYIAIDDIQVLSYPCDKSPHFLRLG 202  
DB 134 GDTTTHRAELAIATFWNFVQVIFEV-VTSGHQYLAIDEVKVLGHPCTRTPHFLRIQ 192  
QY 203 DVEVNAQGNATFCIATGRDAVHNKWLQRRNGEDIPVAQTKNINRRHPAASFRLEQVTK 262  
DB 193 NVEVNAQGFATFCQSAIGRTVAGDRLWLQIGIDVRDAPLKEIKVTSRRFIASFNVNTTK 252  
QY 263 TDQDLRYCVTQBSRGVGNFALIVREPPRIAPQLLGVGPTYLLQLNANSIGDGP 322  
DB 253 RDAGYRCMCTEGGVIGISYAEVVKPEPVPVPIAPQLASVATYLTQLNANSINGDGP 312  
QY 323 IILKEVEYRMTSGSTETHAVNAPYTKLWHLDPDTEYEIRVLLTRPGEGLPGPPLIT 382  
DB 313 IVAREVEYCTAGSNDRQPDVSTSYKIGHLDPDTEYEISVLLTRPGEGLTSGSPALRT 372  
QY 383 RTKCAEPMTPTKIAEQABRIAVDWSLGNITRCHTFNVTICYHYFRGNESKAD- 441  
DB 373 RTKCADEMPGRKLEVEVVKSHQITIRWEPFGVNVTRCHSYNLTVHYGYQVGGQEVREE 432

QY 442 -CLDMDPKAPOHVVNHLPPYTNVSLKMLITNPEGRKESEETIIOTDEVPGPVPVKSLQG 500  
DB 433 VSWDTNSHPQHTITNLSPTYNVSVKILMMPERKESQELTVQDDEPLPAVPTESIQG 492  
QY 501 TSFENKIFLWKEPLDPNGIITQYEISYSSIRSDPAPVAGPPQTYSNLWNSTHHVPMH 560  
DB 493 SAFEKIFLOWREPTQTVGVTILYEITYKAVSSFDPEIDLNSQSGRVSKLGNETHFLFFG 552  
QY 561 LHPOTTYQFFIRASTVKGFGPATVNTVNTISATPLDYEYGDASLNETATITVLLRPA 620  
DB 553 LYPGTYSFTIRASTAKGFGPATNQFTTKISAPSPAYE-FETPLNQTDNTVTVMKXA 611  
QY 621 QAKGAPISAYQIVVEELHPHRTKEAGAMECYQPVTVYQNAMSGAPYFAELPPGNLP 680  
DB 612 QSRGAPSVYQIVVEEERPRTKTKTEILKICYPPIHFNQASILNSYFFAAEPADSQ 671  
QY 681 EPAPFTVGDNRITYQFWNPPLAPRKGYNIYFQAMSSVEKETKTCVRIATKAATEEPEVI 740  
DB 672 AAQFTIGDNKTYNGWNTPLPHKSYRIYQAASRANGETKIDCVRVATKGAV-TPKPV 730  
QY 741 PDPAKQTDVVVKIAGISAGILVFIILLVLLVILVVKSLAKKRDAMGNTQEMTHVNA 800  
DB 731 PEPEKQTDHTVKIAGIAGILLFVIIFLGVVLVKKRKLAKKRKETSSTRQEMTVMVNS 790  
QY 801 MDRSVADQSTLHAEDPLSITFMDQHNFSRY- - - - -ENHS 835  
DB 791 MDRSYAEOGTNCDE- - - - -AFSEMGTHNLNGRSVSPSFTMTNTLSTVSPNSYYPDETH 847  
QY 836 ATABSSRLLDVPRY-LCEGTESPYQTQLHPAIRVADILLOHINLMKTSDSYGFKEEYESF 894  
DB 848 MASDTSSLAQPHYTKKREAADVPYQTQLHPAIRVADILLOHITQMKCAEGYGFKEEYESF 907  
QY 895 FEGQASNDVAKQONRAKNRYGNIYADHSRVILQPVDEDDPSDDYINANVYIDGQRSH 954  
DB 908 FEGQAPWDSAKDENRMKNRYGNIYADHSRVILQMLEGDNNSDYINGNYIDGVRHNH 967  
QY 955 YIATQGPVHETVYDFWMIQEOSACIVMTNLVEGVRKCVKYPDPDTEVVGDPKVTCV 1014  
DB 968 YIATQGPVHETVYDFWMIQEOSACIVMTNLVEGVRKCVKYPDPDTEVVGDPKVTCV 1027  
QY 1015 EMEPLAEYVVRFTFLERRGYNEIREVKQFHTGWPDPHGVYHATGLLSFIRRVKLSNPPS 1074  
DB 1028 DTELLAEVIRTFVAVKEGHEIREIQFHTGWPDPHGVYHATGLLGFRVQVKSPPN 1087  
QY 1075 AGPIVHCSAGAGRTGCVIVIDIMDMAERGVVDIYNCVKALSRRRINMVQTEBOYIFI 1134  
DB 1088 AGPLVHCSAGAGRTGCFIVIDIIMDMAERGVVDIYNCVRELRRRNMVQTEBOYIFI 1147  
QY 1135 HDAILACLCCGTAIPVCEFAAYDFMIRIDSQTNSSHLKDBFOTLNSVTPRLOAEDCSI 1194  
DB 1148 HDAILACLCCGTSIPASQVRSLYYDMNKLDPQTNSSQIKKEFRFLNMVTPTLRVEDCSI 1207  
QY 1195 ACLPRNHDKNRFDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFIVTQPLPNT 1254  
DB 1208 ALLPRNHEKNCMDLLPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFIVTQPLPNT 1267  
QY 1255 VKDFWRLVYDYGCTSIYVLMNEVDLSQGCQVWPBEGMLRYGPIQVECHSCSCMDCVIRI 1314  
DB 1268 VKDFWRLVLDYHCTSVVMLNDVDAQLCPQVWPENGVRHGFQVFEFVSADLEEDIISRI 1327  
QY 1315 FRIENLTPRQSGYLMVQOQFVYLGWASHREVPGSKSFLKILIQVEKQBEWKEGSGRTII 1374  
DB 1328 FRIYNASRPQDHRNVQOQFQLGWPYRDTTPVSKKSFUKLIRQVKNQWEEYNGGPGTVV 1387  
QY 1375 HCLNGGGRSGMFCALIGIVVEMVKNQVVDVFAVKTLENSKPNMVEAPEQYRFCYDVALE 1434  
DB 1388 HCLNGGGRSGMFCALISIVCEMLRQRTVDVFAVKTLENSKPNMVEAPEQYRFCYDVALE 1447  
QY 1435 YLES 1438  
DB 1448 YLNS 1451

## RESULT 14

US-08-991-953A-4  
 : Sequence 4, Application US/08991953A  
 : Patent No. 6083748  
 : GENERAL INFORMATION:  
 : APPLICANT: Cheng, Jill  
 : APPLICANT: Lasky, Laurence A.  
 : TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
 : TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
 : NUMBER OF SEQUENCES: 10  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT, LLP  
 : STREET: 4 Embarcadero Center, Suite 3400  
 : CITY: San Francisco  
 : STATE: California  
 : COUNTRY: United States  
 : ZIP: 94111  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/991,953A  
 : FILING DATE: 16-DEC-1997  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/652,971  
 : FILING DATE: 24-MAY-1996  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Dreger, Walter H.  
 : REGISTRATION NUMBER: 24,190  
 : REFERENCE/DOCKET NUMBER: A-63478-3/WH/D/MTK  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (415) 781-1989  
 : TELEFAX: (415) 398-3249  
 : TELEX:  
 : INFORMATION FOR SEQ ID NO: 4:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1452 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS:  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : US-08-991-953A-4

Query Match 62.18; Score 4791; DB 3; Length 1452;  
 Best Local Similarity 61.38; Pred. No. 0;  
 Matches 885; Conservative 205; Mismatches 320; Indels 34; Gaps 7;

Qy	23	LLGSAQCFAGGCTFDGACDYGQDLYDDFEWVHVSQAEPHYLPPMPQGSYMIIVDS	82
Db	14	LLLLTAAGETSGGLFDEPYSTCGYQADEDFNWEQVNTLTKPTSDPMPGSGFMLVNT	73
Qy	83	SDHDPGKARLQLPMTKENTHCHIDFYLVSQKGLNPGTLNLIVRNKGPLANPIWNT	142
Db	74	SGRPEGQRAHLLPQLKXNDTHCIDPHYFVSSKNAAPGLLVVYKVNNGPLGNPINNIS	133
Qy	143	GFTGRDLRLAEAVSTFWNEYQVIFEAESGGSGSIAIDDDQVLSYPCDKSPHFLRG	202
Db	134	GDPTRTWRAELAISTFWPNFYQVIFEV-VTSGHQGYLAIDEVKVLGHGPTCTRTPHFLRIQ	192
Qy	203	DVEVNAQNTAFQCIATGRDAVHNKMLQRRNGBDIPVAOTKNIHRRRFAASRLQEVTK	262
Db	193	NVEVNAQPFATFQSAIGRTVAGDRLLQGLDVRDAPLKEIKVTSSRFIAFNVNTTK	252
Qy	263	TDQDLYRCVTSQSGSGVSNPAQLIVREPPRIAPPOLLGVGPTYLLIQLNANSIIGDGP	322
Db	253	RDAGKYRCMCTEGGVGISNYAELVVKPEVPVPIAPPQLASVGATYLIQLNANSINGDP	312
Qy	323	IILKEVEYRMTSGSWTETHAVNAPTYKLWLDPDTEYIRVLLTRPGEGTGLPGPPLIT	382
Db	313	IVAREVEYCTASGSNDQRPVDSYSYKIGHLDPDTEYEISVLLTRPGEGTGSPGPAIRT	372

Qy	383	RTKCAEPMRTPKTLKIAEIOARRIAVDWESLGYNITRCHTFNVITCYHYFRGHNESKAD-	441
Db	373	RTKCADPMRGPRKLEVVVEVKSQRTIRWEPFNVNTRCHSYNLTVHYGYVGQEQVREE	432
Qy	442	-CLDMDPKAPQHVNVNHLPPVNTYSLKMLITNPEGRKESEETIIQTDDEDVPGVPVKSLOG	500
Db	433	VSMDDTNSHPQHTITNLSPYTNVSVKLILNPEGRKESQELTQTDDELDLPGAVTESIQG	492
Qy	501	TSFENKIFLNWKEPLDPNGIITQVEISYSSITRSFDPAPVPVAGPPQTVTNLWNSTHHFMH	560
Db	493	SAFEKIFLOWREPTQYVITLYEITYKAVSFDPDEIDLSNQSGRVSKLGNETHFPPG	552
Qy	561	LHPGTYQFFIRASTVKGFGPATINVTNISAPTLDPYEGVDASLNATATITVLLRPA	620
Db	553	LYPGTYSFTIRASTAKGFGPPATNQFTTKISAPSMAYE-FETPLNQTDNTVTVMKPA	611
Qy	621	QAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTYQAMSGGAPYFAELPPGNLP	680
Db	612	QSRGAPVSVYQIVVEEERPRRTKTKTEILKCYVPVPIHFQNASILNSQYIFAAEFPADSLQ	671
Qy	681	EPAPFTVDNRITYQGFWNPLAPRKGYNIYFQAMSSVEKETKTCQVRIATKAAATEEPEVI	740
Db	672	AAQPTIGDNKTYNGYNTTLLPHKSYRIYQAASRANGETKDCVRATKGA-VTPKPV	730
Qy	741	PDPAKQTRVVKIAGISAGILVFIILLVVLVILVVKSKLAKRKDKAMGNTRQEMTHMVA	800
Db	731	PEPEKQTDHTVKIAGVIAGILLFVIIIFLVGVVLMVKRKLAKRKBTSSSTRQEMTMVNS	790
Qy	801	MDRSYADQSTLHAEDPLSITFMQHNFS-PRY-----ENHS	835
Db	791	MDXSAYEQGTNCDE--AFSFMGTHNLNGRSVSSPSSFTMTKNTLTSTSVNYSYYPDETH	847
Qy	836	ATRESSRLLDVPRY-LCEGTESPYQTGLHPAIRVADLLOHINIMKTSDSVGRKEEYESF	894
Db	848	MASDTSLSAOPHYKKREAADVPYQTGLHPAIRVADLLOHITQMKCAEGVGFKEETESF	907
Qy	895	FEQSASMDVAKDONRAKNRYGNIYADHSRVILQPVEDDPSDDYINANYIDGYQRP	954
Db	908	FEQSAPWDSAKKDNRMKNRYGNIYADHSRVRLQMLEGDNDSYINGVIDGYHRPNH	967
Qy	955	YIATQGPVHETVDFWRMIWQBSACIUMTNLVEGRVKCYKYPDPDTEVYGFKTCV	1014
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Qy	1015	EMPLEAYVVTFTLERRGYNEIREVKQFHTGPDHGVPHATGLLSFIRRVKLSNPPS	1074
Db	1028	DTELLAEYVIRTFAVEKRGHIREIRKQFHTGPDHGVPHATGLLSFIRRVKLSNPPS	1087
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Db	1088	AGPLVHCSAGAGRTGCFIVIDIMLDMAREGVVDIYNCVRLSRNRINNVQTEEQYIFI	1147
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Db	1208	ALLPRHDKRMWMLPPORCLPLITIDGESSNYNAALMDSYROPAAFTVTOYPLPNT	1267
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Qy	1315	FRICNTRPQEGYLMVQQFOYLQWASHREVPVSGKRSFLKILQVEKQWKEGEGRTII	1374
Db	1328	FRINYASRPQDGRHWYQFQFLGWPYRDTFVSKRSFLKILQVEKQWKEGEGRTII	1387
Qy	1375	HCLNGGSRGMPCAIGIVVEMVTRQNVVDVFAVKTLLRNSKPNMVEAPQYRFCYDVALE	1434
Db	1388	HCLNGGSRGMPCAIGIVVEMVTRQNVVDVFAVKTLLRNSKPNMVEAPQYRFCYDVALE	1447

QY 1435 YLES 1438  
 Db 1448 YLNS 1451  
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 US-08-652-971-2  
 ; Sequence 2, Application US/08652971  
 ; Patent No. 5814507  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheng, Jill  
 ; APPLICANT: Lasky, Laurence A.  
 ; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE  
 ; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd.  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/652,971  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dregler, Ginger R.  
 ; REGISTRATION NUMBER: 33,055  
 ; REFERENCE/DOCKET NUMBER: P1033  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 225-3216  
 ; TELEFAX: (415) 952-9881  
 ; TELEX: 910 371-7168  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1436 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-652-971-2  
 Query Match 59.5%; Score 4586.5; DB 2; Length 1436;  
 Best Local Similarity 60.3%; Pred. No. 0;  
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 Db 24 RAAGCTFEASDPVFCFSQAQYDDFQWEQVRIHPTGRTFDELPHGAYLMVNASQHTPGQ 83  
 QY 90 KARLQLPTWKENDTHCIDPSYLLYSQKGLNPOTLNLVRVNGKPLANPIVNWGTGRDW 149  
 Db 84 RAHIIFQTLSENDTHCQVSYFLYSRDSGSPGLGVYVRVNGGPIGSAVWNNVTGSHGRW 143  
 QY 150 LPAELAVSTFWPNEVOVIFEAESVSGRSGYIADIDQVLSYPCDKSPHFLRLGDVEVNAG 209  
 Db 144 HQAELAVSTFWPNEVOVIFEAESVSGRSGYIADIDQVLSYPCDKSPHFLRLGDVEVNAG 203  
 QY 210 QNATFQCIATGRDAVHNKMLWLRNGEDIPVAQTKNINHRFAAASFRLOEVTKTDQDLR 269  
 Db 204 QNASFQMAAGRAAEAEHFFLQSGVLVPAAGVRHISHRRFLATFPLASVGRSQDLR 263  
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 Db 264 CVSQAPRGAGVSNFAELIVKEPPTIAPPQLLRAGPTVLIQLNTNSIIGDGPVIRKETE 323  
 QY 330 YMTSGSWTETHAVNAPTYKLWHLDPDTEYIRVLLTRPGEQGTGLPGPPLITRTKCAEP 389

Db 324 YRMARGPWAEEVHAVNLXTYKLVHLWLPDTEYEISVLLTRPGDGTGRPGPPLISRTKCAEP 383  
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 Db 384 TRAPKGLAFAEIQARQLTQWEPLGYNVTRCHTYAVSLCYRYTLGGSHNQITRECVKMER 443  
 QY 448 KAPOHVVNHLPPYTNVSKMLITNPEGRKESEETIIOTDEDPVGPVPVKISQGTGFENKI 507  
 Db 444 GASRYTIKNLLPFNNIHVRLITNPEGRKEKEVTFQTDDEDPVGGIAAESLTFTPLEMDI 503  
 QY 508 FLWKKEFLDPNGIITQYEISYSSIRSPDPAVPVAGPPQTVSNLWNSTHHVFMHLHPGTTY 567  
 Db 504 FLKWEPEQEPNGLITQYEISYQSISSDPAVNVGPRRTISKLRNETVHVPSNLHPGTTY 563  
 QY 568 QFFIRASTVKGFGPATAINVTNISAPTLDPYEGVDASLNETATITVLLRPAQAKGAPI 627  
 Db 564 LFSVRARTSKFGQAALTEITNISAPSF-DYADMPSPLGSESENTITVLLRPAQGRGAPI 622  
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 Db 623 SVYQVVVEERPRRLRREPQADCFSVLTFETALRGLVHYFGAELAAASLEAMPFTV 682  
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 Db 683 GDNQTYRGFWNPPLEPRKAYLIYFQAASHLKGTELNCIRIARKAACKESKRPLEVSQRS 742  
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 Db 743 EEMGLILGICAGGLAVLILLGAILIIRKGPVNMTK-ATVNYRQEKTHMMSAVDRSFT 801  
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 Db 862 PAVRVDLLQHINQMKTAEYGFKEYESPFEG---WDATKKDKLKGGRQEPVAYDR 917  
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 Db 1098 EGVVDIYNCVKTLCSRRVNMITQTEQYIFIHDAILEACLGCGETTTPVNEFRATYEMIRI 1157  
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 Db 1338 RDTPSRKAFHLHLAEVDKQWAE--SGDGRIVHCLNGGGRSGTFCACATVLEMIRCHSL 1395  
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Job time : 39.7887 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:44:18 ; Search time 131.676 Seconds  
(without alignments)  
3777.694 Million cell updates/sec

Title: US-09-887-669-2

Perfect score: 7709

Sequence: 1 MDTTAAALPAFVALLLSP.....EAPQYRVCYDVALEYLESS 1439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	7688	99.7	1439	16	US-10-408-765A-284
3	7571	98.2	1457	9	US-09-887-669-1
4	4838	62.8	1452	9	US-09-887-669-8
5	4784	62.1	1452	16	US-10-408-765A-83
6	4602.5	59.7	1436	14	US-10-205-219-15
7	4564.5	59.2	1444	15	US-10-058-270A-98
8	4564	59.2	1463	14	US-10-176-847-22
9	4564	59.2	1463	14	US-10-205-823-343
10	4555	59.1	1499	15	US-10-296-115-1283
11	4374.5	56.7	1442	16	US-10-408-765A-805
12	4338	56.3	1430	13	US-10-087-993-34
13	2493.5	32.3	623	15	US-10-296-115-1190

14	2210.5	28.7	815	15	US-10-296-115-1390	Sequence 1390, Ap
15	1534.5	19.9	1502	9	US-09-808-602-54	Sequence 54, Appl
16	1534.5	19.9	1502	10	US-09-800-198-44	Sequence 44, Appl
17	1509	19.6	1897	17	US-10-482-029-52	Sequence 52, Appl
18	1505.5	19.5	1907	15	US-10-291-265-250	Sequence 250, Appl
19	1505.5	19.5	1912	7	US-10-772-636-64	Sequence 64, Appl
20	1505	19.5	1948	9	US-09-808-602-55	Sequence 55, Appl
21	1505	19.5	1948	10	US-09-800-198-45	Sequence 45, Appl
22	1491	19.3	1495	15	US-10-258-666-12	Sequence 12, Appl
23	1460.5	18.9	2037	15	US-10-087-684-39	Sequence 39, Appl
24	1460.5	18.9	2037	15	US-10-218-779-39	Sequence 39, Appl
25	1457.5	18.9	2029	15	US-10-087-684-38	Sequence 38, Appl
26	1457.5	18.9	2029	15	US-10-218-779-38	Sequence 38, Appl
27	1349.5	17.5	1585	15	US-10-369-493-5569	Sequence 5569, Ap
28	1349.5	17.5	1585	15	US-10-369-493-5570	Sequence 5570, Ap
29	1284.5	16.7	647	15	US-10-291-265-722	Sequence 722, Appl
30	1187	15.4	793	17	US-10-777-144-3	Sequence 3, Appl
31	1187	15.4	793	17	US-10-777-145-3	Sequence 3, Appl
32	1187	15.4	793	17	US-10-777-186-3	Sequence 3, Appl
33	1172.5	15.2	802	17	US-10-777-144-1	Sequence 1, Appl
34	1172.5	15.2	802	17	US-10-777-145-1	Sequence 1, Appl
35	1172.5	15.2	802	17	US-10-777-186-1	Sequence 1, Appl
36	1170.5	15.2	807	15	US-10-264-049-3138	Sequence 3138, Ap
37	1138	14.8	699	15	US-10-366-547-65	Sequence 65, Appl
38	1138	14.8	774	13	US-10-087-192-1017	Sequence 1017, Ap
39	1132	14.7	700	15	US-10-366-547-63	Sequence 63, Appl
40	1132	14.7	700	15	US-10-444-795B-793	Sequence 793, Appl
41	1132	14.7	700	17	US-10-753-267-100	Sequence 100, Appl
42	1115.5	14.5	642	15	US-10-444-795B-795	Sequence 795, Appl
43	1109	14.4	305	9	US-09-788-626-9	Sequence 9, Appl
44	1107.5	14.4	659	15	US-10-366-547-67	Sequence 67, Appl
45	1085.5	14.1	560	13	US-10-087-192-1020	Sequence 1020, Ap

#### ALIGNMENTS

#### RESULT 1

US-09-887-669-2  
; Sequence 2, Application US/09887669  
; Publication No. US20020082397A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLESINGER, JOSEPH  
; APPLICANT: SAP, JAN M.  
; APPLICANT: ULLRICH, AXEL  
; APPLICANT: VOGEL, WOLFGANG  
; APPLICANT: FUCHS, MIRIAM  
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA  
; FILE REFERENCE: 038602/1246  
; CURRENT FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US/09/887,669  
; PRIOR FILING DATE: 1999-01-21  
; PRIOR APPLICATION NUMBER: 09/234,883  
; PRIOR FILING DATE: 1993-07-01  
; PRIOR APPLICATION NUMBER: 08/087,244  
; PRIOR FILING DATE: 1993-07-01  
; PRIOR APPLICATION NUMBER: 08/049,384  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1439  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-887-669-2

Query Match 100.0%; Score 7709; DB 9; Length 1439;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDTTAAALPAFVALLLSPVLLGSAQGFSDGPGACDVHQDLYDDFEWHV 60

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QY 961 PVHETVYDFWRMIWQESACIYVMTNLVEVGRVKCYKWPDDTEYVYGFKTCVMEPLA 1020
Db 961 PVHETVYDFWRMIWQESACIYVMTNLVEVGRVKCYKWPDDTEYVYGFKTCVMEPLA 1020
QY 1021 EYVWTFTLERGYNEIREVKQFHTGMPDHGVPPHATGLLSFIRRVKLSNPPSPAGPIV 1080
Db 1021 EYVWTFTLERGYNEIREVKQFHTGMPDHGVPPHATGLLSFIRRVKLSNPPSPAGPIV 1080
QY 1081 HCSAGAGRTGCYIVIDIMLDMAREGVVDIYNVCVKAALRSRRINMVQTEEQYIFIHDAILE 1140
Db 1081 HCSAGAGRTGCYIVIDIMLDMAREGVVDIYNVCVKAALRSRRINMVQTEEQYIFIHDAILE 1140
QY 1141 ACLCGETAIPVCEFAKAYFDMIRIDSQTNSSHLKDEFTQNLNSVTPRLQAECDSCIAPRN 1200
```

```
Db 1141 ACLCGETAIPVCEFAKAYFDMIRIDSQTNSSHLKDEFTQNLNSVTPRLQAECDSCIAPRN 1200
QY 1201 HDKNRFDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFIVTQYPLPNTVKDFWR 1260
Db 1201 HDKNRFDMLPPDRCLPFLITIDGESSNYINAAALMDSYRQPAAFIVTQYPLPNTVKDFWR 1260
QY 1261 LVYDYGCTSIYMLNEVDLSQGCPOYWPBEGMLRGPIQVECMSCMDCDVNIRIFRICNL 1320
Db 1261 LVYDYGCTSIYMLNEVDLSQGCPOYWPBEGMLRGPIQVECMSCMDCDVNIRIFRICNL 1320
QY 1321 TRPOEGYLMVQOFOYLGWASHREVPGSKRSFLKILQVEKQWEEWKEGEGRTIIHCLNGG 1380
Db 1321 TRPOEGYLMVQOFOYLGWASHREVPGSKRSFLKILQVEKQWEEWKEGEGRTIIHCLNGG 1380
QY 1381 GRSGMFCAGIGIVEMVKRQNVVDVVFHAVKTLRNSKPNMVEAPEQYRCYDVALEYLESS 1439
Db 1381 GRSGMFCAGIGIVEMVKRQNVVDVVFHAVKTLRNSKPNMVEAPEQYRCYDVALEYLESS 1439
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## RESULT 2

```
US-10-408-765A-284
; Sequence 284, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Watson, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 1439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-284
```

Query Match 99.7%; Score 7688; DB 16; Length 1439;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1436; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MDTTAAALPAFVALLLLSPWPLIGSAQGSAGCTFDDGPGACDYHQDLYDDFEWVHV 60
Db 1 MDTTAAALPAFVALLLLSPWPLIGSAQGSAGCTFDDGPGACDYHQDLYDDFEWVHV 60
QY 61 SAQBPYLPPEMPOGSGYIMVDSDDHDPCEKARLQPTMKENDTHCIDFSYLLYSOKGLNP 120
Db 61 SAQBPYLPPEMPOGSGYIMVDSDDHDPCEKARLQPTMKENDTHCIDFSYLLYSOKGLNP 120
QY 121 GTNLILVRNKGPLANPIWNVTGFTGRDWRDLRAELAVSTFWPNEYQVIFPEAEVSGRSGYI 180
Db 121 GTNLILVRNKGPLANPIWNVTGFTGRDWRDLRAELAVSTFWPNEYQVIFPEAEVSGRSGYI 180
QY 181 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGONATFOCIATGRDAVNKLWLRNGEDIPV 240
Db 181 AIDDIQVLSYPCDKSPHFLRLGDVEVNAGONATFOCIATGRDAVNKLWLRNGEDIPV 240
QY 241 AQTNNHRRFAASFRLEQVTKDODLYRCVTOSESGSGVSNFAQLIVREPPRTIAPPOL 300
Db 241 AQTNNHRRFAASFRLEQVTKDODLYRCVTOSESGSGVSNFAQLIVREPPRTIAPPOL 300
QY 301 LGVGPTYLLIQLNANSIIGDGPILILKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYE 360
Db 301 LGVGPTYLLIQLNANSIIGDGPILILKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDTEYE 360
```

361 IRVLLTRRGGCTGLPGPPLITRTKCAEPMRTPKTLKIAEIQARRIADVMSLGYNITRC 420  
Db IRVLLTRRGGCTGLPGPPLITRTKCAEPMRTPKTLKIAEIQARRIADVMSLGYNITRC 420  
Qy HTFNVTTCYHYFRGHNSKADCLMDPKAPOHVVNHLPPYTNVSLKMLLTNPGRKESSE 480  
Db HTFNVTTCYHYFRGHNSKADCLMDPKAPOHVVNHLPPYTNVSLKMLLTNPGRKESSE 480  
Qy TTIOTDSBVPVGVKSLQGSFENKIFLNKKEPLDPNGIITQYEISYSSIRSDPAVPV 540  
Db TTIOTDSBVPVGVKSLQGSFENKIFLNKKEPLDPNGIITQYEISYSSIRSDPAVPV 540  
Qy AGPPQTVSNLWNSHHVFMHLHPCGTYOFFIRASTVKFGFGATANTVNTNISAPLDYE 600  
Db AGPPQTVSNLWNSHHVFMHLHPCGTYOFFIRASTVKFGFGATANTVNTNISAPLDYE 600  
Qy GVDASLNETAATITVLLRPAQAKAPISAYQIVVEELHPHRTKEAGAMECYQVPVTYQN 660  
Db GVDASLNETAATITVLLRPAQAKAPISAYQIVVEELHPHRTKEAGAMECYQVPVTYQN 660  
Qy AMSGGAPYFAAEPLPGNLPAPFTVGDNRITQGFWMNPLAPRKGNIFYQAMSSVEKE 720  
Db AMSGGAPYFAAEPLPGNLPAPFTVGDNRITQGFWMNPLAPRKGNIFYQAMSSVEKE 720  
Qy TKTCQVRIATKAATEBEVIPPDPKQOTDRVVKIAGISAGILVFILLVILVKKSKLA 780  
Db TKTCQVRIATKAATEBEVIPPDPKQOTDRVVKIAGISAGILVFILLVILVKKSKLA 780  
Qy KKRKDMGNTRQETHMVNAMDRSYADQSTLHAEDPLSITFMDQHNFSRYENHSATAS 840  
Db KKRKDMGNTRQETHMVNAMDRSYADQSTLHAEDPLSITFMDQHNFSRYENHSATAS 840  
Qy SRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHINLMKTSDSYGKKEEYESFEQSA 900  
Db SRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHINLMKTSDSYGKKEEYESFEQSA 900  
Qy SWDVAKQONRAKRYGNIITAYDHSRVLQPVEDDDPSDDYINANIDGYRPSHYIATQG 960  
Db SWDVAKQONRAKRYGNIITAYDHSRVLQPVEDDDPSDDYINANIDGYRPSHYIATQG 960  
Qy PVHETVYDFWRMIWQEOSACIWMVNLVEGRVKCYKYWPDDETVYGFVKTCVMEPLA 1020  
Db PVHETVYDFWRMIWQEOSACIWMVNLVEGRVKCYKYWPDDETVYGFVKTCVMEPLA 1020  
Qy EYVVRTFTLERRGYNEIREVKQFHTGPHQGVPHYHATGLLSFIRRVKLSNPPSAGPIV 1080  
Db EYVVRTFTLERRGYNEIREVKQFHTGPHQGVPHYHATGLLSFIRRVKLSNPPSAGPIV 1080  
Qy HCSAGAGRTGCIIVIDIMLMAEREGVVDIYNCVKALRSRRINNVQTEEQYIFTHDAILE 1140  
Db HCSAGAGRTGCIIVIDIMLMAEREGVVDIYNCVKALRSRRINNVQTEEQYIFTHDAILE 1140  
Qy ACLGGETAIPVCEPKAAYFDMIRIDSQTNSSHLKDEFTQNLNVPRLQAECDSCIAPRN 1200  
Db ACLGGETAIPVCEPKAAYFDMIRIDSQTNSSHLKDEFTQNLNVPRLQAECDSCIAPRN 1200  
Qy HDKXRFMDMLPPDRCLPFLITIDGESSNYINAAIUMDSVROPAAFIYQYPLNVTVDKFWR 1260  
Db HDKXRFMDMLPPDRCLPFLITIDGESSNYINAAIUMDSVROPAAFIYQYPLNVTVDKFWR 1260  
Qy LVYDYGCTSIIVMLNEVDLSQSCPOYWPBEGMLRGPQIQCWCSMDCDVINRIFRICNL 1320  
Db LVYDYGCTSIIVMLNEVDLSQSCPOYWPBEGMLRGPQIQCWCSMDCDVINRIFRICNL 1320  
Qy TRPOEGLVMQOQFYLQWASHREVPGRSPLKILLOVEKWQEBWKEGEGRTIIHCLNGG 1380  
Db TRPOEGLVMQOQFYLQWASHREVPGRSPLKILLOVEKWQEBWKEGEGRTIIHCLNGG 1380  
Qy GRSGMFCAGIIVVEMWKRQNVVDVFHAKVTLRNSKPNWKAPEQYRCYDVALEYLESS 1439  
Db GRSGMFCAGIIVVEMWKRQNVVDVFHAKVTLRNSKPNWKAPEQYRCYDVALEYLESS 1439

RESULT 3

US-09-887-669-1  
; Sequence 1, Application US/09887669  
; Publication No. US20020082397A1

GENERAL INFORMATION:

APPLICANT: SCHLESINGER, JOSEPH  
APPLICANT: SAP, JAN M.  
APPLICANT: ULLRICH, AXEL  
APPLICANT: VOGEL, WOLFGANG  
APPLICANT: FUCHS, MIRIAM

TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA

FILE REFERENCE: 038602/1246

CURRENT APPLICATION NUMBER: US/09/887,669

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: 09/234,883

PRIOR FILING DATE: 1999-01-21

PRIOR APPLICATION NUMBER: 08/087,244

PRIOR FILING DATE: 1993-07-01

PRIOR APPLICATION NUMBER: 08/049,384

PRIOR FILING DATE: 1993-04-21

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1457

TYPE: PRT

ORGANISM: Mus musculus

US-09-887-669-1

Query Match 98.2%; Score 7571; DB 9; Length 1457;

Best Local Similarity 97.3%; Pred. No. 0;

Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

Qy 1 MDTAAALPAFVALLLSLPWLLGSAQGFAGCTFDDGPGACDYHQDLYDDFEWVHV 60  
Db 1 MD-VAAALPAFVALLLWLLYPWLLGSAQGFAGCTFDDGPGACDYHQDLYDDFEWVHV 59  
Qy 61 SAGEPHYLPPEMFGSYNIVDSDHDPGEKARLQLPMTKENDTHCIDFSYLLYSQKGLNP 120  
Db 60 SAGEPHYLPPEMFGSYNIVDSDHDPGEKARLQLPMTKENDTHCIDFSYLLYSQKGLNP 119  
Qy 121 GTNLILRVNKGPLANIPWNTGFTGRDLRAELAVSTFWPNEYQVIFEAHSVGRSGYI 180  
Db 120 GTNLILRVNKGPLANIPWNTGFTGRDLRAELAVSTFWPNEYQVIFEAHSVGRSGYI 179  
Qy 181 AIDDIQVLSYPCDKSPHFLRLGDVENVAGNATPQCIATGRDAVHNLKLQRRNGEDIPV 240  
Db 180 AIDDIQVLSYPCDKSPHFLRLGDVENVAGNATPQCIATGRDAVHNLKLQRRNGEDIPV 239  
Qy 241 AQTKNINHRFAASFRILQEVTKTDQDLYRCVTSERGSVSNFAQLIVREPPPIAPPQL 300  
Db 240 AQTKNINHRFAASFRILQEVTKTDQDLYRCVTSERGSVSNFAQLIVREPPPIAPPQL 299  
Qy 301 LGVGPYVLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPYTKLWHLDPDTEYE 360  
Db 300 LGVGPYVLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPYTKLWHLDPDTEYE 359  
Qy 361 IRVLLTRRPGGGTGLPGPPLITRTKCAEPMRTPKTLKIAEIQARRIADVMSLGYNITRC 420  
Db 360 IRVLLTRRPGGGTGLPGPPLITRTKCAEPMRTPKTLKIAEIQARRIADVMSLGYNITRC 419  
Qy 421 HTFNVTTCYHYFRGHNSKADCLMDPKAPOHVVNHLPPYTNVSLKMLLTNPGRKESSE 480  
Db 420 HTFNVTTCYHYFRGHNSKADCLMDPKAPOHVVNHLPPYTNVSLKMLLTNPGRKESSE 479  
Qy 481 TTIOTDSBVPVGVKSLQGSFENKIFLNKKEPLDPNGIITQYEISYSSIRSDPAVPV 540  
Db 480 TTIOTDSBVPVGVKSLQGSFENKIFLNKKEPLDPNGIITQYEISYSSIRSDPAVPV 539  
Qy 541 AGPPQTVSNLWNSHHVFMHLHPCGTYOFFIRASTVKFGFGATANTVNTNISAPLDYE 600  
Db 540 AGPPQTVSNLWNSHHVFMHLHPCGTYOFFIRASTVKFGFGATANTVNTNISAPLDYE 599  
Qy 601 GVDASLNETAATITVLLRPAQAKAPISAYQIVVEELHPHRTKEAGAMECYQVPVTYQN 660

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Db 600 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQN 659
Qy 661 AMSGAPYFAAEPLPGNLPSPAPPTVGNDRTYOGFWNPPLAPKRGYNIYFOAMSSVEKE 720
Db 660 ALSGAPYFAAEPLPGNLPSPAPPTVGNDRTYOGFWNPPLAPKRGYNIYFOAMSSVEKE 719
Qy 721 TKTCVRIATK-AAETEPEVTPDPAKOTDRVUKTAGISAGILVFTLLLVVILVKKSL 779
Db 720 TKTCVRIATKAAATEEPEVTPDPAKOTDRVUKTAGISAGILVFTLLLVVILVKKSL 779
Qy 780 AKKRKDMGNTRQEMTHMVMANDRSYADQSTLHAEDPLSLTFMDQHNESPRY----- 831
Db 780 AKKRKDMGNTRQEMTHMVMANDRSYADQSTLHAEDPLSLTFMDQHNESPRLPNDPLVPT 839
Qy 832 ----ENHSATSESSRLLDVPRYLCEGTSPTQGTQLHPAIRVADLLQHINLMKTSDSYGF 887
Db 840 AVLDEHNSATAESSRLLDVPRYLCEGTSPTQGTQLHPAIRVADLLQHINLMKTSDSYGF 899
Qy 888 KEEYESFEGOSASWDVAKKONRAKRYGNIIVDHSRVILQPVEDDPSSDYINANYI- 946
Db 900 KEEYESFEGOSASWDVAKKONRAKRYGNIIVDHSRVILQPVEDDPSSDYINANYID 959
Qy 947 -----DGYQRPSHYIATQGPVHETVYDFWRMIWQBSACIIVMVTNLVEGRVKCYKWPD 1001
Db 960 IWLVRDGYQRPSHYIATQGPVHETVYDFWRMWVQBSACIIVMVTNLVEGRVKCYKWPD 1019
Qy 1002 DTEVYDGFVKTCVEMEPLAEYVVRFTTLERRGYNSIREVKQFHFPTGWDHGVPHYATGLL 1061
Db 1020 DTEVYDGFVKTCVEMEPLAEYVVRFTTLERRGYNSIREVKQFHFPTGWDHGVPHYATGLL 1079
Qy 1062 SFIRVKLSNPSPSAGPIVHCSAGAGRTGCVIIVDMLDMAEREGVVDIYNCVKALRSRR 1121
Db 1080 SFIRVKLSNPSPSAGPIVHCSAGAGRTGCVIIVDMLDMAEREGVVDIYNCVKALRSRR 1139
Qy 1122 INMVOTEQYIFIHDAIEALCGBETAIPVCBEKAAYPDMIRIDISQTNSSHLKDBFQTLN 1181
Db 1140 INMVOTEQYIFIHDAIEALCGBETAIPVCBEKAAYPDMIRIDISQTNSSHLKDBFQTLN 1199
Qy 1182 SVTPRLQAECDSCIAPRNHDKNRPMFMLPPDRCLPFLITIDGESSNYINAAALMDSYRQP 1241
Db 1200 SVTPRLQAECDSCIAPRNHDKNRPMFMLPPDRCLPFLITIDGESSNYINAAALMDSYRQP 1259
Qy 1242 AAFIVTQVPLNTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVEC 1301
Db 1260 AAFIVTQVPLNTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCPOYWPBEGMLRYGPIQVEC 1319
Qy 1302 MSCSMDCDVINRIFRICNLTRPQEGYLMVQOYQYILGWASHREVPGSKRSFLKLILQVEKW 1361
Db 1320 MSCSMDCDVINRIFRICNLTRPQEGYLMVQOYQYILGWASHREVPGSKRSFLKLILQVEKW 1379
Qy 1362 QSEWKEGEGRTIIHCLNGGSGMFCAGIVVEMVKRQNVVDVFAHVKTLRNSKPNMVEA 1421
Db 1380 QSEWKEGEGRTIIHCLNGGSGMFCAGIVVEMVKRQNVVDVFAHVKTLRNSKPNMVEA 1439
Qy 1422 PQYRRCYDVALEYLESS 1439
Db 1440 PQYRRCYDVALEYLESS 1457
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## RESULT 4

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US-09-887-669-8
; Sequence 8, Application US/09887669
; Publication NO. US20020082397A1
; GENERAL INFORMATION:
; APPLICANT: SCHLESSINGER, JOSEPH
; APPLICANT: SAP JAN M.
; APPLICANT: ULLRICH, AXEL
; APPLICANT: VOGEL, WOLFGANG
; APPLICANT: FUCHS, MIRIAM
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
; FILE REFERENCE: 038602/1246
; CURRENT APPLICATION NUMBER: US/09/887,669
```

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; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/234,883
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 08/087,244
; PRIOR FILING DATE: 1993-07-01
; PRIOR APPLICATION NUMBER: 08/049,384
; PRIOR FILING DATE: 1993-04-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-669-8
```

## Query Match 62.8%; Score 4838; DB 9; Length 1452;

Best Local Similarity 61.2%; Pred. No. 0;  
Matches 896; Conservative 203; Mismatches 322; Indels 42; Gaps 8;

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Qy 4 TAAALPAFVALILLSPWLLGSAQGFSSAGGCTFDGPGACDYHQDLYDDFEWVHVSQA 63
Db 3 TLGTCLATLALL-----TAAGETFGGCLDFDEPYSTCGYSQSEGGDFNWEQNTL 54
Qy 64 EPHYLPPEMPQGSYMIVDSSDHDPEKARLQLPTMKENDTHCIDFSYLLYSQKGLNPGTL 123
Db 55 TKPTSDPMPGSGSLMVAASGRPEGQRAHLLLPOLKENDTHCIDFHYFVSSKSNPPGLL 114
Qy 124 NILVRNKGPLANIMVNTGTFGRDMLRAELAVSTFWPNEYQVTPAEAVSGRSGYIAID 183
Db 115 NVYKVNNGPLGNIDINISGDPTRTNRAELAISTFWPNFYQVIFEV-ITSGHGYLAID 173
Qy 184 DIQVLSYPCDKSDFLRLGDEVNAGQNAFOCTATGRDAVHNKLMWQRRNGEDIPVAQT 243
Db 174 EVKVLGHPCRTPLFLRIQNVENAGOFATQCQSAIGRTVAGDRLWLQGDIVDRDAPLKEI 233
Qy 244 KNINHRFPAASFRLOEYTKTDQDLRYCVTOSERSGSVNFAQLIVREPRPIAPPQLGV 303
Db 234 KYTSRRFLASFVNVVTKRDAGKYRCMIRTEGGVGISNYAELVVKPEPVPPIAPPQASV 293
Qy 304 GPTYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPYKLMHLDPDTEYETRV 363
Db 294 GATYLIQLNANSINGDGPVAREVEYCTASGSWNRQPVDSYKIGHLDPDTEYETISV 353
Qy 364 LLTPGSGGCLPGPPLITRTKCAEPWRTPKTLKIAEIQARRIADVDESIGVNTTRCHTF 423
Db 354 LLTPGSGGCGPAPALRTRTKCADPMRGPRLKEVEVKRQITIRWEPFGVNTTRCHSY 413
Qy 424 NVTICYHYFRGHNESKAD--CLDMDPKAPQHVNVNHLPPYTNVSLKMLTNPEGRKESBET 481
Db 414 NLTVHYCYVQGGQVREEVSWDTENSHPOHTITNLSPYTNVSVKLIILNPEGRKESQEL 473
Qy 482 IIQTDVDPGVVPVKSLQGTSGFENKIFLNWKEPLDPNGIITQYEISYSISRSFDPAPVA 541
Db 474 TVQTDDELPGAAPTESIQQSTFEKIFLQWREPTQTYGVITLYEITYKAVSDFDEIDLS 533
Qy 542 GPQTVSNLWNSTHHVFNHLHPGTYOFFIRASTVKGFGPATAINVNTNI SAPLPDVEG 601
Db 534 NQSGRVSKLGNETHFLPFLGYPGTYSFTIRASTAKGFGPPATNQFTTKISAPSAPAYE- 592
Qy 602 VDASINETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMECYQVPVYQNA 661
Db 593 LETFLNQTDNTVTVMKPAQSRGAPSVYQIVVEERPRRTKTKTEILKCPVPIHFQNA 652
Qy 662 MSGGAPYFAAEPLPGNLPPEPAPPTVGNDRTYOGFWNPPLAPKRGYNIYFOAMSSVEKET 721
Db 653 SLLNSQYFFAAEFPAADSLQAAPPTIGDNKTYGWNTPLLPYKSYRIYFQAASRANGET 712
Qy 722 KTQCVRIATKAAATEEPEVTPDPAKOTDRVUKTAGISAGILVFTLLLVVILVKKSLAK 781
Db 713 KIDCVQVATKGA--TPKPVPEPEKQTDHTVKIAGVIAGILLFVIFLGVVLWKKRKLAK 771
Qy 782 KRKDMGNTRQEMTHMVMANDRSYADQSTLHAEDPLSLTFMDQHNESPRY----- 831
```

Db 772 KRKETSSTREMTVMVNSMDKSYAEQGTNCDE---AFSFMDDTHNLNGRSVSSPSSFTMK 828  
Qy 832 -----ENHSATAESRLLDVPY-LCEGTESPYQTGOLHPAIRVADLLQH 875  
Db 829 TNLSTSVNPNYYPDETHWASDTSSLVQSHYTKKREPADVQYTGOLHPAIRVADLLQH 888  
Qy 876 INLMKTSYGFKEEYESFFEGOSASWDVAKQDNRAKRYGNIIAYDHSRVILQPVEDD 935  
Db 889 ITQMKCAEGYGFKEEYESFFEGOSASWDVAKQDNRAKRYGNIIAYDHSRVILQPVEDD 948  
Qy 936 PSSDIYINANYIDGQRPSHYIATQGPVHETVYDFWMIWQOSACIVMVTNLVEGRVKC 995  
Db 949 TNSDYINGNYIDGVRPNHYIATQGPQETIYDFWVWHEHTASIIIMVTNLVEGRVKC 1008  
Qy 996 KYKPPDDTEVYDGPVKTCVMEPELAEYVVRFTLERRGYNIREVKQPHFTGWDHGVY 1055  
Db 1009 CKYPPDDTEIYKDIKLTIELLAEEYVIRTFAVEKRGIIIEIRIQPHFTGWDHGVY 1068  
Qy 1056 HATGLLGFIRVRLSNPPSAGPIVVHCSAGAGRTGCTIVIDIMLDMAREGVVDIYNCVK 1115  
Db 1069 HATGLLGFVRQVKSPPSAGPLVHCSAGAGRTGCTIVIDIMLDMAREGVVDIYNCVR 1128  
Qy 1116 ALRRRNVMVQTEQYIFIHDAILEACLCGETAIPVCEFKAAYPDMDIRIDISOTNSSHLKD 1175  
Db 1129 ELRSRVNMVQTEQYIFIHDAILEACLCGETSPASQVRSRYLYDMKLDPTQNSSQIKE 1188  
Qy 1176 EFQTLNVTPLQAECDSCIACLRNHDQRMFMDLPPDRCLPFLITIDGESSNYINAALM 1235  
Db 1189 EFTLNMTPLTRVEDCSIALPRNHEKRCMDILPPDRCLPFLITIDGESSNYINAALM 1248  
Qy 1236 DSVROPAFIVTQPLNVTQDFRLVYDYGCTSIIVMLNEVDLSQGCQYWPESGMLRYG 1295  
Db 1249 DSYKQPSAFIVTQPLNVTQDFRLVYDYGCTSVMLNVDVDPALCPQYWPENGVRHG 1308  
Qy 1296 PIQVECMSCMDQVINRIFRINLTPQEGYLMVQOQFYLGWASHREVPKRSFLKI 1355  
Db 1309 PIQVEFSADLEEDIIISRFIYNAARPDQGYRMVQOQFYLGWEMYRDTVPKRSFLKI 1368  
Qy 1356 LQVEKWQEWKQEGRGRTIICLNGGGRSGMFCAGIVVEMVKRQNVVDVHAKVTLRNSK 1415  
Db 1369 RQVDKWQEEYNGGBGTVPVHCLNGGGRSGTFCALSIVCEMLRHQRTVDVHAKVTLRNNK 1428  
Qy 1416 PNWVEAPEQYRFDVDALEYLS 1438  
Db 1429 PNWDLDDQYKFCYEVALEYLS 1451

## RESULT 5

US-10-408-765A-83  
; Sequence 83, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Fahy, Eoin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 83

; LENGTH: 1452

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-408-765A-83

Query Match

62.1%; Score 4784; DB 16; Length 1452;

Best Local Similarity 60.5%; Pred. No.:0;  
Matches 885; Conservative 208; Mismatches 328; Indels 42; Gaps 8;  
Qy 4 TAAALPAFVALLLLSPWLLGSAQGFSDGPGACDYHQDLYDDFEWVHSAQ 63  
Db 3 TLGTCLATLACLL-----TAAGTFFSGGCLFDEPSTCGYSQSEGGDFNWEQVNTL 54  
Qy 64 EPHVLPPEMPOGSMVVDSDHDGPEKARLQLPMTKENDTHCIDFSYLLYSOKGLNPOTL 123  
Db 55 TKPTSDPMPSSGLMLVNASRPEGORAHLLLPOLKENDTHCIDFHYFVSSKSNPPGLL 114  
Qy 124 NILVRNKGPLANPINVTGFTGDMRLAEALVSTFWPNEYOVLFPEAEVSGRSGYIAID 183  
Db 115 NVYKVNNGPLGNPINWISGPTTWNRAELALSTFWPNFYQVIFEV-ITSGHQGYLAID 173  
Qy 184 DIQVLSYPCDKSPHFLRLGDVEVNAGQATFQCIATGRDAVHNLKLQRRNGEDIPVAQT 243  
Db 174 EVKVLGHPCTRTPHFLRIQNVENAGQATFQCSAIGRTVAGDRMLQGDIVDRAPLKEI 233  
Qy 244 KNINHRFAASFRLOEVTKTDDLYRCVTOSEGRSGVSNFAQLIVRPPRIAPPQLGV 303  
Db 234 KVTSSRRFIASFNVVNTTKRDAKYRCWIRTEGGVGSNTVAELVVKPEPVPPIAPPQASV 293  
Qy 304 GPTVLLIQLANANSIIGDPRIILKEVEYRMTSGSWTETHAVNAPYKLMHLDPDTEYETRV 363  
Db 294 GATYLTQLNANSINGDPVAREVEYCTASGWNDRQPDVDSYKIGHLDPDTEYETRV 353  
Qy 364 LLTRPGSGGTGLPGPLITRTKCAEPMRTPKLXIABIQARRIAVDWESLGYNITRCHTF 423  
Db 354 LLTRPGSGGTGSGPALRTTKADPMRGRKLEVEVEKSRQITIRWEPFGYNTRCHSY 413  
Qy 424 NVTCYHYFRGHNESKAD--CLDMDPKAQHVNVHLLPYTNVSLKMLITNPEGRKESBE 481  
Db 414 NLTVHYCYQVGGQOQREVEVSWDTSNHPQHTITNLSPYTNVSVKLILMNPGRKESQEL 473  
Qy 482 IIQTDDEVCPVPVKSLQSTSPENKIPLNWKEPLDPNGIITQYISISSIRSPDPAPVA 541  
Db 474 IVQTDDELPAVPTESIQGSTPEEKIFLOWREPTQTYGVITLXEITYKAVSSFFPEIDL 533  
Qy 542 GPQVTSNLNWSNTHVFMHLHPGTYQFFIRASTVKGFGPATAINVTNTISAPTLDPYEG 601  
Db 534 NQSGRVSKLGNETHFLFGLYPGTYSFTIRASTAKGFGPATNQFTTKISAPSWPAYE- 592  
Qy 602 VDAENETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTVYQNA 661  
Db 593 LETPLNQDNTVTVMLKPAHSRGAPSVYQIVVEEERPRRTKTKTEILKCYVPVPIHFQNA 652  
Qy 662 MSGGAPYFAELPPGNLPEPAPFTVGDNRTYQGFNPPPLAPRGYNIYFOAMSSEKET 721  
Db 653 SLLNSQYFAAEFPADSLAAQPFITGDNKTYNGYWNTPLLPYKSYRIYQAASRANGET 712  
Qy 722 KTCQVRIATKAATEEPEVIPPDAKOTDRVVKIAGISAGILVFIILLVLLVILVKKSLAK 781  
Db 713 KIDCVQVATGAA--TPKPVPEPEKQTDHTVKIAGIAGILVFIIFLGVLVWKKRKLAK 771  
Qy 782 KRKDMGNTRQEMTHVMVNMADRSYADQSTILHABDPLSITFMDQHNFSPPY----- 831  
Db 772 KRKETSSITQEMTMVNSMDKSYAEQGTNCDE---AFSFMDDTHNLNGRSVSSPSSFTMK 828  
Qy 832 -----ENHSATAESRLLDVPY-LCEGTESPYQTGOLHPAIRVADLLQH 875  
Db 829 TNLSTSVNPNYYPDETHWASDTSSLVQSHYTKKREPADVQYTGOLHPAIRVADLLQH 888  
Qy 876 INLMKTSYGFKEEYESFFEGOSASWDVAKQDNRAKRYGNIIAYDHSRVILQPVEDD 935  
Db 889 ITQMKCAEGYGFKEEYESFFEGOSASWDVAKQDNRAKRYGNIIAYDHSRVILQPVEDD 948  
Qy 936 PSSDIYINANYIDGQRPSHYIATQGPVHETVYDFWMIWQOSACIVMVTNLVEGRVKC 995  
Db 949 TNSDYINGNYIDGVRPNHYIATQGPQETIYDFWVWHEHTASIIIMVTNLVEGRVKC 1008  
Qy 996 KYKPPDDTEVYDGPVKTCVMEPELAEYVVRFTLERRGYNIREVKQPHFTGWDHGVY 1055  
Db 1009 CKYPPDDTEIYKDIKLTIELLAEEYVIRTFAVEKRGIIIEIRIQPHFTGWDHGVY 1068

Db 1009 CKYPPDDTEIYKIDKVTLIETELLAAYVIRTFAVEKRGVHEIREIQPHFTGMPDHGVY 1068  
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Db 1069 HATGLLGFVRQVKSPPSAGPLVHCSAGAGRTGCTFIVIMLMDAREGGVWIDYNCVR 1128  
Qy 1116 ALRSRINNVQTEEQYIFIHDAILEACLCGETAIVCFKAAYPDMIRIDISQTNSSHLKD 1175  
Db 1129 ELRSRVNVQTEEQYIFIHDAILEACLCGDTSPASQVRSLYIDYMNKLDQTNSSQIKE 1188  
Qy 1176 EFTLNSVTPRLQABDCSIACLPRNHDKNRDMMLPPDRCLPFLITIDGESSNYNAALM 1235  
Db 1189 EFTLNMVTPTRLVEDCSIALPRNHKNRCWIDILPPDRCLPFLITIDGESSNYNAALM 1248  
Qy 1236 DSYROPAAFIQYPLPNTVKDFWRLVYDYGCTSIWMLNEVDLSGCGQYWPBEGMLRYG 1295  
Db 1249 DSYQPSAFIVTQHPLPNTVKDFWRLVLDYHCTSVVMLNDVDPALCQYWPENGVRHKG 1308  
Qy 1296 PLOVECMSCSDCVINRIFRICNLTRPOEGVLMVQOXYLGMASHREVPGSKRSFLKLI 1355  
Db 1309 PLOVEFVSADLEEDIISIRIFRYNARPDQGRHMVQOQFLGWPMYRDTPVSKRSALLLI 1368  
Qy 1356 LOVERKQBEWKEGEGRTIHCINGGGRSGMFCAGIIVVMVKRQNVVDVFFHAVKTLRNSK 1415  
Db 1369 RQVDKQBEYNGEGPTVVHCLNGGGRSGTFCAISIVCEMLRHQRTVDVFFHAVKTLRNNK 1428  
Qy 1416 PNWEAPQYRCYDVALEYLES 1438  
Db 1429 PNWDLLOQYKFCYEVALEYLNS 1451

## RESULT 6

US-10-205-219-15  
; Sequence 15, Application US/10205219  
; Publication No. US20030138803A1  
; GENERAL INFORMATION:  
; APPLICANT: Warner-Lambert Company  
; APPLICANT: Lee, Kevin  
; APPLICANT: Dixon, Allistair  
; APPLICANT: Brooksbank, Robert  
; APPLICANT: Pinnock, Robert  
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain  
; FILE REFERENCE: WL-A-018200  
; CURRENT APPLICATION NUMBER: US/10/205,219  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: GB 0118354.0  
; PRIOR FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 1436  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Receptor protein tyrosine phosphatase-lambda  
US-10-205-219-15  
Query Match 59.7%; Score 4602.5; DB 14; Length 1436;  
Best Local Similarity 60.3%; Pred. No. 0;  
Matches 855; Conservative 214; Mismatches 329; Indels 19; Gaps 9;  
Qy 33 AGCTFTDGGPG---ACDHYQDLYDDPEWVHVSQAQEPHYLPPEMPOGSMYIVDSSDHPGE 89  
Db 24 AAGCTFEESDPVWPCFESQAQYDDFQWEQVRIHFETGRTPEDLPHGAVLMVNASQHTFQG 83  
Qy 90 KARLQLPTWKENDTHCIDPSYLLYSQGLNPGCTNLTLVRVNGKPLANPIWVNTGFTGRDW 149  
Db 84 RAHIIFQTLUSENDTHCVQSFYFLYRDGHSPTGLGVYVNVNGPGLGSAVNMWIGSHGRQW 143  
Qy 150 LRAELAVSTFWPNEQVIFAEVSGRSGYIAIDDIQVLSYPCDKPSFLRLGDEVVNAG 209  
Db 144 HQAELAVSTFWPNEFQVLFALISPDHKGYIGLDDILLFSPFCAPAKPHFSRLGDEVVNAG 203

Qy 210 QNATFQCIATGRDAVHNKMLQRRNGEDIPVAOTKNINHRFAASFRLEQVTKTDQDLYR 269  
Db 204 QNASFQCAAGRAAEAEHFFLQSGVLVPAAGVYRHLSHREFFLATFPPLASVGRSEQDLYR 263  
Qy 270 CVTQSGRGVSNPAQLIVREPPPIAPPQLLGVPYVLLIQLNANSIIGDPILKEVE 329  
Db 264 CVSQAPRGAGVSNPAELIVKEPPTPIAPPQLLRAGTYLIIQLNTNSIIGDPVIRKEIE 323  
Qy 330 YRMTSGSWTETHAVNATYKLIWHLDPDTEYFIRVLLTRPGCGGTGLCPPLITITKCAEP 389  
Db 324 YRMARGPMAEVAHNLQYKLIWHLDPDTEYFISVLLTRPGDGGTGRPPPLISRTKCAEP 383  
Qy 390 MRTPKTLKIAEIOARRIADWESLGYNITRCHTFNVATICVHYFRG--HNESKADCLMDMP 447  
Db 384 TRAPKGLAFIEIQARQLTQWEPGLCYNVTRCHTAVSLCYRYTLGGSNQTIRECVKMER 443  
Qy 448 KAPOHVNHLPPYTNVSLKMLTNPEGRKESEETIIQTDEDVPGVPVVKSLQGSTFENKI 507  
Db 444 GASRYTIKNLLPPRNHVRILITNPEGRKEKEVTFQTDDEVPGGIAAESLTFTPLEDMI 503  
Qy 508 FLANKPELDPNGIITQYEISYSSITRSDPPAVPVPAGPQTVSNLWNSHTHVMHLPGTTY 567  
Db 504 FLKWEPEQEPNGLITQYEISYQSIESSDPAVNVFPPRRTISKLRNETHYVFSNLHPGTTY 563  
Qy 568 QFFTRASTVKGFPATAINVTNINISAPLTPDYEGVDASLNETATTITVLLRPAQAKGAPI 627  
Db 564 LFSVARTSKFGQAALTEITNINISAPF-DYADMPSPLGSESENTITVLLRPAQGRGAPI 622  
Qy 628 SAYQIVVEELHPHRTKREAGAMECYQVPVTVYQNASMGAPYFAAEPLPGNLPBPAPPTV 687  
Db 623 SVYQVWVEERPRRLRREPQAQDCFSVPLTETALARGLVHFGAELAAASLLEAMPPTV 682  
Qy 688 GDNRTYQGFNPPPLAPRKGNIYFQAMSSVEKETQCVRITATKAATEPEVEIPDPAKQT 747  
Db 683 GDNQTYGFNPPPLEPRKAVLIYFQAASHLKGTELNCIRIARAKAACKESKRPLEVRSORS 742  
Qy 748 DRVVKIAGISA-GILVFTLLLVILIVKSKLAKRKDAMGNTROEMTHVMVNDMSYA 806  
Db 743 EEMGLIIGICAGGLAVLILLGALIVIRKQKPVNMTK-ATVNYRQEKTHMSAVDRSFT 801  
Qy 807 DQSTLHAEDPLSITFMDQHNFSPRYENHS--ATAESSRLLDVPRYLCBGTSPYOTGQLH 864  
Db 802 DQSTLQEDERLGLSFMADAPGYSPRGDORSQGVTEASSLLGSGPRPCGRKSGPYHTGQLH 861  
Qy 865 PAIRVADLLQHINLMKTSDSYGFKEEYBSPFEGQSASWDVAKQONRAKNRYGNIIADH 924  
Db 862 PAVRVADLLQHINQMKTAEYGFQYBSPFEG----WDATKKDKDKLGGKQEPVSAYDR 917  
Qy 925 SRVILQPVEDDPSDDYINANYIDGVRPSHYIATQGPVHETVYDFWRMIWQESACIVMV 984  
Db 918 HHVKLHPMLADPDADYISANYIDGVRSHNHFIATQGPXPEMIYDFWRMVWQEQACSIWMI 977  
Qy 985 TNLVEGVRKCYKMPDDTEYVGDYKVTCEVMEPLAEYVVRFTTLERRGYNEIREVKQPH 1044  
Db 978 TKLVEGVRKCSYWPEDSDMYGDIKITLVKTETLAEYVVRFTFALERRGYSARHEVRQPH 1037  
Qy 1045 FTGHPDHGVPHATGLLSFIRRVKLSNPPSAGPIVHCSAGAGRTGCTYIVIMLMDARE 1104  
Db 1038 FTAWPEHGVPHYHATGLLAFIRRVKASTPPDAGPIVHCSAGTGTGCTYIVLDMWMDMAEC 1097  
Qy 1105 EGVVDIYCNCKVALRSRRINMVQTEBOYIFIHDAILEACLCGETAIPVCFEKAAYFDMIRI 1164  
Db 1098 EGVVDIYCNCKVALRSRRINMVQTEBOYIFIHDAILEACLCGETTIPVNEFRATYEMIRI 1157  
Qy 1165 DSQTNSSHLKDEFTLNSVTPRLQABDCSIACLPRNHDKNRDMMLPPDRCLPFLITIDG 1224  
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Qy 1225 ESSNYINAAALMDSTROPAAFIQYPLPNTVKDFWRLVYDYGCTSIWMLNEVDLSQG--- 1281  
Db 1218 DPNNYINAAALDSTRSAAFIQYPLPNTVKDFWRLVYDYGCTSIWMLNQLNQSNSAMP 1277  
Qy 1282 CPQYWPBEGMLRYGFIQVECMSCSDCVINRIFRICNLTRPOEGVLMVQOXYLGMASH 1341

Db 1278 CLQWPGGQQYGLMEVFGSTANEDLVSRFRVQNSKRLQBGHLVHRFQELRWSAY 1337  
Qy 1342 REVPGSKRSFKLILQVKEWKEGEGRTIIHCLNGGGRSGMFCAGIIVEMVKRQNV 1401  
Db 1338 RDTSDSKAFHLHLAEVDKQAB--SGDGRVTVHCLNGGGRSGTFCACATVLEMIRCHSL 1395  
Qy 1402 VDVFHAKTILRNKPNMVEAPEQYRFCYDVDALEYLE 1438  
Db 1396 VDVFHAKTILRNKPNMVEAPEQYRFCYDVDALEYLEA 1432

RESULT 7  
US-10-058-270A-98  
; Sequence 98, Application US/10058270A  
; Publication No. US20040029114A1  
; GENERAL INFORMATION:  
; APPLICANT: Mack, David H.  
; APPLICANT: Gish, Kurt C.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and  
; TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer  
; FILE REFERENCE: 018501-005210US  
; CURRENT APPLICATION NUMBER: US/10/058,270A  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: US 60/263,965  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: US 60/265,928  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 09/829,472  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: US 60/282,698  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: US 60/288,590  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: US 60/294,443  
; PRIOR FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 98  
; LENGTH: 1444  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-058-270A-98

Query Match 59.2%; Score 4564.5; DB 15; Length 1444;  
Best Local Similarity 58.0%; Pred. No. 0;  
Matches 844; Conservative 239; Mismatches 343; Indels 29; Gaps 8;

Qy 1 MDTTAAALPAFVALLLSFWPLLGSAQGFSGGCTFFDGPACDYHQDL-YDDFEWVH 59  
Db 1 MASIALAL---SLLRLQLPLPGARASAPGCSFDEHYSNCGYSVALGTNGFTWEQ 56  
Qy 60 VSAQEPHYLPPEMQGSYMIIVDSDDHDPGEKARLQLPTMKENTHCTIDFSLYLSQKGLN 119  
Db 57 INTTEKPMLOQAVPTGSFMMVNSGRASGQKALHLLPTLKENDTHCIDFHYFSSRRSS 116  
Qy 120 PGTILNIVRNKGPLANPINNVGTGRDMLRAELAVSTFWPNEYQVIFEAESVGGSGY 179  
Db 117 PGALNVVKNVGGFGQGNPWNVSGVTEGWVKAELAISTFWPHFYQVIFESVLKGGHPY 176  
Qy 180 IAIIDIOVLSPYCDKSPHFLRLGDEVNAGONATFOCIATGRDAVHNKMLQRRNGEDIP 239  
Db 177 IANDEVRLAHPEKAPHFRLQNVENVNQNATFOCIAGCKWSQHDKMLQOQNGRDTA 236  
Qy 240 VAQTKNINHRPFAASFRLOEVTKTDQDLXRCVTQSERGSGVSNFAQLIVREPPRIAPPO 299  
Db 237 LMVTVVNHRRFSATSVADTAQRSVSKYRCVIRSDDGSGVSNVAELIVKEPTPIAPPE 296  
Qy 300 LLGVGPTLLIQLNANSIIGDPIILKEVEYRTSGSWTETHAVNAPTYKLWHLDDPTEY 359  
Db 297 LLAVGATYLIWKNANSIIGDPIILKEVEYRTTGTGTAETHIVDSNPNYKLWHLDDPVEY 356

Qy 360 EIRVLLTRPGEQGTGPGPPLIIRTKCABPMRTPTKLIKIAEQARRIAVDWESIGYNITR 419  
Db 357 EIRVLLTRPGEQGTGPGPAPLITRTKCADPVHGQPNVEIVDIRARQLTLQWEPFGYAVTR 416  
Qy 420 CHTFNVTICVHYFRGHNESKADCLDMDPKAPQHVHNLPPVTVNYSKMLITNPNREKSE 479  
Db 417 CHSYNLIVQYQV--FNQOQYEAEEVLOTSSHTLRGLRPFMTIRLLLSNPNREKSE 474  
Qy 480 ETIIQTDDEDVPGVPVKSLQGSTFENKIFLNWKEPLDPNGIITQYBISYSIRSIRDFPAPV 539  
Db 475 ELVVQTEEDVPGAVPLESIQGGPFEEKIYIQWKPNETNGVITLIEYNKAVGSLDPSAD 534  
Qy 540 VAGPPQTVSNLWNSHTHVFMHLHPGTYQFFIIRASTVKGFGDATAINVTNISAPTLPDY 599  
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Qy 600 EGVDAISINETATITITLLRPAQAKGAPISAYQIVVEELHPRHTKREAGAMECVQVPVYQ 659  
Db 595 D-TDTPLNETDITITVNLKPAQGRGAPSVQIVLVEERLQKRRADIIIECSVPVSIR 653  
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Qy 720 ETKTQCVRIATKAATEEPEVIPPAKQTDRTVVKIAGISAGILVPIILLVILVKK--- 776  
Db 714 ETKINCVRLLATTGASTQNSNTVEPEKQVNDTVKMGVIAGLLFIILLGLVMLTIKRRN 773  
Qy 777 -----SKLAKKRDAMNGTROEMTHVNMDBSYADQSLTHAEDPLSITFMDOHN 826  
Db 774 AYSYSYLSQRLAKKQKQKQTSQAQREMGPVASA-DKPTTKLSASRNDEGFSSSQVNG 832  
Qy 827 FSPRYNHSATBSSRLLDV---PRYLCEGTSPYQTGQLHPAIRVADLQHLNLMKTS 883  
Db 833 FT----DGRGELSQTTLTIQTHPYRTCDPVMSYPRDQQLAIRVADLQHLQITOMKRG 888  
Qy 884 SYGFKSEYSFFEGQSASMDVAKDQNRKRNRYGNIAYDHSRVLQFVDEDDPSSDYNA 943  
Db 889 GYGFKSEYALPEGQTASMDTAKEDENRNKNRYGNIISYDHSKVRLLVLDGDPHSDYNA 948  
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Qy 1304 CSMDCVINRIFRICNLTRPQEGYLMVQOQYQYLGWASHREVPGSKSFLKILQVEKQOE 1363  
Db 1309 ADIDEDIHRIFRICNWARPDGYRIVQHLQYIGWPAYRDTTPSKSLLKVVRLKQOE 1368  
Qy 1364 EWKEGEGRTIIHCLNGGGRSGMFECAIGIVVMVKRQNVVDVFAVKTLRNSKKNVPEAPE 1423  
Db 1369 QYDREGRTVHCLNGGGRSGTFCALCSCEMIQQQNIIDVFHIVKTLRNNKNMWTLE 1428



;	TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
;	TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;	TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
;	FILE REFERENCE: MRI-044
;	CURRENT APPLICATION NUMBER: US/10/205,823
;	CURRENT FILING DATE: 2002-07-25
;	PRIOR APPLICATION NUMBER: 60/307,982
;	PRIOR FILING DATE: 2001-07-25
;	PRIOR APPLICATION NUMBER: 60/314,356
;	PRIOR FILING DATE: 2001-08-22
;	PRIOR APPLICATION NUMBER: 60/325,020
;	PRIOR FILING DATE: 2001-09-25
;	PRIOR APPLICATION NUMBER: 60/341,746
;	PRIOR FILING DATE: 2001-12-12
;	PRIOR APPLICATION NUMBER: 60/362,158
;	PRIOR FILING DATE: 2002-03-05
;	NUMBER OF SEQ ID NOS: 455
;	SOFTWARE: FastSeq for Windows Version 4.0
;	SEQ ID NO 343
;	LENGTH: 1463
;	TYPE: PRM
;	ORGANISM: Homo sapiens
;	US-10-205-823-343
	Query Match 59.2%; Score 4564; DB 14; Length 1463;
	Best Local Similarity 57.5%; Pred. No. 0;
	Matches 847; Conservative 238; Mismatches 341; Indels 48; Gaps 9;
Qy	1 MDTTAAALPAFVALLLLSPWLLGSAQGGSAGGCTFDDPGACDQHDQL-YDDFEVWH 59
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Qy	60 VSAQEPHYLPPEMPQGSYMIYDSSDDHPGSEKARLQLPTMKENDTHCIDFSYLLYSQKGLN 119
Db	57 INTTEKPMLOQAVPTGSGFMVNSGRASGQKALLLPTLAKENDTHCIDFHYFESSRDRSS 116
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Db	117 P GALNVYKVGNGPQGNPVMVNSGVVTEGWKAEALAISTFWPHFYQVIPESVSLKHPGY 176
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Db	177 IAVDEVRLAHPCKRAPHFRLQNVENVNGONATFOCIAGGKWSQHDKLWLQWNGRDTA 236
Qy	240 VAOTKMINHRRFAASFLQEWTKTDQDLYRCVTSQSERGSVNSFAOLIVREPPRTAPPO 299
Db	237 LMWTRVVNHRFSATVSVADTAQRSYSKYICVIRDSGSGSVNYAELIVKEPTPIAPPE 296
Qy	300 LLVGPTYLLIQNANSIIGDGPILKEVYRMTSGSWTETHAVNAPTYKLMHLDPDTEY 359
Db	297 LLAVGATYLIWKPNANSIIGDGPILKEVYRMTTGTWAEITHVDSFNYKLMHLDPDVEY 356
Qy	360 EIRVLLTRPEGGTLPGPPLITRTKCAEPMRPTKTLKIAEIOARIVDWESLGNITR 419
Db	357 EIRVLLTRPEGGTPPGAPLITRTKCADPVHGQNVETIDIRARQLTLQWEPFGYAVTR 416
Qy	420 CHTFNVITCYHFRGHNESKADCLDDMPKAPQHVWHLPPVTNVSLKMLITNPEGRKESE 479
Db	417 CHSYNLTVQYV--FNQQYAEAEVITQSSHYTLRGLRFPWIRLULLSNPEGRWESE 474
Qy	480 ETIIQTDDEVPVPVKSLQGTGFENKIFLNWKEPLDPNGIIITQYEISYSSIRSFDPAPV 539
Db	475 ELVVQTEEDVEGAVPLESIQGGPFEEKIYIQWKPPNETNGVITLYEINYKAVGSLDPSAD 534
Qy	540 VAGPPQTVSNLWNSHTHVFWHLHPGTYQFFIRASTVKGFGPATAINVITNIISAPTLPOY 599
Db	535 LSSQRGKVFKLRNETHHLFVGLYPGTYTSFTIKASTAKGFGPPVTRTIATKISAPMPEY 594
Qy	600 EGYDASINETAATTITVLLRPAQAKGAPISAYQIIVLELHPHRTKRBAGAMECYQVPVTVQ 659
Db	595 D-TDTPLNETDTTITVLMKEPARGAPSVYQLVVKERLQKRAADIIIECFSPVSVYR 653
Qy	660 NAMSGGAPYFAAELPFGNLPEPAPFTVGDNRITYQGFNPNPLAPRGYNIYFOAMSVEK 719

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1283

Query Match      59.1%; Score 4555; DB 15; Length 1499;
Best Local Similarity 59.7%; Pred. No. 0;
Matches 856; Conservative 208; Mismatches 328; Indels 43; Gaps 13;

QY 35 GCTDDGPG---ACDYHQDLVDDFEWVHVSAQEPHYLPPEMPQGSYMTVDSDDHPGKA 91
DB 71 GCTFEESDPAVPCEYSQAQYDDFQEWQVRIHPGTRAPADLPHGSLYLVMTVSHQAPGORA 130
QY 92 RLQPLTKMKNETHCIDFSYLLYSQGLNPGTLNLTIVRNKGPLANPINWVTGFTGRDWLR 151
DB 131 HVIFQSUSENTHCQFSYFLYSRDSGSPGLGVTVRVNNGPLGSVAVNMTGSHGRQHW 190
QY 152 AELAVSTFWPNEYQVIFEAESYSGRSGYIAIDDIQVLSYPCDKSPHFRLRLGDEVNAGQN 211
DB 191 AELAVSTFWPNEYQVLFALISPDRCYVGLDILLISYPCAKAPHFSLGDEVNAGQN 250
QY 212 ATFQCIATGRDAVHNKMLQRNGEDIPIVATQKNINHRFAASFLQBLQVTKTDQDLRCV 271
DB 251 ASFOQMAAGRAAEERFLQROSGALVPAAGVRIHSHRRFLATFLAAVSRABQDLRCV 310
QY 272 TQSERGSGVS-NFAQLIVREPRPTAPQLLGVGPTYLLIQLNANSIIGDGPILLKEVEY 330
DB 311 SQAPRGRTSLNFAEFMVKPEPTPIAPQLLRAGPTYLLIQLNANSIIGDGPVVRKEIEY 370
QY 331 RMTSGSWTEHAVNAPTIVKHLWLDPDTEYEVIRVLLTRPGEGTGLPGPPLITRTKCAEPM 390
DB 371 RMARGPWAEEVAVSLQTKLWHLDPDTEYEVISVLLTRFGDGTGRGPPLISRYKCAEPM 430
QY 391 RTPKTLKIAEIQAARIVADWESLGVNITRCHTFNVTICYHYFRG--HNESKADCLMDMPK 448
DB 431 RAPKGLAEIAQARQLTQWEPGLGVNTRCHTYTVSLCVHYTLGSSHQITRECVKTRQG 490
QY 449 APQHVNHLPPTVTVSLKMLTNPRKESBETIIOETDEDVPGVPVKSLOGTSFENKIF 508
DB 491 VSRVYTMKNLLPYRVNHHVRLVLTNPGRGKEVETFTQDEDVPSGIAAESLFTPLEDMIF 550
QY 509 LNWKEPLDNGIITVEISYSIRSIFDPAVPAGPPTVSNLWNSHTRHVFVHLHPGTTYQ 568
DB 551 LKWEPPQENGLITVEISYSIESDSDPAVNVGPRRIISKURNEYVFNHSLHPGTTYL 610
QY 569 FFIRASTVKGFGPAPAINVTNNISAPTLDPYEGVDASLNETAATTITVLLRPAQAKAPIS 628
DB 611 FSVARTCKGFGQAALTEITTNISAPSF-DYADMPSPLGSESENTITVLLRPAQGRGAPIS 669
QY 629 AYQIVVEELH-PRHTRKAGAMECYQVPTYTONAMSGGAPYFAELPPGNLPEPAPPTV 687
DB 670 VYQIVVEEQQSRRLRREPPGQDCFPVLTFFAALARGLVDFYFGAELAASSLPEAMPPTV 729
QY 688 GDNRTYQGFNPPPLAPRGYNIYFOAMSSVEKETKTCVRIATKAATBEPEVIPDPKATQ 747
DB 730 GDNKTYRGFWNPPLPRKAYLIYFOAASHLKGELNLCIRIARAKAACKESKREPLEVSORS 789
QY 748 DRVVKIAGISA-GILVIFILLAVLILVKKSK-----LAKRKDAMGNTRQOE 793
DB 790 BEMGLILGICAGGLAVLILLGAIIVITIRKGRDHVAYSYPKPVNMTK---ATVNYRQE 845
QY 794 MTHVNVNMDRSVADOSTLHAEDPLSTFMDQNFSPRYENHS--ATAESSRLLDVPRYLC 851
DB 846 KTHMNSAVDRSFTQDSTQLQEDERLGLSFMDMTHGYSTRGDQRSGGYTEASSLLGSGPRPC 905
QY 852 ECTGSPYOTGQLHPAIRVADILLQHLNLMKTSYSGYKEEYESFEFGQSASMDVAKDQNR 911
DB 906 GRKGSFYHTGQLHPAIRVADILLQHLNLMKTAGYGFKEYESFEFG-----WDATKKDKV 961
QY 912 AKNRYGNIAYDHSVILQPVDEDDPSDYINANYID-----GYQRPSHYIATQGVPHET 965
DB 962 KGSRQEPMPAYDRHRVTKLHPMLGDDPNADYINANYIDIRINRGGYHRSNHFIATQGVKPEM 1021
QY 966 VYDFWRMIWQESACTIVMNLVVEGRVKCYKYWPDDETVYGDFTVCVEMEPLAEYVVR 1025

; Db 1022 VYDFWRMIWQESSIVMTKLVVGRVKSRYPEDSDTYGDIKIMLVTKETLAEYVVR 1081
; QY 1026 TFTLERRGYNEIREVKQFHFTGPDHGVVPYHATGLLSFIRRVKLSNPPSAGPIVVHCSAG 1085
; Db 1082 TFALERRGYSARHEVRQFHFTAWDEHGVVPYHATGLLAFIRRVKASTPPDAGPIVIHCSAG 1141
; QY 1086 AGRTGCVIVDIDMLDMAEREGVVDIYNCVKALRSRRINWQTERQYFIHDAILEACLCG 1145
; Db 1142 TGRGTCVIVLDWMLDMAECEGVVDIYNCVKTLCSRRVNMIOQTERQYFIHDAILEACLCG 1201
; QY 1146 ETALPVCFEKAAAFDMIRIDISOTSSHLKDEFOFLNSVTPRLQAEDECSIACLPRNHDQNR 1205
; Db 1202 ETTIPSEFKATYKEMIRIDISQSSQLREFOFLNSVTPPLDVEECSIALLPNRDQNR 1261
; QY 1206 FMDLPPDRCLPFLITIDGESSNYINAALMDSYRQAAFIYQYPLPNTVKDFWRLVYDY 1265
; Db 1262 SMDVLPDRCLPFLISTDGSNNYINAALTDSYTRSAAFIVTLHPLQSTTPDFWGLVYDY 1321
; QY 1266 GCTSIVMLNEVDLSQG---CQYWPBEGMLRYGPIOVCEMCSMDCDVINRIFRICNLTR 1322
; Db 1322 GCTSIVMLNQLNQSNSAMPCLQYWPBEGMQYGLMEVEFMGSGTADEDIVARVFRVQNTSR 1381
; QY 1323 PQEGYLVMOQFOYGLGWSHREVPGSKRSFLKLILQVEKWOBEWKEGERTIICHCLNGGGR 1382
; Db 1382 LQEGHLLVRHFQFURWSAYRDTPSKKAFLHLLAEGDKWQAE--SGDGTIVHCLNGGGR 1439
; QY 1383 SGMFCALGIVVEMVKRQNVVDVFAVHATLRNSENKEMVEAPEQYRFCYDVALEYLE 1437
; Db 1440 SGTECATVLEMRCHNLVDVFFAAKTLRNYKENVETMDQYHFCYDVALEYLE 1494

RESULT 11
US-10-408-765A-805
; Sequence 805, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Zhang, Eoin D.
; APPLICANT: Faby, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Watnick, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 805
; LENGTH: 1442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-805

Query Match      56.7%; Score 4374.5; DB 16; Length 1442;
Best Local Similarity 58.5%; Pred. No. 6e-314;
Matches 840; Conservative 202; Mismatches 332; Indels 63; Gaps 18;

QY 35 GCTDDGPG---ACDYHQDLVDDFEWVHVSAQEPHYLPPEMPQGSYMTVDSDDHPGKA 91
DB 33 GCTFEESDPAVPCEYSQAQYDDFQEWQVRIHPGTRAPADLPHGSLYLVMTVSHQAPGORA 85
QY 92 RLQPLTKMKNETHCIDFSYLLYSQGLNPGTLNLTIVRNKGPLANPINWVTGFTGRDWLR 151
DB 86 HVIFQSUSENTHCQFSYFLYSRDSGSPGLGVTVRVNNGPLGSVAVNMTGSHGRQHW 145
QY 152 AELAVSTFWPNEYQVIFEAESYSGRSGYIAIDDIQVLSYPCDKSPHFRLRLGDEVNAGQN 211
DB 146 AELAVSTFWPNEYQVLFALISPDRCYVGLDILLISYPCAKAPHFSLGDEVNAGQN 205
```





Qy 1008 DFKVTCVEMELAEYVVTFTLERRGYNEIREVQFHTGPHDGVPHATGLLSFIRRV 1067  
Db 192 DIKVTLLTELLAEYVIRTFVBERKGVHEIREIQFHTGPHDGVPHATGLLGFVRQV 251  
Qy 1068 KLSNPPSAGPVTWCHSAGAGRTGCVIVIDIMLDMAREGVVDIYNCVKALRSRRNMVQT 1127  
Db 252 KSKSPSAGPVTWCHSAGAGRTGCVIVIDIMLDMAREGVVDIYNCVKALRSRRNMVQT 311  
Qy 1128 BEQYFIFHDAILEACLCGETAIPVCEFKAAFYDMIRIDSQTNSSHLKDEFOFLNSVTPRL 1187  
Db 312 BEQYFIFHDAILEACLCGETSVPASQVRSYLYDMNKLDPQTNSSQIKEEFTLNWVPTL 371  
Qy 1188 QAEDCSIACLPRNDKXRFMDMLPDRCLPLIITIDGESSNYINAALMDSYRQAAFIIVT 1247  
Db 372 RVEDCSIALPRNHEKRCMDILPDRCLPLIITIDGESSNYINAALMDSYRQAAFIIVT 431  
Qy 1248 QYPLPNTVKDFWRLVYDYGCTSIYMLNEVDLSQCPQVWPEEGMLRGVPIOVEMCSMD 1307  
Db 432 QHPLPNTVKDFWRLVLDYHCTSVMLNDVDPAQLCPQVWPEEGMLRGVPIOVEMCSMD 491  
Qy 1308 CDVINRIFRICNLTRPOEGYLMVQFQYLGWASHREVPGSRKSLKLILQVEKMQEEMKE 1367  
Db 492 EDIISRIFRINYAARPQDGYRMVQFQYLGWASHREVPGSRKSLKLILQVEKMQEEMKE 551  
Qy 1368 GEBRTIHLNGGSGRMFCAIGIVEMVRQNVVDVPHAVKTLRNSKPNMVEAPEQYRF 1427  
Db 552 GEBRTVHCLNGGSGRTFCAISIVCEMLRQRTVDVPHAVKTLRNNKPNMVDLLDQYKF 611  
Qy 1428 CYDVALEYLES 1438  
Db 612 CYEVALEYLNS 622

## RESULT 14

US-10-296-115-1390  
; Sequence 1390, Application US/10296115  
; Publication No. US20040053248A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq Inc  
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 784PCT  
; CURRENT APPLICATION NUMBER: US/10/296,115  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR FILING DATE: US09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR FILING DATE: US09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 1478  
; SEQ ID NO 1390  
; LENGTH: 815  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-296-115-1390

Query Match 28.7%; Score 2210.5; DB 15; Length 815;  
Best Local Similarity 53.2%; Pred. No. 3.2e-154;  
Matches 412; Conservative 123; Mismatches 227; Indels 13; Gaps 5;  
Qy 4 TAAALPAFVALLLSLSPWLLGSAGQFSGAGCTFDDGPGACDYHQDYDDFEWVHSAQ 63  
Db 3 TLGTCLATLALLL-----TAAGETFSGCLFDEFPYSTCGYSQSEGGDDFNWEQNTL 54  
Qy 64 EPHYLPPEMPOGSMYVDSDDHDPGEKARLQLPMTKENDTHCIDFSYLLYSOKGLNPGTL 123  
Db 55 TKPTSDPWFMSGSMFLVNAGRPGQRAHLLLPOLKENDTHCIDFHFVSKSNSPPGLL 114  
Qy 124 NILVRNKGPLANPIWNTGTGRDLWRAELAVSTFWPNEYQVIFAEVSGRSYTAID 183  
Db 115 NVYKVNGLPLNPIWNSIGDPTWRAELAISTFWPNEYQVIFEV-ITSGHQYLAID 173  
Qy 184 DIQVLSYPCDKSFLRLGDEVNAGQATFQCIATORDAVNKLWLRNGEDIPVAQT 243  
Db 174 EVKVLGHPCRTTHPLFLRIQNVNAGOFATFQCSAIGRTVAGDLRLWLQGDIVRDAPLKEI 233

Qy 244 KNINHRFAASFRLOEVTKTDQDLYRCVTOBSRGSGVSNFAQLIVREPPRIAPPQLGV 303  
Db 234 KVTSSRRFIASFNVTNTKRDAGKYRCMIRTEGGVIGSNVYAEVAVKEPPVPIAPPQLASV 293  
Qy 304 GPTVLLIQLNANSIIGDPIILKEVEVMTSGSWTETHAVNAPYKLMHLPDDEYEIRV 363  
Db 294 GATYLLIQLNANSINGDPIVAREVEYCTASGWNDRQPDVDSYKIGHLDPDEYEISV 353  
Qy 364 LLTRPGGGTGLPGPPLITRTKCAEPMRTKTLKIAEIOARRIAVDWESLGYNITRCHTF 423  
Db 354 LLTRPGGGTGSFGPALRTKCADPMRGPKLEVEVKSQIITIRWEPFGYNVTRCHSY 413  
Qy 424 NVTCYHYFRGHNESKAD--CLDMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKESET 481  
Db 414 NLTVHYCYVQGGQVREEVSWDTEHSPQHTITNLSPTNVSVKILMNEGRKESQEL 473  
Qy 482 IIQTDDEVPVGVKSLQCTSFENKIPLNKEPLDPNGIITQYBISVSSRSRFPDPAVVA 541  
Db 474 IVQTDDELPGAVPTESIQGSTFEKIFLOWREPTQTYGVITLYEITYKAVSSFPDEIDL 533  
Qy 542 GPPTQVSNLWNSHTHVFMHLHPGTYQFFIRASTVKGFGPATAINVTNITISAPTLPDYEG 601  
Db 534 NQSRVSKUGNETHFLFGYPGTYFTIRASTAKGFGPPATNQFTTKISAPMPAYE- 592  
Qy 602 VDAISNETATTITVLLRPAQAKGAPISAYQIVVVEELHPHRTKREAGAMECYQVVPVYQNA 661  
Db 593 LETPLANTDNTVTVMKAPHSAGPVSQYQIVVEEERPRRTKKTTEILKCYVPPIHFQNA 652  
Qy 662 MSGGAPYFAAELPPGNLPEPAPPTVGDNRTYQGFVWNPPLAPRGYNIYFOAMSVEKET 721  
Db 653 SLLNSQYFAAEFFPADSLQAAQPTTIGDNKTNGYNTPLLPYKSYRIYFOAASRANGET 712  
Qy 722 KTCVRIATKAATEEPEVIPPDAKOTDRVVKIAGISAGILVFIILLVWILLVKK 776  
Db 713 KIDCVQATKGA--TPRPVPEPEKQTDHTVKIAGIAGILLVFIILLVWILLVKK 766

## RESULT 15

US-09-808-602-54  
; Sequence 54, Application US/09808602  
; Patent No. US20020155115A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine A  
; APPLICANT: Fernandes, Elma  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Herriman, John L  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Mezes, Peter S  
; APPLICANT: MacDougall, John  
; TITLE OF INVENTION: No. US20020155115A1el Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-697 CIP  
; CURRENT APPLICATION NUMBER: US/09/808,602  
; CURRENT FILING DATE: 2001-03-14  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR FILING DATE: 2000-03-03  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 54  
; LENGTH: 1502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-808-602-54

Query Match 19.9%; Score 1534.5; DB 9; Length 1502;  
Best Local Similarity 30.7%; Pred. No. 8.1e-104;  
Matches 422; Conservative 213; Mismatches 480; Indels 259; Gaps 46;  
Qy 205 EVNAGQATFQCIATGRDAVHKNLWLRNG--EDIPVAQTKNINHRFAASFRLOEV 260  
Db 195 EVNAGQATFQCIATGRDAVHKNLWLRNG--EDIPVAQTKNINHRFAASFRLOEV 260

Db 242 EIMPGGNVITCVAVGSMPYVK-WMOGAEDLTPEDDMPVG--RNV-----LELTDV 290  
Qy 261 TKTDODLVRCTVQSRGSGVNFQAOLIVREPRPIAPQLLGVGPTYYLLIQNANSIGD 320  
Db 291 -KDSANYHPCVAMSSLVG-IEAVAQITVKSLPKAPGTPMVTENTATSIITWDSGN---P 345  
Qy 321 GPIILKEVEYRMTS--GSWTETHAVNAPTYKLIHLDPDTEVEIRVLLTRPBGEGTGLPGP 378  
Db 346 DVSYYVIEYKSKODGPYQIKEDITTRYSIGGLSPNSEYEIUV--SAVNSIGQPPSE 403  
Qy 379 PLITRTKCAEPMRTKTLKIAEIQARRIAVJWES-----LGYN----- 417  
Db 404 SVWTRTGQAAPRPRNVQARMLSATMIWQEEBPVEPNGLIRGYRVYVYTWEPEHPVGNW 463  
Qy 418 -----T 418  
Db 464 QKHNVDLSLLTTVGSLLDETVTVRVLAFTSVGDGLSDPIQVKTQCGVPQPMNLRAEA 523  
Qy 419 RCHTFNVITCYH-----YFRGHNESKADCLDMDPKAQOHVNVHLPVYTNVSLK 466  
Db 524 RSET-SITLSWSPPROESI I KYELLFREGDHGREVGRTFDP-TTSYVVEDLKPNTYAFR 581  
Qy 467 MILTNPEG-----RKESEBETIQTDEDVPGVPVKSLQTSFENKIFLNWKEPLDPN 518  
Db 582 LAARSPQGLGAFTPVVRQRTLQSI-----SPKNFKVKWIMKTS-----VLSWEP-DNY 630  
Qy 519 GIITOYEISYSIRSIRFDPNAVAGPPQTVNSIWNSTHVFHMLHPGTTYQFFI--RASTV 576  
Db 631 NSPTPKIQYNGL-----TLVDVG-----RTTKKLIHLKPHTFYFVLTNRGSSL 676  
Qy 577 KGFGPA---TAINVTT-NISAPTLPDYEGVDASLNETAATTITVLLRPAQAKGAPISAYQ 631  
Db 677 GGLQQTWTAWTAFNLNGKPSVAPKPDADGF-----IMVYLPDQGSF-VEVQSIF 725  
Qy 632 IVVEELHPR-----TKREAGAMECYO-----VPVTYQNMAGSGAPYFPA--AE 673  
Db 726 IVMVPRLKSRGQOFLTPLGSPEDMDLEELIQDISRLQRSLRHSRQLVPRPYIAARFSV 785  
Qy 674 LPPGNLPEPAPPTVGDNRTYQGFWNPPILAPRGYNIYFOAMSSVEKETKTQCVRATKAA 733  
Db 786 LPP-----TPHPGDQXQGGFNRKLEPGHRYVFLAVL--LQKSEPT-----FAASP 831  
Qy 734 TEEPEVI--PDPAKOTDRVVKIAGISAGILVFILLLVLI-LIVKSKLAKRKDAMGNT 790  
Db 832 FSDPFQLNDPDPQPIVDGEEGLIWIWGPVLAVFIIICIVAILLYKNKPDSCRKDSERPRT 891  
Qy 791 RQEMTHMVMNDRSVADOSTLHAEDPLSITFMDQHNFGSPRYENHSATAESSRLLDVPRYL 850  
Db 892 KCLINN-----ADLAPHKDPVE---MRRINF----- 916  
Qy 851 CEGTESPYQTGOL-HPAIRVADLLOHINIMKTSDSYGFKEYESFFEGOSASWDVAKKDQ 909  
Db 917 ----QTP---GMLSHPPPIADMAEHTERLKAANDSLKSQYESIDPGQOFTWEHSNLEV 969  
Qy 910 NPAKRYGNI IAYDHSRVLQVEDDPSDDYINANYIDQYQRPSPHYIATQGPVHETVYDF 969  
Db 970 NKPKRYANVIAVDHSRVLQPIEGIMGSDYINANYVDGRRQONAYIATQGPLPETFGDF 1029  
Qy 970 WEMIWQEOSACIVMTNVLVEGRVKYKYPD-DTEVVYVGDVCTVEMEPLAEYVVVTRFT 1028  
Db 1030 WRMWQORSATIVMTRLEEKSRICKDQWPNRGHTYGFIOVTLDTIELATFCVTFIS 1089  
Qy 1029 LERRGYNEIREVKQHFHTGPDHGVPPYHATGLLSFIRRVKLSNPPSAGPIVVHCSAGAGR 1088  
Db 1090 LHKNGSSEKREVRQOFTAMPDGHVPYPTPLAFLRRVKTCTNPPDAGPIVVHCSAGVGR 1149  
Qy 1089 TGCYIVIDIMDMAEREGVVDIYNCVKALRSRINMVQTESQYIIFIHDAILEACLGETA 1148  
Db 1150 TGCFFIDAMLERIKPEKTVDVYGHVTLMRSORNYMVQTESQYFIHEALLAEGVCGNTE 1209  
Qy 1149 IPVCFKAAYFOWIRIDSQTNLSHLKDEFOTLNSVTPRLQAEDCSIACLPNRHDKNRFMD 1208  
Db 1210 VPARSYAVIQLAQVEPGEHVTGMELEFKRL--ANSKHTSRFFISANLPCKKFKNRLVN 1267

Qy 1209 MLPPDRCLPFLITIDG-ESSNYINAALMDSYRQPAAEIVTQYPLPNTVKDFWRLVYDYGC 1267  
Db 1268 IMPYESTRVCLOPIRGVGEVDYINASFIDGRQOKAYIATQGPLAEFTTDFWRLWENNS 1327  
Qy 1268 TSIWMLNEVDL--SQGCPQYWPBEGMLRYGPIQVECMSCSDCDVINRIFRICNLTRPQE 1325  
Db 1328 TIVVMLTKLRMGREKCHQYWPABERSARYQYFVVDPA---EYNMPQVILLREFKVTDARD 1384  
Qy 1326 GY-LMWQOQYVLGASHREVPVGSKRSLKILQVEKQOEWEKSGEGRTIIHCLNGGGRSG 1384  
Db 1385 QOSRTVRQFQFTDW-PEQGVPKSGEGFIDFTIGQVHKTKXEQFGQ-DGPISVHCSAGVGRGTG 1442  
Qy 1385 MFCAIGIVVEMVKEQNVVDVPHAVKTLRNSKPNVVEAPEQYRPCYDVDALEYLES 1438  
Db 1443 VFITLSIVLERMRYEGVVDIFQTVMLRTORPAMVQTEDEYQFCYQAALLEYLGS 1496

Search completed: June 1, 2005, 14:02:15  
Job time : 138.676 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2005, 13:40:58 ; Search time 38.2607 Seconds  
(without alignments)  
3618.750 Million cell updates/sec

Title: US-09-887-669-2  
Perfect score: 7709  
Sequence: 1 MDTTAAALPAFVALLLSP.....EAPQVRFYVDVALEYLESS 1439

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7595.5	98.5	1440	2 JC6312	protein-tyrosine-p
2	7571	98.2	1457	1 A48066	protein-tyrosine-p
3	4807	62.4	1452	1 S17669	protein-tyrosine-p
4	4791	62.1	1452	1 S17670	protein-tyrosine-p
5	4632	60.1	1436	2 JC5290	protein-tyrosine-p
6	4374.5	56.7	1442	2 S72441	protein-tyrosine-p
7	1529.5	19.8	1501	2 I58148	protein-tyrosine-p
8	1517.5	19.7	1898	2 S46216	leukocyte antigen-
9	1509	19.6	1897	1 TDHULK	leukocyte antigen-
10	1508.5	19.6	1499	2 I50212	protein-tyrosine-p
11	1505.5	19.5	1912	2 A56178	protein-tyrosine-p
12	1490.5	19.3	1496	1 A48758	protein-tyrosine-p
13	1483	19.2	1691	1 D54689	protein-tyrosine-p
14	1483	19.2	1894	2 C54689	protein-tyrosine-p
15	1470.5	19.1	1290	2 A56493	leucocyte common a
16	1462.5	19.0	1863	2 S46217	protein-tyrosine-p
17	1457.5	18.9	2029	1 TDFLJK	protein-tyrosine-p
18	1446	18.8	1907	2 S50893	protein-tyrosine-p
19	1426	18.5	1231	2 S53089	protein-tyrosine-p
20	1366	17.7	1437	2 T31093	probable protein-t
21	1349.5	17.5	1585	2 T19121	probable protein-t
22	1324	17.2	2051	2 T30938	receptor tyrosine
23	1255	16.3	582	2 A57068	protein-tyrosine-p
24	1196	15.5	796	1 JC1285	protein-tyrosine-p
25	1172.5	15.2	802	1 A36065	protein-tyrosine-p
26	1164.5	15.1	832	2 JC8051	protein tyrosine p
27	1153	15.0	829	1 A47373	protein-tyrosine-p
28	1143	14.8	699	2 JC6132	protein-tyrosine-p
29	1132	14.7	700	1 S12053	protein-tyrosine-p

30	1106	14.3	1262	1 B48758	protein-tyrosine-p
31	1071	13.9	680	2 JC8052	protein tyrosine p
32	1023.5	13.3	2314	1 A46151	protein-tyrosine-p
33	1017.5	13.2	1442	1 B48148	protein-tyrosine-p
34	996.5	12.9	1445	1 A48148	protein-tyrosine-p
35	979.5	12.7	1422	2 T42636	protein-tyrosine-p
36	953	12.4	1301	1 A41622	protein-tyrosine-p
37	952.5	12.4	1462	1 B36182	protein-tyrosine-p
38	940.5	12.2	1273	1 TDRTLT	leukocyte common a
39	940	12.2	1291	1 A28334	protein-tyrosine-p
40	931.5	12.1	1304	1 A46546	leukocyte common a
41	908	11.8	1200	2 T43148	probable protein-t
42	882.5	11.4	1409	2 T42522	protein-tyrosine-p
43	875.5	11.4	1237	2 A54080	protein-tyrosine-p
44	866	11.2	1422	2 T30111	hypothetical prote
45	765	9.9	711	2 T23738	probable protein-t

ALIGNMENTS

RESULT 1  
JC6312

protein-tyrosine-phosphatase (EC 3.1.3.48) receptor-type - human  
C;Species: Homo sapiens (man)

C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jan-2000

C;Accession: JC6312

R;Yang, Y.; Gil, M.C.; Choi, E.Y.; Park, S.H.; Pyun, K.H.; Ha, H.

Gene 186, 77-82, 1997

A;Title: Molecular cloning and chromosomal localization of a human gene homologous to th

A;Reference number: JC6312; MUID:97199372; PMID:9047348

A;Accession: JC6312

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1440 <YAN>

A;Cross-references: GB:L77886

C;Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe

-tyrosine-phosphatase homology

C;Keywords: phosphoric monoester hydrolase

F;31-194/Domain: MAM homology <MAM>

F;209-272/Domain: immunoglobulin homology <IMM>

F;294-372/Domain: fibronectin type III repeat homology <3FR>

F;911-1131/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 98.5%; Score 7595.5; DB 2; Length 1440;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1421; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

Qy 1 MDTTAAALPAFVALLLSPWLLGSAQGFSAAGGCTFDDPGACDYHQDLYDDFEWVHV 60

Db 1 MDTTAAALPAFVALLLSPWLLGSAQGFSAAGGCTFDDPGACDYHQDLYDDFEWVHV 60

Qy 61 SAQEPHYLPPEMPOGQSYMIYVSSDHPDGEKARLQPTMKENDTHCIDFSYLLYSQKGLNP 120

Db 61 SAQEPHYLPPEMPOGQSYMIYVSSDHPDGEKARLQPTMKENDTHCIDFSYLLYSQKGLNP 120

Qy 121 GTLNILVRVNGKPLANPIWVTGTGRDLRAELAVSTFWPNEYQVTFEAEVSGSRGYI 180

Db 121 GTLNILVRVNGKPLANPIWVTGTGRDLRAELAVSTFWPNEYQVTFEAEVSGSRGYI 180

Qy 181 AIDDIQVLSYPCDKSPHFLRLGDEVEVNAQNATFQCIATGRDAVHNKLWLQRRNGEDIPV 240

Db 181 AIDDIQVLSYPCDKSPHFLRLGDEVEVNAQNATFQCIATGRDAVHNKLWLQRRNGEDIPV 240

Qy 241 AQTKNINRRFAASFRLOEVTQDQLYRCVTQSERGSGVSNFAQLIVRPPPIAPPOL 300

Db 241 AQTKNINRRFAASFRLOEVTQDQLYRCVTQSERGSGVSNFAQLIVRPPPIAPPOL 300

Qy 301 LGVGPYLLIQLNANSITIGDPIILKEVEVRMTSGSWTETHAVNAPTYKLWHLDPDTEYE 360

Db 301 LGVGPYLLIQLNANSITIGDPIILKEVEVRMTSGSWTETHAVNAPTYKLWHLDPDTEYE 360

Qy 361 IRVLLTRPGSGGTGLPGPPLITRTKCAEPMRTPKTLKIAEQARRIADVWESLGYNITRC 420

Db 361 IRVLLTRRGEGTGLPGPLLTTRTKCAEPMRTPTKLKIAEQARRIADVMSLGVNLTTC 420  
Qy 421 HTFNVTICYHYFRGHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGRKSEEE 480  
Db 421 HSFNVTICYHYFRGHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLTNPGRKSEEE 480  
Qy 481 TTIOTDEVDVPGVPVKSLQGTSTFENKI FLNWKPELDPNGITTOYEISYSSRSRSDPAVPV 540  
Db 481 TTIOTDEVDVPGVPVKSLQGTSTFENKI FLNWKPELDPNGITTOYEISYSSRSRSDPAVPV 540  
Qy 541 AGPPTVSNLWNSTHVFMHLHPGTYTOFFTRASTVKGFGPATAINVTNTNISAPTLPDYE 600  
Db 541 AGPPTVSNLWNSTHVFMHLHPGTYTOFFTRASTVKGFGPATAINVTNTNISAPTLPDYE 600  
Qy 601 GVDASLNETAATITVLLRPAQAKGAPISAYQIIVVEELHPHRTKREAGAMECYQVPVTYQN 660  
Db 601 GVDASLNETAATITVLLRPAQAKGAPISAYQIIVVEELHPHRTKREAGAMECYQVPVTYQN 660  
Qy 661 AMSGAPYFPAELPPGNLPEPAPPTVGDNRITYQGFWNPPPLAPRKGYNIFYQAMSSVEKE 720  
Db 661 AMSGAPYFPAELPPGNLPEPAPPTVGDNRITYQGFWNPPPLAPRKGYNIFYQAMSSVEKE 720  
Qy 721 TKTQCVRIATK-AAETEPEVIPPDAKQTDVVVKIAGISAGILVFTLLLLVWILIVKSKL 779  
Db 721 TKTQCVRIATKAAATEPEVIPPDAKQTDVVVKIAGISAGILVFTLLLLVWILIVKSKL 780  
Qy 780 AKKRKDMGNTRQEMTHVMNMDRSYADQSTLHAEDPLSITFMDQHNFSPRYENHSATAE 839  
Db 781 AKKRKDMGNTRQEMTHVMNMDRSYADQSTLHAEDPLSITFMDQHNFSPRYENHSATAE 840  
Qy 840 SSRLLDVPRLCEGTESPYQTQLHPAIVADLLOHINLMKTSDSYGKEYESPFEGQS 899  
Db 841 SSRLLDVPRLCEGTESPYQTQLHPAIVADLLOHINLMKTSDSYGKEYESPFEGQS 900  
Qy 900 ASWDVAKKQDNRAKRYGNI IAYDSRVLQOVEDPSSDYINANYIDGQRPISHYIATQ 959  
Db 901 ASWDVAKKQDNRAKRYGHI IAYDSRVLQOVEDPSSDYINANYIDGQRPISHYIATQ 960  
Qy 960 GPVHETVDFWRMIWQEOSACIVMVTNLVGRVKCYKYPDDTEVYGDVKVTCVEMEP 1019  
Db 961 GPVHETVDFWRMIWQEOSACIVMVTNLVGRVKCYKYPDDTEVYGDVKVTCVEMEP 1020  
Qy 1020 ABYVVRTFTLERRGNEIREVKQFHTGWPDHGVPHYATGLLSFTRVKLSNPPSAGPIV 1079  
Db 1021 ABYVVRTFTLERRGNEIREVKQFHTGWPDHGVPHYATGLLSFTRVKLSNPPSAGPIV 1080  
Qy 1080 VHCASAGRTGCVIVIDIMLMAEREGVVDIYNCVKALRSRRINNMVQTEEQYIFTHDAIL 1139  
Db 1081 VHCASAGRTGCVIVIDIMLMAEREGVVDIYNCVKALRSRRINNMVQTEEQYIFTHDAIL 1140  
Qy 1140 EAELCGETAIPVCEPKAAAYFDMIRIDSQTNSSHLKDEFQTLNSVTPRLQAECDSCIAPLR 1199  
Db 1141 EAELCGETAIPVCEPKAAAYFDMIRIDSQTNSSHLKDEFQTLNSVTPRLQAECDSCIAPLR 1200  
Qy 1200 NHDKNRFMDMLPPDRCLPLITIDGESSNYINAAALMDSYRQPAAFIVTQYPLPNTVKQFW 1259  
Db 1201 NHDKNRFMDMLPPDRCLPLITIDGESSNYINAAALMDSYRQPAAFIVTQYPLPNTVKQFW 1260  
Qy 1260 RLVDYDGGCTSIWLNNEVDLSQGCPOYWPBEGMLRYGPIQVECMSCMDCDVNIRIFLCN 1319  
Db 1261 RLVDYDGGCTSIWLNNEVDLSQGCPOYWPBEGMLRYGPIQVECMSCMDCDVNIRIFLCN 1320  
Qy 1320 LTRPQEGYLMVQOFOYLGWASHREVPGRSKRSFLKLIQVEKQWEEKGEGRITIIHCLNG 1379  
Db 1321 LTRPQEGYLMVQOFOYLGWASHREVPGRSKRSFLKLIQVEKQWEEKGEGRITIIHCLNG 1380  
Qy 1380 GRSQMFCAIGIIVEMVKQNVVDVPHAVKTI RNKSKPNVWEAPEQVRFICYDVALYBLS 1439  
Db 1381 GRSQMFCAIGIIVEMVKQNVVDVPHAVKTI RNKSKPNVWEAPEQVRFICYDVALYBLS 1440

A48066  
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type kappa precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 21-Jan-1994 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
C;Accession: A48066  
C;Jiang, Y.P.; Wang, H.; D'Eustachio, P.; Musacchio, J.M.; Schlessinger, J.; Sap, J.  
Mol. Cell. Biol. 13, 2942-2951, 1993  
A;Title: Cloning and characterization of R-PTP-kappa, a new member of the receptor prote  
ion.  
A;Reference number: A48066; MUID:93233655; PMID:8474452  
A;Accession: A48066  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1457 <JIA>  
A;Cross-references: UNIPROT:P35822; GB:L10106; NID:G293771; PIDN:AAA40021.1; PID:G293772  
A;Experimental source: brain  
A;Note: sequence extracted from NCBI backbone (NCBIP:129880)  
C;Complex: after cleavage by a furin-like endopeptidase, the two chains remain associate  
C;Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe  
tyrosine-phosphatase homology  
C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tran  
F;1-28/Domain: signal sequence #status predicted <SIG>  
F;29-1457/Product: protein-tyrosine-phosphatase, receptor type kappa, uncleaved #status  
F;29-641/Product: protein-tyrosine-phosphatase, receptor type kappa, chain 1 #status pre  
F;29-641,644-755/Domain: extracellular #status predicted <EXT>  
F;30-193/Domain: MAM homology <MAM>  
F;208-271/Domain: immunoglobulin homology <IMM>  
F;293-371/Domain: fibronectin type III repeat homology <FN3A>  
F;388-477/Domain: fibronectin type III repeat homology <FN3B>  
F;489-581/Domain: fibronectin type III repeat homology <FN3C>  
F;593-682/Domain: fibronectin type III repeat homology <FN3D>  
F;644-1457/Product: protein-tyrosine-phosphatase, receptor type kappa, chain 2 #status  
F;756-772/Domain: transmembrane #status predicted <TMN>  
F;773-1457/Domain: intracellular #status predicted <INT>  
F;841-1457/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F;922-1148/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F;1218-1442/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F;100,139,210,415,423,435,461,551,585,589,606,689/Binding site: carbohydrate (Asn) (cova  
F;215-269/Disulfide bonds: #status predicted  
F;643-644/Cleavage site: Arg-Glu (furin-like endopeptidase) #status experimental  
F;1100/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1106/Binding site: substrate phosphate (Arg) #status predicted  
F;1394/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1400/Binding site: substrate phosphate (Arg) #status predicted

Query Match 98.2%; Score 7571; DB 1; Length 1457;  
Best Local Similarity 97.3%; Pred. NO. 0;  
Matches 1419; Conservative 13; Mismatches 6; Indels 20; Gaps 4;

Qy 1 MDTTAAALPAFVALLLSLSPHLLGSAGQSFAGGCTFDDGGACDYHQDLYDDFEWVHV 60  
Db 1 MD-VAAALPAFVALWLLYPHLLGSALGQSFAGGCTFDDGGACDYHQDLYDDFEWVHV 59  
Qy 61 SAQEPHYLPPEMPOGYSYMI VDSDDHDPCEKARLQLPTMKENDTHCIDFSYLLYSQGLNP 120  
Db 60 SAQEPHYLPPEMPOGYSYMWVDSNHDPEKARLQLPTMKENDTHCIDFSYLLYSQGLNP 119  
Qy 121 GTLNILVRNKGPLANPIWNVGTGTRDMLRAELAVSTFWPNQYQVIFEAEVSGRSGYI 180  
Db 120 GTLNILVRNKGPLANPIWNVGTGTRDMLRAELAVSTFWPNQYQVIFEAEVSGRSGYI 179  
Qy 191 AIDDIQVLSYPCDKSPHFLRLGDVEVNAQNATFCIATGRDAVNKLQORNGEDIPV 240  
Db 180 AIDDIQVLSYPCDKSPHFLRLGDVEVNAQNATFCIATGRDAVNKLQORNGEDIPV 239  
Qy 241 AQTKNINRRFAAASFRLEQVTKDQLYRCVTSQSRGSGVSNFAQLIVREPPRPPIAPOL 300  
Db 240 AQTKNINRRFAAASFRLEQVTKDQLYRCVTSQSRGSGVSNFAQLIVREPPRPPIAPOL 299  
Qy 301 LGVGPTYLLIQLNANSIIGDGPILKVEYRMTSGSWTETHAVNAPTYYKLMLHLDPDTEYE 360  
Db 300 LGVGPTYLLIQLNANSIIGDGPILKVEYRMTSGSWTETHAVNAPTYYKLMLHLDPDTEYE 359

Qy 361 IRVLLTRPGEQGLPGPPLITRTKCAEPMTPTKTLKIAEIOARRIAVDWESLGNITRC 420  
Db 360 IRVLLTRPGEQGLPGPPLITRTKCAEPMTPTKTLKIAEIOARRIAVDWESLGNITRC 419  
Qy 421 HTFNVTICYHYFRGHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKSEEE 480  
Db 420 HTFNVTICYHYFRGHNESKADCLMDPKAPQHVNVNHLPPYTNVSLKMLITNPEGRKSEEE 479  
Qy 481 TIIOTDEVDVPGPVKSLQGTSPFNKIPLNKKEPLDNGIITQVEISYSSIRSDPAPVPV 540  
Db 480 TIIOTDEVDVPGPVKSLQGTSPFNKIPLNKKEPLDNGIITQVEISYSSIRSDPAPVPV 539  
Qy 541 AGPQTQVSNLWNSHHVFMHLPGTQYOFFTRASTVKGFGPATINVTNLSAPLDPYE 600  
Db 540 AGPQTQVSNLWNSHHVFMHLPGTQYOFFTRASTVKGFGPATINVTNLSAPLDPYE 599  
Qy 601 GVDASLNATETITVLLRPAQAKGAPISAYQIVVEELPHPTKREAGAMECYQVPVTYQN 660  
Db 600 GVDASLNATETITVLLRPAQAKGAPISAYQIVVEELPHPTKREAGAMECYQVPVTYQN 659  
Qy 661 AMSGAGPYFAAELPPGNLPPAPFTVGDNRTYQGFNPPPLAPRGYNIYFOAMSSVEKE 720  
Db 660 ALSGAGPYFAAELPPGNLPPAPFTVGDNRTYQGFNPPPLAPRGYNIYFOAMSSVEKE 719  
Qy 721 TKTCQVRIATK-AATEPEVTPDPAKQTDVVVKIAGISAGILVFIILLVILVVKSKL 779  
Db 720 TKTCQVRIATKAAATEPEVTPDPAKQTDVVVKIAGISAGILVFIILLVILVVKSKL 779  
Qy 780 AKKRDAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSITFMDQHNFSRY----- 831  
Db 780 AKKRDAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSITFMDQHNFSRPLNDPLVPT 839  
Qy 832 ----ENHSATAESRLLDVPRYLCEGTSPYQTQLHPAIRVADLLOHINLMKTSDSYGF 887  
Db 840 AVLDEHSATAESRLLDVPRYLCEGTSPYQTQLHPAIRVADLLOHINLMKTSDSYGF 899  
Qy 888 KEEVESFEFGOSASWDVAKDONAKRYGNI IADHSRVILQVEDDPSSDIYANVYI- 946  
Db 900 KEEVESFEFGOSASWDVAKDONAKRYGNI IADHSRVILQVEDDPSSDIYANVYI 959  
Qy 947 ----DGYQPSHYIATQGPVHETVDFWRMIWQEQSACIWMVNLVGEVRKCYKWPD 1001  
Db 960 IWLVRDGYQPSHYIATQGPVHETVDFWRMWQEQSACIWMVNLVGEVRKCYKWPD 1019  
Qy 1002 DTEVYGDVKVTCVEMSEPLAEYVVRFTLERRGYNEIREVKQFHTGWPDHGVPYHATGLL 1061  
Db 1020 DTEVYGDVKVTCVEMSEPLAEYVVRFTLERRGYNEIREVKQFHTGWPDHGVPYHATGLL 1079  
Qy 1062 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCVIIVIDIMLDMAREGVVDIYNCVKALRSRR 1121  
Db 1080 SFIRRVKLSNPPSAGPIVHCSAGAGRTGCVIIVIDIMLDMAREGVVDIYNCVKALRSRR 1139  
Qy 1122 INNVQTEQYIFIHDAILEACLCGETAIPVCEPKAAVDFMIRIDSQTNSSHLKDEFQTLN 1181  
Db 1140 INNVQTEQYIFIHDAILEACLCGETAIPVCEPKAAVDFMIRIDSQTNSSHLKDEFQTLN 1199  
Qy 1182 SVTPRLQAECDCSIACLPRNHDKNRFMDMLPDRCLPFLITIDGSSNYINAALMDSYRQP 1241  
Db 1200 SVTPRLQAECDCSIACLPRNHDKNRFMDMLPDRCLPFLITIDGSSNYINAALMDSYRQP 1259  
Qy 1242 AAFIVTQYPLNTVKDFWRLVYDYGCTSI VMLNEVDLSQGCPOQVWPEEGLRYGPIQVEC 1301  
Db 1260 AAFIVTQYPLNTVKDFWRLVYDYGCTSI VMLNEVDLSQGCPOQVWPEEGLRYGPIQVEC 1319  
Qy 1302 MSCMDCDVNRIPIRINLFRPOBYLWVOQFYLGHASHREVPGSRKFLKILQVEKW 1361  
Db 1320 MSCMDCDVNRIPIRINLFRPOBYLWVOQFYLGHASHREVPGSRKFLKILQVEKW 1379  
Qy 1362 QEEWKEGEGRTIHLNGGGRSGMFCAGIIVEMVKQNVVDVPHAVKTLRNSKPNVEA 1421  
Db 1380 QEEWKEGEGRTIHLNGGGRSGMFCAGIIVEMVKQNVVDVPHAVKTLRNSKPNVEA 1439  
Qy 1422 PEQRYFCYDVALEYLESS 1439

Db 1440 PEQRYFCYDVALEYLESS 1457

## RESULT 3

S17669

Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type mu precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 22-Nov-1993 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: S17669

FEBS Lett. 290, 123-130, 1991

A:Title: Cloning, expression and chromosomal localization of a new putative receptor-like

A:Reference number: S17669; MUID:92008644; PMID:1655529

A:Accession: S17669

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1452 <GEB>

A:Cross-references: UNIPROT:P28827; EMBL:X58288; NID:g32455; PIDN:CAA41226.1; PID:g32456

A>Note: the authors translated the codon TAT for residue 1340 as His, TTC for residue 13

C:Genetics:

A:Gene: GDB:PTPRM; PTPRL1

A:Cross-references: GDB:128093; OMIM:176888

A:Map position: 18p11.2-18p11.2

C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe

-tyrosine-phosphatase homology

C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tran

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-1452/Product: protein-tyrosine-phosphatase, receptor type mu #status predicted <MAT

F:21-745/Domain: extracellular #status predicted <EXT>

F:22-184/Domain: NAM homology <NAM>

F:199-262/Domain: immunoglobulin homology <IMM>

F:284-364/Domain: fibronectin type III repeat homology #status atypical <FN3A>

F:379-470/Domain: fibronectin type III repeat homology <FN3B>

F:482-574/Domain: fibronectin type III repeat homology <FN3C>

F:586-674/Domain: fibronectin type III repeat homology <FN3D>

F:746-762/Domain: transmembrane #status predicted <TM>

F:763-1452/Domain: intracellular #status predicted <INT>

F:842-1452/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:923-1143/Domain: protein-tyrosine-phosphatase homology <PTP>

F:72,92,131,249,406,414,448,454,534,544,598,651,681/Binding site: carbohydrate (Asn) (co

F:206-260/Disulfide bonds: #status predicted

F:1095/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1101/Binding site: substrate phosphate (Arg) #status predicted

F:1389/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1395/Binding site: substrate phosphate (Arg) #status predicted

Query Match 62.4%; Score 4807; DB 1; Length 1452;

Best Local Similarity 60.8%; Pred. No. 1.4e-318;

Matches 889; Conservative 206; Mismatches 326; Indels 42; Gaps 8;

Qy 4 TAAALPAFVALLLSPWLLGSAQGSAGGCTFDGPGACDYHQLYDDFEVHVSQAQ 63

Db 3 TLGTCLATLGLL-----TAAGTFFGGCLFDFEPYTCGYSQSEGGDFNWEQVNTL 54

Qy 64 EPHVLPPEMQGSVMIVDSDDHDPGEKARLQLPMTKENDTHCIDFSYLLXSOKLNPOTL 123

Db 55 TKTSIDPFWPSSGSLMVNAGREGQARHLLLPOLKENDTHCIDFHFVSKSNPGLL 114

Qy 124 NILVRNKGPLANPINVVTGTRDMLRAELAVSTFWPNEYQVIFEAEVSGSGSYIAID 183

Db 115 NVYKVNNGPLGNPINWISGDPTRTNRAELAISTFWPNEFQVIFEV-ITSGHQYLAI 173

Qy 184 DIQVLSYPCDKSPHFLRLGDEVNAGQATFQCIATGRDAVHNKLMWORNGEDIPVAQT 243

Db 174 EVKVLGHPCRTTRHFLRIQNEVNAGQFATFQCSAIGRTVAGDRLMTQGGIDVRDAPLKEI 233

Qy 244 KTNHRRFAASFRLEQVTKTDQDLRYCVTQSESGSVNFAQLIVRPPRPIAPPPQLLGV 303

Db 234 KVTSSRRPIASFNVNTTKEDACKYRCWIRTEGVSIGNSIAELVKEGPPPIAPPPQLASV 293

Qy 304 GPTYLLIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMHLPDPTETEYIRV 363

Db	294	GATYLMITQLNANSINGDGPVAREVEYCTASGWNDRQPVDSYKIGHLDPOTEYISV	353
Qy	364	LLTRPGGGTCLPGPLITRTKCAENRWTPKTKIAEIOARRTADWDESLGYNTTCHTF	423
Db	354	LLTRPGGGTSGPGALRTRTKCADPWGRPKUEVVEVKSRQITIRWEPPGYNVTRCHSY	413
Qy	424	NVTICYHYFRGHNSKAD--CLWMDPKAPQHVNVNHLPPYTNVSLKMLITLTPGKRESEET	481
Db	414	NLTVHYCYVGQGOVREEVSWDTENSHPOHTITNLSPYTNVSKLILMNPGRKESQEL	473
Qy	482	IIQTDENVPGVPVKSLQGTSEFNKIFLNKKEPLDPNGIIITQYEISYSSIRSDPVPVPA	541
Db	474	IVOTDEDLPGAVPTEISQGSTFEBKIFLOWREPTQTYGVITLVEITYKAVSSDPDEIDL	533
Qy	542	GPQTVNLNNSHTHVFMHLHPCGTYOFFTRASTVKGFGPATAINVNTNLSAPLDDYEG	601
Db	534	NQSGRVSKLGNETHFLFGLPGTYGTYFTTRASTAKFGPPANQFTTKLSAVSMPAYE-	592
Qy	602	VDASLNETAATTITVLLRPAQAKGAPIISAYQIVVEELHPHRTKREAGAMECVQPVTVQNA	661
Db	593	LETPLAQTDNTVTVMKXPAHSRGAPVSVYQIVVEEERPRETKTTELKCYPPVPIHQNA	652
Qy	662	MSGGAPYFAABLDPGNLPBAPPTVGDNRTYQGFWMNPPLAPRGYNIYFOAMSSVEKET	721
Db	653	SLNLSQYVFAAEFPADSLQAAPPTIGDNKTNGYWNVTLLPYKSVRIYFQAASRANGET	712
Qy	722	KTCOVRTAKTAATEPEBEVIDPPAKOTDRVVKIAGISAGILVFIILLIWLVLVKKSKLAK	781
Db	713	KIDCVQVATGAA--TPKPVPEPEQOTDHTVKIAGVIAGILFVIIIFGVVLVMMKRRKLAK	771
Qy	782	KRKDAMGNTQREMTWMVNMADRSVADOSTLHAEDPLSITFMDQHNFSPRY-----	831
Db	772	KXKETMSTQREMTVMVNSMDKSVABQGTNCDE---AFSPMDTHNLNCRSVSPSSFTMK	828
Qy	832	-----ENHSATAESSRLLDVPRY-LCEGTESPYQTQQLHPAIRVADLLQH	875
Db	829	TNTLSTSVPSNSYYPDETHMTWASDTSLSVQSHYTKREPADVPYQTQQLHPAIRVADLLQH	888
Qy	876	INLMKTSDDSFGFKEEYESFPQGSASWDVAKQONRAKNRYGMIAYDHSRVILQPVEDD	935
Db	889	ITQMKCAEGYGFKEEYESFPQGSAPWDSAKKDNRNMKNRYGMIAYDHSRVLRLOTIEGD	948
Qy	936	PSSDIYINANYIDGYORPSHYIATQCPVHETVYDPFWRMIWOQSACIYVWVTLNVEVGRVKC	995
Db	949	TNSDIYINGNYIDGTHRPNNHVIATQCPHQEIIYDFWRMVWHTASIIWVTLNVEVGRVKC	1008
Qy	996	YKYWPDDETVYDGPVKTCVMEPLAEYVYVFTTLRERGYNREIRVVKQFHFTGMPDHGVPY	1055
Db	1009	CKYWPDDTEIYKDIKVTLIETELAEYVIRTFPAKEKRGVHEIREIRQFHFTGMPDHGVPY	1068
Qy	1056	HATGLLSPFIRVKLSNPSGAPIVVHCSAGAGRTGCYIVIDIMLDMAREGVWDIYNVCVK	1115
Db	1069	HATGLLGFVRQVKSKSPSAPGLVVHCSAGAGRTGCFYIVIDIMLDMAREGVWDIYNVCR	1128
Qy	1116	ALRRRRNMVQTEBQYFIHDAILEACLCEBETAPVCEKAAYPDMIRIBDSQTNSSHLD	1175
Db	1129	ELRSRRNMVQTEBQYFIHDAILEACLCEGDTSPASQVRSLYYDMKMLDPQTNSSQIKE	1188
Qy	1176	EFQTLNSVTPRLQADECSIACLPRNHDKNRPMDLPPDRCLPLFLITIDGESSNYINAALM	1235
Db	1189	EFRTLNMVTPTLRVEDCSIALPRNHEKNRCMDILPDRCLPLFLITIDGESSNYINAALM	1248
Qy	1236	DSYEQPAAFIYQYPLNTWKDFWRLIYDYDCTSIUMLNEVDLSQGCPCQYWPBEGMLRYG	1295
Db	1249	DSYEQPSAFIYQYPLNTWKDFWRLIYDVHCTSVNMNLNDVDPALQCFQYWPENGVRHG	1308
Qy	1296	PIQVECKMSCMDCDVINRIFRICMLTRPOEGLVMVQOYFVLGWAHSREVPGSKRSFLKLI	1355
Db	1309	PIQVEFFSADLEEDIISRIFRINYAARPQDGYRMVQOYFVLGWPWYRDTVPVSKRSFLKLI	1368
Qy	1356	LQVEKQWBEWKEGBGRITIIHCLNGGGRSGMPCAIIGIVEMVQRQNVYDVFAVKTLENSK	1415

Db 1369 RQVDKMQBEYNGGEGFTVVHCLNCGGRSGTFCFAISIVCEMLRHQRTVDVPHAVKTLLRNKK 1428

Qy 1416 PNWVEAPQRYRCFYDAVALEYLBS 1438  
||||| :|||:|||:|||||

Db 1429 PNWDLLDQYFCYEVALEYLNS 1451  
||||| :|||:|||:|||||

RESULT 4

S17670 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type mu precursor [validated] - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Nov-1993 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
C;Accession: S17670  
R;Gebblink, M.F.B.G.; van Etten, I.; Hateboer, G.; Suijkerbuijk, R.; Beijersbergen, R.L.,  
FEBS Lett. 290, 123-130, 1991  
A;Title: Cloning, expression and chromosomal localization of a new putative receptor-like  
tyrosine-phosphatase homology  
A;Reference number: S17669; MUID:92008644; PMID:1655529  
A;Accession: S17670  
A;Molecule type: mRNA  
A;Residues: 1-1452 <GB>  
A;Cross-references: UNIPROT:P28828; EMBL:X58287; NID:g53234; PIDN:CAA41225.1; PID:g53235  
C;Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe-  
tyrosine-phosphatase homology  
C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tran-  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-1452/Product: protein-tyrosine-phosphatase, receptor type mu #status predicted <MAT>  
F;21-745/Domain: extracellular #status predicted <EXT>  
F;22-184/Domain: MAM homology <MAM>  
E;199-262/Domain: immunoglobulin homology <IMM>  
F;284-382/Domain: fibronectin type III repeat homology <FN3A>  
F;379-470/Domain: fibronectin type III repeat homology <FN3B>  
F;482-574/Domain: fibronectin type III repeat homology <FN3C>  
F;586-674/Domain: fibronectin type III repeat homology <FN3D>  
F;746-762/Domain: transmembrane #status predicted <TMN>  
E;763-1452/Domain: intracellular #status predicted <INT>  
F;842-1452/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F;923-1143/Domain: protein-tyrosine-phosphatase homology <PTP>  
F;1213-1437/Domain: protein-tyrosine-phosphatase homology <PP2>  
F;72\_92\_131\_249\_406\_414\_448\_454\_534\_544\_598\_651\_681/Binding site: carbohydrate (Asn) (co-  
F;206-260/disulfide bonds: #status predicted  
E;1095/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1101/Binding site: substrate phosphate (Arg) #status predicted  
F;1389/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1395/Binding site: substrate phosphate (Arg) #status predicted

Query Match 62.1%; Score 4791; DB 1; Length 1452;  
Best Local Similarity 61.3%; Pred. No. 2.le-317;  
Matches 885; Conservative 205; Mismatches 320; Indels 34; Gaps 7;

Qy 23 LLGSAGQGFSAAGCTFDGPGACDYHDLYDDPEWHVSQAEPHYLPENPQGSMYIVDS 82  
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

Db 14 LLLTAAGETFSGGCLFDEPYSTCYGSAQEDDFNWEQVNTLTTRPTSDPWMPSGSFMVLNT 73  
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

Qy 83 SDHDPGEKARQLQPMTKENDTCIDFSLYSQGLNPGLTNILVRNKGPLANPIWNVT 142  
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

Db 74 SKCPBGCAHLLPLQKENDTHCIDPHYVSSKSNAAPGLLVKNVNGPLGNPNIS 133  
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

Qy 143 GFTGRDWLRAEALVSTFWPENYQVIPAEAYSGRSRGYAIIDDIQVSPCDKSPHFRLG 202  
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

Db 134 GDPTRTWRAELAISTFWPENFYQVIFEV-VTSCHQGVLAIDEVKVLGHPCPTRTEPHFLRIQ 192  
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

Qy 203 DVENVAGNAVPOCIATGRDAVHNKLWLQRNGEDI PVAQTKNINHRFPAAASFLOEVTK 262  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 193 NVEVNAGOFATPQCISAIGRTVAGDLRWLGQIDVRDAPLKEIKVTSRRFTASFNWVNTTK 252  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 263 TDODLYRCVTOSERGSGVSNFAOLI VREPRPIAPPOLLGVGPPTYLLIQLNANSIIIGDGP 322  
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

Db 253 RDAGKYRCMI CTGEGVGISNYAELVVKPEPVPIAPQLASVGATYLWIQLNANSINGDGP 312  
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

Qy 323 IILKEVEYRMTSGSWTETHAVNAPTYYKLWHLDPDPTTEYIRVLLTPGEGGTGLPGPPLIT 382  
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

Db 313 IVAREVEYCTASGSWNDRDPVDSYKI GHLDPDTEYISVLLTPGEGGTGSGPALRT 372  
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

QY 383 RTKCAEPMRTPKTLKIAEIQARRIADVWESLGYNIITRCHTFNVTICHYHFRGHESKAD- 441  
DB 373 RTKCADPMRGPRKLEVVVEVSRQITIRWEPFGYNVTRCHSYNLTVHYGYQVGQGVRRSE 432  
QY 442 -CLDMDPKAQHVNVNHPPTVNSLKMILNPNPEGRKESEETIIQTDSDVPGVPVKSLQG 500  
DB 433 VSWDTDNHSHQHITITNLSPYTVNSVKLIJLNNPEGRKESQELTVQTDSDLPNAVPTESIQG 492  
QY 501 TSPENKILFNWKEPLDNGIITQVEISYSIRSPPDPAVPVAGPQPTQVSNLWNSTHHVFMH 560  
DB 493 SAFEKEKIFLOWREPTQTYGVTITLYEITYKAVSSPDPBIDLSNQSGRVSKLGNETHPLFPFG 552  
QY 561 LHPGTTTYQFFIRASTVKGFGPATVNTNISIAPTLDPYEGVDASINETAITITVLRLPA 620  
DB 553 LYFGTTTYSFIRASTAKFGGPPATNQFTTKISAPSPAYE-FETPLNQTDNTVTVMLKPA 611  
QY 621 QAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTVYQAMSGAPYFAAEALPPGNLP 680  
DB 612 QSRGAPSVVQIVVEERPRRTKKTTEILKCYVPVPIHFQNASILNSQYFAAEFPADSLQ 671  
QY 681 EPAPFTVGDNRITYOGFWNPPLAPRGKYNIIYFQAMSSVEKETQCVRIATKAATEPEVI 740  
DB 672 AAQPFTIGDNKTYNGVWNTPLPHKSYRIYVQAASRANGETKIDCVRVATKGAV-TPKPV 730  
QY 741 PDPAKQTDVVKIAGISAGILVFIILLVILVVKSLAKKRDAMGNTROETHWVNA 800  
DB 731 PEPEKQTDHTVKIAGVITAGLILFVIFLGVVLVMMKRLAKRKETMSSRQENTVMVNS 790  
QY 801 MDRSYAQDQSLHAEDPLSITFMDOHNSPRY-----ENHS 835  
DB 791 MDKSYAEQGTNCDE---AFSGMTHNLNGRSVSPSFTWKTNTLSTSVNSYVPDETHI 847  
QY 836 ATAESRLDLDPVRY-LEGTESPYQTQQLPAIRVADLLOHINLMKTSDSYGFKEEYESF 894  
DB 848 MASDTSLSLAQPHYTKKREAADVPQTQQLPAIRVADLLOHIQMKCAEGYGFKEEYESF 907  
QY 895 FEQGSASVDVAKQDNRAKRYGNIITAYDHSRVLQVPEDDPSDDYINANYIDGYQRPSPH 954  
DB 908 FEQGSAPWDSAKDENMKRYGNIITAYDHSRVLQVLEGNDSYINGYIDGYRPNH 967  
QY 955 YIATQGVPHVTVDVFWEMIWEOESACIVMTVNLVEGVRKCYKVPDDETVYGFKVTVCV 1014  
DB 968 YIATQGVPMQETIYDFMRWVHENTASIIIMTVNLVEGVRKCYKVPDDETVYIDKIKVTLI 1027  
QY 1015 EMPLAEYVYVTRFTLERRGYNEIREVKQHFHTGMPDHGVPHYATGLLSFIRRVKLSNPPS 1074  
DB 1028 DTELLAEYVIRTAFAVEKRGHIREIRQHFHTGMPDHGVPHYATGLLGFVRQVKSPPN 1087  
QY 1075 AGPIVHCSAGAGRTGCVIIVIDIMLMAEREGVVDIYNCVKALRSRRINNVQTEEQYIFI 1134  
DB 1088 AGPLVHCSAGAGRTGCFIIVIDIMLMAEREGVVDIYNCVRELRSRRINNVQTEEQYVI 1147  
QY 1135 HDAILAEACLCGETAI PVCEFKAAVFMIRIDSTQNSSHLKDEFQTLNVTPLRQAECSI 1194  
DB 1148 HDAILAEACLCGDSIPSASQVRSYLYDMKNLDPQTNSSQIKEEFTLNMVPTPLRVEDCSI 1207  
QY 1195 ACLPRNHDKRFDMLPDRCLPELITIDGESSNYINAAIMDSYROPAAFIIVTQYPLPNT 1254  
DB 1208 ALPLRHNKRCMDILPDRCLPELITIDGESSNYINAAIMDSYKQPSAIVTQHPLPNT 1267  
QY 1255 VKDFWRLIYDYGCTSIYVLMNEVDSLQSCQCPQYWPBEGMLRYGPIQVECMSCMDVINRI 1314  
DB 1268 VKDFWRLIYDYGCTSVVLMNDVDPALCPQYWPBEGVHRGPIQVEFVSADLEEDIISRI 1327  
QY 1315 FRICNLTRPQEGYLMVQFOYLWASHREVPGSKRSPFLKILQVEKKQBEWKEGEGHTII 1374  
DB 1328 FRIYNASRPQDGRHVMVQOFLGMPMYRDTFVSKRSPFLKILRQVDMQEEYNGEGEPTVV 1387  
QY 1375 HCLNGGGRSGMFCAGITGVWBMVKRONVVDVFAVKTLRNSKPNVPEAPGYRFCYDVALE 1434  
DB 1388 HCLNGGGRSGTFCASIVCEMLRHQRTVDVFAVKTLRNKNPNVLLDQYKFCYCEVALE 1447  
QY 1435 YLES 1438

Db 1448 YLNS 1451

## RESULT 5

JC5290

protein-tyrosine-phosphatase (EC 3.1.3.48) - human

N/Alternate names: Phosphotyrosine phosphatase

C/Species: Homo sapiens (man)

C/Date: 16-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 09-Jul-2004

C/Accession: JC5290

R/Wang, B.; Kishihara, K.; Zhang, D.; Hara, H.; Nomoto, K.

Biochem. Biophys. Res. Commun. 231, 77-81, 1997

A/Title: Molecular cloning and characterization of a novel human receptor protein tyrosi-  
ma cells.

A/Reference number: JC5290; MUID:97223402; PMID:9070223

A/Accession: JC5290

A/Molecule type: mRNA

A/Residues: 1-1436 &lt;MAN&gt;

A/Cross-references: UNIPROT:O00197; GB:U73727; NID:91923222; PIDN:AA551343.1; PID:9192323

C/Comment: This enzyme belongs to type II receptor protein tyrosine phosphatase which me  
and an immunoglobulin-like domains.

C/Genetics:

A/Gene: hprt-J

C/Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe

-tyrosine-phosphatase homology

C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F/22-188/Domain: MAM homology &lt;MAN&gt;

F/203-266/Domain: immunoglobulin homology &lt;IMM&gt;

F/288-366/Domain: fibronectin type III repeat homology &lt;3PR&gt;

F/826-1436/Domain: leukocyte common antigen cytosolic domain homology &lt;LAC&gt;

F/903-1123/Domain: protein-tyrosine-phosphatase homology &lt;PTP1&gt;

F/1193-1418/Domain: protein-tyrosine-phosphatase homology &lt;PTP2&gt;

F/1075/Active site: Cys (phosphocysteine intermediate) #status Predicted

F/1081/Binding site: substrate phosphate (Arg) #status Predicted

F/1370/Active site: Cys (phosphocysteine intermediate) #status Predicted

F/1376/Binding site: substrate phosphate (Arg) #status Predicted

Query Match 60.1%; Score 4632; DB 2; Length 1436;

Best Local Similarity 60.1%; Pred. No. 1.4e-306;

Matches 867; Conservative 211; Mismatches 339; Indels 26; Gaps 10;

QY 6 AAALPAFVALLLSLPMLLGSAQGFSAAGCTFD---DGFACDYHQDLVDFEWHVSA 62  
DB 4 AQALVALATFQLCAP-----ETETPAAGCTFEASDPAVPCEYSQAQYDDFQWEQVRI 56  
QY 63 QEHYLPPEMQSGSYMLVDSSDDHDPGEKARLQLPYTKENDTHCIDSYLLYSQKLNPGT 122  
DB 57 HPTRAPADLPFGSYLMVNTSQAPQORAHVIFQSLSENTHCQVFSYFLYSRDGHSPT 116  
QY 123 LNTLVNKGPLANPIWNVTFGRDWLRAELAVSTFWPNEYQVIFPAEYSGRSGYIAI 182  
DB 117 LGYVAVNGGPGLSAVWNTGSHGRWQHQAELAVSTFWPNEYQVIFALLSPDRGYMGL 176  
QY 183 DDIOVLSYPCDKSPHFLRLRGDVEVNAQONATFCIATGRDAVNKMLQRRNGEDIPVAQ 242  
DB 177 DDILLSPYCAKAPHFSRLGSDVEVNAQONASFOCAAGRAAEERFLQSQGALVPAAG 236  
QY 243 TKNINIRRAASFRLEQVTKDQDLVRCVTSQSRGSGVSNFAQLIVREPRPTAPPOLLG 302  
DB 237 VRHISRRFLATPPLAAVSRAEQDLVRCVSAQPRGAGVSNFAELIVKEPPTTAPPOLLR 296  
QY 303 VGPYLLIOLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTLYKLWHLDDPDEYIR 362  
DB 297 AGTYLIILQNTNSIIGDGPVIRKEIEYRMARGFWAEVHVAISLQTYKLWHLDDPDEYIS 356  
QY 363 VLTATREBEGGTGLPGPLITRTKCAEPMRTPKTLKIAEQARRIADVWESLGYNITRCHT 422  
DB 357 VLLTRFGDGGTGRPGPLISRTKCAEPMRAPKGLAFAEIQARQLTLQWEPLGYNVTRCHT 416  
QY 423 FNTVICYHVRG--HNESKADCLMDPKAPQHVNVNHPPTVNSLKMILNPNPEGRKESEE 480  
DB 417 YTVSLCYHVTLGSSHNQITRECVCYKTSRYTIKNLLPYRNVHVRVLTNPPEGRKEGKE 476

Qy 481 TIIQTDEVDVGPVPVKSLQGTSPFNKIFLNKKEPLDPNGIITQYBEISYSSSTRSDPAVPV 540  
Db 477 VTQFDEDPVSGIAAESLFTPLEDMIFLKEEPEQENGLITQYBEISYQSSTESSDPAVV 536  
Qy 541 AGPPTVSNLWNSTHHVMHLHPGTYGFFTRASTVKGFGPATAINVTNINSAPLDPYE 600  
Db 537 PGPRTIISKLNETHYVSNLHPGTYLFSVARTGKGFGQAALTEITNINSASF-DYA 595  
Qy 601 GVDASLNETAATTITVLLRPAQAGAPISAYQIVVEELHPHRTKRBAGAMECYQVPVTVQN 660  
Db 596 DMPSPLGSESENTITVLLRPAQGRGAPISVYQIVVEERARLRREPQGGQDCCFPVPLTPEA 655  
Qy 661 AMSGAPYFAAELPPGNLPPAPPTVGDNRITYQGFNPPPLAPRKGYNIYQAMSSVEKE 720  
Db 656 ALARGLVHYFGAELAASSLPAMPPTVGDNTYRGFNPPLEPRKAYLIYFQAASHLKG 715  
Qy 721 TKTCVRIATKAATEPEVIPPQAKQTRVVKIAGISA-GILVFTLLLVLLVILVKSKL 779  
Db 716 TRLNCIRIARKAACKESKRPLEVSORSSEMGILIGICAGGLAVLILLGALIIIVIRKGP 775  
Qy 780 AKRKDAMGNTRQEMTHVMNANDRSYADQSTLHAEDPLSITFMDQHNFSRYENHS--AT 837  
Db 776 VNMTK-ATVNYRQETHMMSAVDRSFTDQSTLOEDERGLGSFMDTHGYSTRGQDRSGVT 834  
Qy 838 AESSRLLDVPRVLCBGTSPYOTQOLHPAIRVADLLQHLINLWKTSDSYGFKEEYSPFEG 897  
Db 835 EASSLLGSGRRPCRGKSPVHTGQHPAVRVADILLQHLINQWKTAEYGFKEEYSPFEG 894  
Qy 898 QSASDVAKKQNRKAKRYGNIIVDHSRVILQPVDEDDPSDYINANYIDGQRPESHVIA 957  
Db 895 ---WDATKKDKKVGSKQEPMPAYDRHRVKLHPLMGDPNADYINANYIDGTHSRNHPIA 950  
Qy 958 TQGPVHETVDFWRMIWQESACIYVMVNLVEVGRVKCYKYPDQTEYVYGFKYTCVEME 1017  
Db 951 TQGPKEVNYDFWRVWQEHCSIIWMIKLVGVGRVKSRYWPEDSDTYGDIKMLVKTE 1010  
Qy 1018 PLAEVYVTFTLRRGYNEIREVKQFHTGWPDHGVPHATGLLSFIRRVKLSNPPSAGP 1077  
Db 1011 TLAEVVVRTFALERRGYSARHEVRQFHTAWPEHGVPHATGLLAFIRRVKASTPPDAGP 1070  
Qy 1078 IIVHCSAGAGTCYIVIDIMDMAERGVVDIYNCVKALSRRLNMVQTEQYIFIHDA 1137  
Db 1071 IIVHCSAGTGTGCVIYLDVMDMAECGVDIYNCVKTLCSRRVNMVQTEQYIFIHDA 1130  
Qy 1138 ILEACLGETAIPVCEFAAYPDMIRIDSQTNSSHLKDEFOTLNSVTPRLQAEDCSIACL 1197  
Db 1131 ILEACLGETTIPVSEFKATYKEMIRIDPQSNSSQLREFFQTLNSVTPRLQAECSIAL 1190  
Qy 1198 PRNHDKNRMDLPPDRCLPFLITIDGSSNNYINAAALMDSVRQPAAFIVTQYPLNVTKD 1257  
Db 1191 PRNDRKNRMDLPPDRCLPFLISTDGSNNYINAAALTSYTRSAAFIVTLHLPLQSTTPD 1250  
Qy 1258 FRLVYDYGCYSIVMLNEVDLSQ---CEQYWPESGMLRYGPIQVECHSCSMDCDVINRI 1314  
Db 1251 FRLVYDYGCYSIVMLNQLNSNSAWPCLQYWPESGQOYGLMEVFEVSGTAEDELVARV 1310  
Qy 1315 FRI CNLTPRQEGYLMVQFOYLGMASHREVPGSKSFLKLILQVEKWQEBEWEKGEGRITII 1374  
Db 1311 FRVQNISRLQEGHLLVRHFQLRWASAYRDTPSKAFLLHLLAEVDKQAE--SGDGRITV 1368  
Qy 1375 HCLNGGSGRMFCAIGIVVMVKRQNVVDVFAVHTLRNSKNMVEAPEQYRVCYDVALE 1434  
Db 1369 HCLNGGSGSGTCACATVLEMIRCHNLVDVFPAAKTLRNYKNMVTMDQYHFCYDVALE 1428  
Qy 1435 YLE 1437  
Db 1429 YLE 1431

RESULT 6  
S72441

protein-tyrosine-phosphatase (EC 3.1.3.48) pi - human

N:Alternate names: FMI protein; receptor-like protein tyrosine phosphatase pi  
C:Species: Homo sapiens (man)  
C>Date: 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 09-Jul-2004  
C:Accession: S72441  
R:Crossland, S.; Smith, P.D.; Crompton, M.R.  
Biochem. J. 319, 249-254, 1996  
A:Title: Molecular cloning and characterization of PTP-psi, a novel receptor-like protein  
A:Reference number: S72441; MUID:97024447; PMID:8870675  
A:Accession: S72441  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1442 <CRO>  
A:Cross-references: UNIPROT:Q92735; EMBL:X95712; NID:gi666422; PIDN:CAA65016.1; PID:gi666422  
A:Experimental source: mammary; cell line MCF-7  
C:Genetics:  
A:Gene: fmi  
C:Function:  
A:Description: regulates cellular function by dephosphorylating phosphotyrosine residues  
C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repe  
-tyrosine-phosphatase homology  
C:Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase  
F:29-188/Domain: NAM homology <MAM>  
F:288-366/Domain: fibronectin type III repeat homology <3PR>  
F:910-1130/Domain: protein-tyrosine-phosphatase homology <PTP>  
Query Match 56.7%; Score 4374.5; DB 2; Length 1442;  
Best Local Similarity 58.5%; Pred. No. 4.7e-289;  
Matches 840; Conservative 202; Mismatches 33; Indels 63; Gaps 18;

Qy 35 GCTPDDGPG--ACDYHQDLYDDFEWVHVSAQEAPHYLPEMPQGSYMLVSDSDHDPGSKA 91  
Db 33 GCTPEESGDPAVPCYSAQYDDDFQWDPGS-----PADDPHGSYLMVNTSQHAPGORA 85  
Qy 92 RLQIPLTKWKNETHCIDFSYLLSQKGLNPGTFLNLRVKNKGLANPIWNVTGFTGRDWLR 151  
Db 86 HVIQSLSENDTHCVQSYFLYSRDGHSPGLTVGVVRVNGGFLGSAAVNMVMTGSHGRWHQ 145  
Qy 152 AELAVSTFWPNEYQVIFEAEEVSGRSGYIAIDDTQVLSYPCDKSPHFLRLGDVEVNAQON 211  
Db 146 AELAVSTFWPNEYQVLFALISPDPRGYMGDDICILSYPCAKAPHFHSRLGSDVEVNAQON 205  
Qy 212 ATFOCIATGDAVHKNLWLRNGEDIPVAQTKNINHRFAASPLQSVTKTDQDLYPCV 271  
Db 206 ASFOCMAAGR-AEAERFLQKQSGALVPAAGVRHSHRSFLATPLAAVSAEQLYRCV 264  
Qy 272 TQSRGSGVS-NFAQLIIVREPPRIAPPQLLGVPPTLLIQLNANSIIGDGPILKVEY 330  
Db 265 SQAPRGRGTSLNFAEFWVKEPPTPIAPPQLLRAGPTYLIQLNTNSIIGDGPVIRKEIY 324  
Qy 331 RMTSGSWTETHAVNAPYKLMHLDPDTEYEIRVLLTRPGEGGTGLPPLTRTKCABPM 390  
Db 325 RMARGPMAEVHAVSLQTYKLMHLDPDTEYEISVLLTRPFGDGTGRLGPPFISRTKCAEPM 384  
Qy 391 RTPTKLTAETQARRIADVESLGVNTRCHTENVTCYHYFRG--HN-----ESKAD 441  
Db 385 RAPKGLFABIQAQQLTLQWEPLGVNVRCHTYTVSLCYHYTLGSSHQTTTPRVCEDDR 444  
Qy 442 CLMDPKAPQVNVNHLPPYTNVSLKMLITNPEGRKESEETIIQTDEDVPGVPVVKSLQGT 501  
Db 445 CQPLHHEEPAL-----SERSREVLTNPEGRKEGKVEVTFQTDVPSGIAAESLTFT 497  
Qy 502 SFENKIFLNWKEPLDPNGIITQYBEISYSSISFSDPAVPAGPQPTVSNLWNSHTHVFHML 561  
Db 498 PLEDIMFLKWEPEQENGLITQYBEISYQSISSDPAVNVQA--TSTISKLRNETHYVFSNL 556  
Qy 562 HPGTYTQFFIRASTVKGEGPATAINVTNINSAPLDPYEGVDASINETAATTITVLLRPAQ 621  
Db 557 HPGTYLFSVGARTKKGFGQAALTEITYIISAPSL-DYADMPSPGSENNITVLLRPAQ 615  
Qy 622 AKGAPISAYQIVVEBELH--PHRTKRBAGAMECYQVPVTVQNAMSGAPYFAAELPPGNLP 680  
Db 616 GRGAPISYQIVVEEQSGRRRLRREPQGGQDCCFPVPLTFEAAALARGLVDFYFGAELAASSLP 675

Qy	681	EPAPFTVGDNR	TYQFGFNPP	PLAPRKGN	YIYQAMSS	VEKETK	TOCVRIAT	KAATPEE	PEVI	740
Db	676	EA	MPFTVGDN	KTYGFWGN	PPLEPRKAL	YIYQAA	SHLKG	ETRLNC	IRIAR	735
Qy	741	PDPAKOTDR	VVVKIAG	IA-GTLVF	ILLV	LVILV	IKKSK	-----	-LAKK	786
Db	736	LEV	QSEEMGL	IIGICAG	HAUVILL	GALLI	VIIRKGR	DHAYSY	PKPVNM	791
Qy	787	MGNTRQEM	THMVNADR	SYAQOST	HAEDPL	SIITFMD	QHNFS	PRYENH	S--ATAE	844
Db	792	TNVYRQEK	THMWSADR	SFTDOSTL	---QPP	GLSFM	DTHGYS	TRGEQR	SGGVTEA	848
Qy	845	DVPRYL	CEGTBSP	QOTGOLH	PAIRVAD	LLOHIN	LKMTSD	SGVFKEE	VEYSP	904
Db	849	GSPRRP	CGRKSG	PYHTTQ	LHPFAVR	ADLLOH	INOMK	TAEGY	PGFKQ	904
Qy	905	AKQONRA	KNGYGN	IAYDHS	RVILQ	PVEDD	SPSDY	INANY	IDGQ	964
Db	905	TKKXDK	VKSGQ	EBMPAY	DRHRV	KLHPM	LGDPN	ADYIN	NANY	964
Qy	965	TVYDFWR	MWOB	SACIY	MMVTNL	VEVGR	VCKYK	YKYPD	DTVEY	1024
Db	965	MVYDFWR	MWQEH	CSYIM	ITKLVE	VAGC	KCSR	YMPED	SDTYG	1024
Qy	1025	RTFTLRR	GYNEI	BEVQF	HTGPD	HGVPV	HATGL	LSF	RRVK	1084
Db	1025	RTFALRR	GYSAR	VEVRQ	FHTPA	WEHG	VPYHTT	GLLAF	IRRVK	1084
Qy	1085	GAGRTGC	VIVIDML	DMAER	GVVDI	YNCVK	ALSR	RINNV	OTEEO	1144
Db	1085	GTGRIGC	VIVDVM	LMAEC	BGVVDI	YNCVK	TLSC	RNVMI	QTEBQ	1144
Qy	1145	GETAIP	CEFAAY	FD	MIRID	SO	TNSH	LKDE	FOTL	1204
Db	1145	GETTIP	VEFKA	TYKEM	IRIDP	QSN	SQ	REEF	OTLNS	1204
Qy	1205	RFMDML	PPDRCL	PLPIIT	IDGESS	YIN	AA	LMDS	TQ	1264
Db	1205	RSMDLV	PPDRCL	PLP	ISITD	GSNNY	IN	AA	LTDSY	1264
Qy	1265	YGCTSI	VMLNE	VDLSQ	G--C	POY	WPE	GM	LR	1321
Db	1265	YGCTSI	VMLNQL	NOGNS	AWPCL	QYWP	BPGQ	YQGL	MEV	1324
Qy	1322	RPQBGY	LMVQO	FQY	LGHASH	REV	PGSK	SFLK	LQ	1381
Db	1325	RLQEGH	LLVRH	FQFL	RSAYR	DT	PDSE	KAF	LHLLA	1382
Qy	1382	RS	GMFCA	IGIV	EMVK	QNV	VDV	PHAV	KTL	1438
Db	1383	RRGTS	CA	LR	TVLE	MIR	CHNL	VDVS	FA	1439

RESULT 7  
I58148  
protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat  
N:Alternate names: leukocyte common antigen-related phosphatase  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I58148  
E:Walton, K.M.; Wartell, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.  
Neuron 11, 387-400, 1993  
A:Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogen-  
esis  
A:Reference number: I58148; MUID:93357030; PMID:8352946  
A:Accession: I58148  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1501 <WAL>  
A:Cross-references: UNIPROT:Q64605; GB:L19333; NID:G310242; PIDN:AAA42309, 1; PID:G310243  
A:Note: in Genbank entry RATTVPFPHOS, release 113.0, the source is designated as Rattus norvegicus  
R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.  
Biochem. J. 302, 39-47, 1994  
A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase

A:Reference number: S46216; MUID:94347119; PMID:8068021  
A:Accession: S46218  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-1501 <ZHA>  
A:Cross-references: EMBL:U12329; NID:G294573; PIDN:AAC37657.1; PID:G294574  
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
ogy  
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi  
F:47-109/Domain: immunoglobulin homology <IMM1>  
F:149-209/Domain: immunoglobulin homology <IMM2>  
E:246-300/Domain: immunoglobulin homology <IMM3>  
F:413-506/Domain: fibronectin type III repeat homology <3PR>  
F:882-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:963-1190/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F:1258-1481/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status predicted  
F:1148/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted  
F:1433/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted  
F:1439/Binding site: substrate phosphate (Arg) #link PTP2 #status predicted

Query Match	19.8%; Score 1529.5; DB 2; Length 1501;
Best Local Similarity	30.1%; Pred. No. 2.5e-95;
Matches	419; Conservative 207; Mismatches 470; Indels 296; Gaps 46;
Qy	205 EVNAGQNTQCIGTGEDAVHKNLWLRNG---EDIPVAQYKYNHRRFAASFRLOEV 260
Db	242 EIMPGGNVITCAVAGSPMPYVK-WMGAEDLTPEDDMPVG---RNV-----LELT 288
Qy	261 TKTDQDLYRCVTOSERGSGVSEFAQLIVRPPRPPIAPPQLLGVGPTVLLQLNANSIIGD 320
Db	289 DVKDSANYTCVAMSSLGV-IEAVAQITVKSLPKAPGTPVVTENTATSIITVWSGN--P 344
Qy	321 GPILKEVYRMTS--GSWTETHAVNAPTYKLMHLPDDEYEIRVLLTRPGEGGTGLPGP 378
Db	345 DPVSYYVIEYKSKSQDGPYQIKEDIITTRYISIGGLSPNSEYIYW--SAVNSIGQGPPSE 402
Qy	379 PLITRTKCAEPMETPKTLKIAETQARRIADVDES-----LGYNITRCHTFNVTICYH 430
Db	403 SVVTRTGEQAPASAPRVQARMLSATTMIQWSEEPVEPNGLIRGYV-----449
Qy	431 YFRGHNESKADCLDMPDKAPQHVVNHLPPYTNVSYLSKMLITNPGRKESBETIIQT--- 485
Db	450 YY-----TWBEHPVGNWQKH-NVD-DSLLTTVGSLLDEDEYTVRVLAFTS 493
Qy	486 --DEDVGPVPVKSLOG-----TSFENKIFLNKWEKDPDNGIITQYSEISYSS-- 530
Db	494 VGDGPLSDPTQVKTQCGVPGQPQPNMLRAEAKSETSIGLSWAPRQES--VIKYLEFREGD 551
Qy	531 ----TRSDPAVPVAGPPQTVSNLWNSTHHVFMHLLHGGTYOFFIRASTVKFGGPATAI 585
Db	552 RGREVGTFDP-----TTAFVVEDLKPNTEYAFRLAARSPOGLGAPTAV 595
Qy	586 --CQORTLQAI SPKNFKVMKTMKTSVLLSWEEPDPNYSPT-PYKIQYNGLLTDVGRITKKL 634
Db	596 VCORTLQAI SPKNFKVMKTMKTSVLLSWEEPDPNYSPT-PYKIQYNGLLTDVGRITKKL 654
Qy	614 TVLLRP-----AQAKGAPISAIQYVVEELHPHRTKREA-----GAM 649
Db	655 ITHLKPHRTFNFVLTRNGSSLGLQQTV-----TARTAFNMLSGKPSVAPKPDNDGSI 707
Qy	650 ECV---QVPVTYQNAMSGGAPYYEAEPL-----PQNL P-----680
Db	708 VTLDPGQSPVTQV-----YFIVMPLRKSRGGQFPILGSPEDMDLEELIQLSLR 759
Qy	681 -----BPAPPTVGDNRITYQGFWMNPPLAPRKGYNIYFQAMS 715
Db	760 LQRSLRHSRQLEVPYPIYAARSFILLPAVPHPCNQKQYGGFDRNGLEPGHRYVLFVLAV- 818
Qy	716 SVBEKTKTCQVRATKAATEEPEVI--PDPAKOTDRVKVIAGTSAGILVFILLLVVIL- 772
Db	819 -LQKNBPT-----FAASPFSDPQLQNDPDPQPTVDGDEGLIWIWGFVLAVVFICTVIAI 872





QY 169 EAEVSGRSYIAIDIOVLSPYC-DKSPHFL-----RLG-----DVEVNAGQNA 212  
Db 538 WAAEDEDQHKVTFDPTS--SYTLEDLPDITLYRFQLAARSDMGVFTPTIEARTQST 595  
QY 213 -----TFOCIATGRDAVHNKLWL-----QRRNGEDIPVAQTKNINHRFAASFRLOEYV- 261  
Db 596 PSAPPQKVMCSGSGTTRVRS-WVPPPADSRNG-----VITQYSVAHEAVDGEDRSHVVD 650  
QY 262 -----KTQDDL-----YRCVTO--SERGSGVSNFAQLIVREPRPIAPPQLLGVP- 305  
Db 651 GISRSHSSMDLVGLEKWTYRVMVRAHTDVGPSPSSPVLVTRTDBDVPSPKRVVEPL 710  
QY 306 -----TYLLIQNLNAN-----STIGDGPILLKEVEVRMTSG 335  
Db 711 NSTAVHVYWKLPVPKQHGQIRGYQVTVYRLE-NGEPRGLPIIQD--VMLAEAQWRPEES 767  
QY 336 SWTETHAVNAPTYKLVHLDPPDEYERIV-LLTRPCEGGTGLPGPPLITRTKCAEPMRTPK 394  
Db 768 EDYET-----TISGLTPETYSVTVAAYTTKGDGAR---SKPKIVTTTCAVPCR--P 814  
QY 395 TLKIAEIQARRIADW-----ESLGYNIITRCHTFNVTICYHYFRGHNESKADCLDMD 446  
Db 815 TWMISTAMNTALLQWHPKELPGLGLGYRLQYCR-----DEARPTIDFG 861  
QY 447 PKAPQHVNVHLPPTYNVSLKMLTNPGEKKESEETIIQTDENVPGVP-----VKSLQTS 502  
Db 862 KDDQHTVTGLHGKGTYYTFLAAKNRAGLGEFEKEIRTPEDLPSPGPNLHVTLTST 921  
QY 503 PENKIFLNWKEPL--DPNGIITQYRISYSSIRSPDPAVPVAGPPQTVSNLMNSTHVFWMH 560  
Db 922 TE-----LAWDPVLAERNRIISYTVVFDINS-----QBELQNIITDTRFTLTG 967  
QY 561 LHPGTTYQFFIRASTVKGFGPATAINVTNIGAPTLPDYGVDASLNETAFTI--TVLLR 618  
Db 968 LKPDTTYDIKVRWTSKSGSP-----LSPSIQRTMP-VEQVFAKNFRVAAMAKTSVLLS 1021  
QY 619 ---PQAQKA-----PISAYQIVV----- 634  
Db 1022 WEVPDSYKSAVPFKILYNGSQSVEVDGHSMRKLIADLPQNTSEYFVLMNRGSSAGGLQHLV 1081  
QY 635 -----EELPHPR-----TKREAGAM----- 649  
Db 1082 SIRTAPDLLPHKPLPASAVIEDGRFDLSMPHVQDPSLVRFVIVVVPIDRVGSGMLTPRW 1141  
QY 650 -----ECYQVPVTVYQNAWSGGAPY-----YFAAEPLPGNLPPEPAPFTVGNRTYQ 694  
Db 1142 STPELELDELLEATEQGEQERRRRQERLKPVVAQLDV--LPE--TFTLGDKKNYR 1197  
QY 695 GFWNPPLAPRKGYNIYFQAMSSVEKETQCVRIATKAATERPEVIPDPKQTRDVVKIA 754  
Db 1198 GFYNRPLSPDLSYQCFVLASLKEPMDQK-----RYASSPSYSDIIVVQVTPAQOQEE-PEML 1252  
QY 755 GISAGILVPIILLVLLVILVKSLAKKRKADAMGNTROBMTWNVAMDR---SYADQSTL 811  
Db 1253 WTPGPVLAVILILIVIAL-----LLPKRK-----RTHSPSKQEQSGICLKDLSLLA 1298  
QY 812 HAEDPLSITFMDQHNPSRYENHSATSESSRLLDVPRYLCEGTSESPYQGL--HPAIRV 869  
Db 1299 HSSDPV-----EMRRL-----NYQTPEGMRDHPPIPI 1324  
QY 870 ADLLOHINLMKTSDSYGFKEEYESPEGQSASWDVAKQDNQAKRYGNIIDYHSRVL 929  
Db 1325 TDLADNIERLKANDGLKFSQYESIDPDQOQFTWENSLNVNPKRYANVIAIDHSRVL 1384  
QY 930 QPVDDPSSDYINANYIDQYRPSHYIATQGPVHETVYDFWMTWEOQSACTVMTNIVE 989  
Db 1385 TSIDVPGSDYINANYIDGRKQNAVYATQGPPEMGDFWRVWQRTATVMMTRLEE 1444  
QY 990 VGRVKCYKTYMP--DDETVYGDVFKVCEMEPLAEYVVRFTLRRRGYNEIREVKQHFHTGW 1048  
Db 1445 KSRVKQDQWPARGTETCGLIQVTLTLDVTVELATYTVRTFALHKSGSSSEKRELQRQFQMAW 1504

QY 1049 PDHGVVPYHATGLLSFIRRVKLSNPPSAGPIVVHCSAGAGRTGCTYIVDIMLMDAERGVV 1108  
Db 1505 PDHGVPEYPTPILAFARVKACNPLDAGPMVHVHCSAGVGTGCFIVIDAMLERMKHKTIV 1564  
QY 1109 DIYNVCVKALRRRRNNMVQTERQYIFIHDAILEACLGCETAIPVCEFFKAAYFDMIRIDSQT 1168  
Db 1565 DIYHVTCMRSQRYNVQTEQYVFIHEALLEAATCGHTEVPARNLYAHIKLQGVPPGE 1624  
QY 1169 NSSHLKDEFFQTLNSVTPLQAEDECSIACLPRNHDKNRMMLPPDRCLPFLITIDG-ESS 1227  
Db 1625 SVTAMELEFKLLAS--SKAHTSRFISANLPCNKFKNRLVNIIMPVELTVCVQLPIRGVSGS 1682  
QY 1228 NYINAAALMDSYRPAAFIVTOYPLPNTVKDSWRVLVYDYGCTSI VMLNVDL--SQGCPQY 1285  
Db 1683 DYINASFUDGVRQKAYIATQPLAESTEDFWMLWEHNSTIIVMLTKLREMGREKCHQY 1742  
QY 1286 WPEEGMLRYGIQVECMSCSDCVINRIFRICMLTRPOEGY-LMVQOFOYQLGWASHREV 1344  
Db 1743 WPAERSARYQYFVVDPMW---EYNMPQYILREFKVTDARDGQSRTIRQFQFTDW-PEQGV 1798  
QY 1345 PGSKRSFKLILQVEKQWKEGEGERTIIHCLNGGSGRSMFCAIGIVVEMVQRNVVDV 1404  
Db 1799 PKTGEFTDFTGQVHKTKQEQFGQ-DGPITVHCSAGVGTGVFTILSVILERMRYEGVYDM 1857  
QY 1405 FHAVKTLRNSKPNVVEAPEQYRVCYDVALEYLES 1438  
Db 1858 FQTVKTLRTQRPAMVQTEQYQLCYRAALEYLG 1891

RESULT 10  
I50212  
Protein-tyrosine-phosphatase (EC 3.1.3.48) - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I50212  
R:Stoker, A. W.  
Mech. Dev. 46, 201-217, 1994  
A:Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase at  
A:Reference number: I50212; MUID:95001563; PMID:7918104  
A:Accession: I50212  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-1499 <STO>  
A:Cross-references: UNIPROT:Q90815; GB:I32780; NID:g485746; PIDN:AAA64460.1; PID:g485747  
C:Genetics:  
C:Gene: CRYPalphal  
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
F:148-208/Domain: immunoglobulin homology <IMM1>  
F:245-299/Domain: immunoglobulin homology <IMM2>  
F:317-399/Domain: fibronectin type III repeat homology <IMM3>  
F:881-1499/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:1257-1479/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:1141/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1147/Binding site: Cys (phosphocysteine intermediate) #status predicted  
F:1432/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1438/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.6%; Score 1508.5; DB 2; Length 1499;  
Best Local Similarity 29.0%; Pred. No. 6.6e-94;  
Matches 463; Conservative 219; Mismatches 533; Indels 383; Gaps 58;  
QY 38 FDDGFGACDYHQDLYD--DFEWVHVSAQEPH-----YLPPEMQGSYMLV 80  
Db 82 FDESAGAVLRIOPLRTPRDIYECVQNPHEVTVHAKLTVLREDQLPPGPF----- 134  
QY 81 DSSDHPDPEKARLQLPWKENDTHCIDFSYLLYSQKGLNPGTLNLVVRNKGPLANPIWN 140  
Db 135 -NIDMGP-----QLKVVERTRT-----ATMLCAASG-----NPDPE 164  
QY 141 VTGTGRDLWRAELAVSTFWPNEYQVFEAVESGSGVIAIDDIQVL---SYPCDKS-- 195

Db 165 ITWF--KDFLPVDPST-----NGRIKQLRSGGLQIESSEETDQKQECYCAVNS 211  
Qy 196 -----PHELRIG-DVEYNAGQATFOCIATGRDAVHNKLMQRRNG 235  
Db 212 AGVRYSSPANLYVRVRVAPRFSILPVSGHEIMPGGNNVITCVAVGSPMPYK-WMQGAED 270  
Qy 236 ----EDIPVAQTKNINHRFAASFLQEVTKTDQDLYRCVQSGSGSVNFAQLIVREP 291  
Db 271 LTPBDDMPVG--RNV-----LELTDVKDSANYTCVAMSSLGV-IEAVAQITVKS 317  
Qy 292 PRPIAPPOLLGVPTLLIQLNANSIIGDGPIILKEVEYRMTS--GSMTEHAVNAPYK 349  
Db 318 PKAETPVVTTATISITWDSGN--PDFVSYVVIYKSKSQDGPQIKEDITITRYS 374  
Qy 350 LWHLDPTDEYRVLVTRPGGGTGLPGPPIILITRKCAEPMRTPTKLKIAEIQARRIAD 409  
Db 375 IGLSPNSEYEW--SAVNSIGQPPSPESVVTTRTEQAPASAPRNVQGRMLSTMIQ 432  
Qy 410 WES-----LGYNITFCHTFNVTICVHYPRGHNESKADCLMDPKAP-----OHVNH 456  
Db 433 WEBPVEPNQIRGYRV-----YY-----TMEPDQPVSNWQKHND- 467  
Qy 457 LPPYTNVSLKMLNPEGRKESEETIQT-----DEDVPGVPVKSLOG----- 500  
Db 468 -----DSLLITVGSLLDEYTVRVLAFTSVGDGPLSDPIQVTKQQGPGQPMNFR 518  
Qy 501 --TSFENKIFLNWKEPLDPNGIITQYEISYSS-----IRSFDPAPVAVGPPQTVSNLW 551  
Db 519 AEAKTETSIVLSWSPRQE--IIVKYELLFKEGDHGREVPENFEP----- 561  
Qy 552 NSTHHVFMHLHPGTYOFFPRASTVKGFGPAT-----AINVTT----- 589  
Db 562 --TTSFTVEGLKPNTEYVFLRAARSGALGAPTPBVRTLOSILPKNFKVQVTKTSVLL 620  
Qy 590 ----NISAPTLR--DYEG--VDASINETAITIT----- 614  
Db 621 SWEPENYNSPT-PYKIQYNGLVNDVGRITTKLITNLKPHTFYFVLMNRGNSMGGLQQ 679  
Qy 615 -----VLLRPAQAKGAPISAYQIVW-----BELH 638  
Db 680 NVAATAANMLSRKPEVTHKPDADGNVVILPDVKSSVAVQAYIVVPLEKSRGGQFLN 739  
Qy 639 PHRTKREAGMECYQ-----VPVTYQNAMSGAPYVFAELPGNLPPEPAPFTVGDNR 691  
Db 740 PLGSPEDMLEELTQDIARLRRSLRHSRQLDFPKP-YIARF--RSLPN--HFLVGLDMK 794  
Qy 692 TYQGFWNPPLAPRGYNYLFOAMSSVEKETQCVRIATKATBEPEVI-----PDPAKQT 747  
Db 795 HYDNFENRALEPGQRYVIFILAVIQ-BPE-----ATFAASPFDPPIQLNDPDPPII 845  
Qy 748 DRVVKIAGISAGILVIFILLIIVTI-LIVKKSKLAKRKDAMGNTRQEMTHMVNAMDRSYA 806  
Db 846 DGEGLIHWIGPVLAVFIICIVAILLYKNKPSKDKSEPRTKCLNN-----A 896  
Qy 807 DQSTLHAEDPLUSITFMDQHNPSPRYENHSATAESSRLLDVPRYLCEGTSPYQTGL-HP 865  
Db 897 EITPHPKDPE---MRRINF-----QTP-----GMLSHP 923  
Qy 866 AIRVADILLOHNLNMTSDSYGFEKEYESFFEGQSASWDVAKKQONRAKNRYGNIAYDHS 925  
Db 924 PIPVSELAETHHLKANDNLKLSOYESIDFGQOFTWEHSNLEYNKPNRYANIAYDHS 983  
Qy 926 RVILQPVDEDDPSDIYINANYIDGQRPSHYTATQGVHETVYDFPWRMIWQOSACIYVMT 985  
Db 984 RVILLPIEGIVGSDIYINANYIDGRKQNAVYATQGLPTEGDFWRMVWQORSATIYVMT 1043  
Qy 986 NLVEVGRVKCYKWPD-DTEYVGDGFKVTCVEMEPLAEYVVRFTFLRRGYNEIREVQKFH 1044  
Db 1044 KLEBSRIKQDQWYFGRGTDYGMQVTLTDLTIELATFCVTFSLHKNKSGSEKEVQFQ 1103  
Qy 1045 FTGWPDHGVPHATGLISFTRVRKLSNPPSAGPIVHVCHSAGAGRTGCVIIVIDIMLMAER 1104  
Db 1104 FTAMPDGHVPEYPTFFLAFLRRVKTCPDPDAGPIVHVCHSAGVGRGTGCFVIDAMLERIKH 1163

Qy 1105 EGVVDIYNCVKALRRRINMVQTEBQYIFIHDAILEACLCGETAIPVCFKAAVDFMIRI 1164  
Db 1164 EKTVDIYGHVITLMSQRNVMVQTEDQYSFIDHALLAEVACGNTEVPARNLYTIQKLAQI 1223  
Qy 1165 DSQTNSSHLKDEFQTIASVTPRLQAECDSCIACLRNHDKNRPMQMLPPDRCLPFLITIDG 1224  
Db 1224 EVGSHVTGMELFEKRL--ANSKAHTRSPISANLPCNFKPNLNVIMPYETTRVCLQPIRG 1281  
Qy 1225 -ESSNYINAALMDSYROPAAFIVTQYPLPNTVKDFWRLVYDYGCTSIIVMLNEVDL--SQG 1281  
Db 1282 VEGSDYINASPIDGYROOKAYIATQGLAETTEDFWRLWENNSTIVVMLTKLBEMGREK 1341  
Qy 1282 CPQYWPBEGMLRYGPIQVECHSCMDCDVINRIFRICNLTRPQBGY-LMWQOQFOYLGWAS 1340  
Db 1342 CHQYWPAAERSARYQYFVVDPMMA--EYNNMPOYLREBFKVTARDGQSRVTRVQFOTDW-P 1397  
Qy 1341 HREVPGSKRSPFLKILLQVEKQWEEKSEGEETIITCLNGGORSQMFCAIGIHWVEMVKRON 1400  
Db 1398 EQGPKSGEGFIDFIGVHKTKQFGQ-DGPISVHCSAGVGTGVFTLSIVLERMYEG 1456  
Qy 1401 VVDVFHAVKTLRNSKPNWAEPOYRFCYDVVALEYLES 1438  
Db 1457 VDIQTVKMLR-TQPAWVQTEDEYQCYQAALBYLGS 1493

## RESULT 11

A56178

N;protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human  
N;Alternate names: protein-tyrosine-phosphatase BPTP-2  
C;Species: Homo sapiens (man)  
C;Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text\_change 09-Jul-2004

C;Accession: A56178; S12052; B44929  
R;Pulido, R.; Krueger, N.X.; Serra-Pages, C.; Saito, H.; Streuli, M.

J. Biol. Chem. 270, 6722-6728, 1995  
A;Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.

A;Reference number: A56178; UID:95204468; PMID:7896816

A;Accession: A56178  
A;Status: preliminary

A;Molecule type: mRNA  
A;Residues: 1-1912 <PUL>

A;Cross-references: UNIPROT:P23468; GB:L38929; NID:g755652; PIDN:AAC41749.1; PID:g755653

R;Krueger, N.X.; Streuli, M.; Saito, H.  
EMBO J. 9, 3241-3252, 1990

A;Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatase

A;Reference number: S12049; UID:9106018; PMID:2170109

A;Accession: S12052  
A;Status: preliminary

A;Molecule type: mRNA  
A;Residues: 390-1912 <KRU>

A;Cross-references: GB:X54133; NID:g35789; PIDN:CAA38068.1; PID:g35790

A;Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-T

R;Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yac  
Cancer Res. 52, 737-740, 1992

A;Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.

A;Reference number: A44929; UID:92119637; PMID:1370651

A;Accession: B44929  
A;Molecule type: mRNA

A;Residues: 1756-1804, 'C', 1806-1845 <ADA>

A;Cross-references: GB:S78086; NID:g243545; PIDN:AA21147.1; PID:g243546

A;Experimental source: pre-B cell NALM-6

A;Note: the sequence extracted from NCBI backbone (NCBIN:78086, NCBI:P:78087)

A;Note: the authors did not report the entire codon for residue 90

C;Genetics:  
A;Gene: GDB:PTPRD

A;Cross-references: GDB:131384; OMIM:601598

A;Map position: 9p24-9p24

C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
cgy

C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

F;38-100/Domain: immunoglobulin homology <IMM1>

F;140-209/Domain: immunoglobulin homology <IMM2>





Db 420 SWQPPVSKQNGIITEYSLKVAADVGEDYKPEHEIIGNSSDTTKYLLEQLEKWTY--RIT 477  
Qy 365 LTRPGEGETGLPPLIIRTKCAEPMRTPKTLKIAEIOARRIADWES-----LG 414  
Db 478 VTAHTDVGPWPESLSVLRTDEDVSPGPPRKVEEAVNATAVKVSWRSPVFNKQHGQIRG 537  
Qy 415 YNITRCHTFNVTICVHYPRGHN--ESK-----ADCLDM----- 445  
Db 538 YQV-----HYVKMENGEPKSAMLKDVMLADAQDMIIISGLQPETSYSLTAYT 585  
Qy 446 -----DPAQOHVAVHLLPYTNVSLKMLITNPE-----G 474  
Db 586 TKGDGARSKPLVSTGSPGKPLRVINH-----TQMTALIQMHPVDVTFGLQGVRLKFG 641  
Qy 475 RK-----ESEETIIQTD-----EDVPQPV 493  
Db 642 RKDMPLTLTFSEKEDHFTATDIHKGASYVPRLSARNKVGFBEMVKEISVPEEIPGF 701  
Qy 494 PVKSQGTSPENKIFLNKWEPL--DPNGIITQYEISYSIRSFPDPAVPAG---PPQTVS 548  
Db 702 PQNLHSEGTSTSVQSLWSPQVPLAERNGVITKYTLRYDINV--PLLPMHEHLIVPADTSM 759  
Qy 549 NLWNSTHVFVHLLHGTYYQPIRASVKGCGPATAINVTNINISAPTLDPYEGVDASL-- 606  
Db 760 TLTG-----LKSDDTYDVKVRHTSKRGP-----YSPSPQRTLP-----VDQSMFA 802  
Qy 607 -----NETATTITVLIR--PAQAKAPISAVOI-----VBEELHPHRTKR---EAGAMEC 651  
Db 803 KNFHVKAVMKTSVLLSWEIPENYNPAILSKFPMMDGKWEVDEGRAQKLVNLKPEKS 862  
Qy 652 YQVPTYQNMGGSGAPYPAABELPG-----NLPE----- 681  
Db 863 YSFVLTRNGNSAGGLQHRVTAKTAPDVLRTKPAFIGKTNLDMGTIVQLPDPVANENIKGY 922  
Qy 682 -----HPTDPEVLRRLN-----P 682  
Db 923 YIIIVPLKKSROKFKIPWESPDEMBELDLKEISKRKRSIRYGREVELKPYIAAHFDVLP 982  
Qy 683 APFTVGDNRITYGFNPPPLAPKGYNIYFOAMSSVEKETKTQCVRIATKAATEEPEVIP- 741  
Db 983 TEFTLGDDKHGYGFTNKQLSQOEY--VFVLAVMDHAESK-----MYATSPYSDPVMSD 1036  
Qy 742 -DPAQOTDRVVKIAGISAGIL--VFILLVVLIVKSKL-AKKRKDAMGNTRQEMTH 797  
Db 1037 LDPQITDEEGLIIVGVPLAVVFIICIVIAILLYKRAESRKSLSPLNSKEVPSH- 1095  
Qy 798 VNAMDRSYADQSTLHAEDPLSITFMDQHNFSRYENHSATAESSRLLDVPRVLCBGTSP 857  
Db 1096 -----HPTDPEVLRRLN----- 1107  
Qy 858 YQTGOL--HPAIRVADLLQHLNLMKTSDSYGFKEEVEFPFQSQASWDVAKKQDNRAKNR 915  
Db 1108 FOTPGVASHPPPIELADHIELKANDNLKESQEVESIDPCQQTWEHSLNVLNPKNR 1167  
Qy 916 YGNIIAYDHSRVILQVEDDPSDYINANYIDGQRPSHYIATQGPVHETVYDFWRMIWQ 975  
Db 1168 YANVIAYDHSRVLLSAIEGIPGSDYVANYIDGQRKQNAVYATQGLSPETFGDFWRMIW- 1226  
Qy 976 EQSACTVMVNLVEGRVKCYKXWPD--DTEVYGDFKVTCTVMEPLAEYVVRFTLERGY 1034  
Db 1227 EQEATVMMTKLEERSRVKCDQVWPSRGTETGLGVQLVLLDTVELT-YCVRTFALYNNGS 1285  
Qy 1035 NEIREVKQFHFTGWPDHGVPHYHATGLLSPIRVKLSNPPSAGPIVVHCSAGAGRTGCYIV 1094  
Db 1286 SEKKVRQOFTAWPDHGVPEHPTFLAFLRRVKTCTNPPDAGPMVHCSAGVGRGCFIV 1345  
Qy 1095 IDIMLMAEREGVVDIYNVCVKALRSRRINNVQTEQYIFIHDAILEACLCGSTAIPVCEB 1154  
Db 1346 IDAULERIKHEKTVDIYGHVTLMAQRNVMVQTEQYIFIHDALEAVTCGNTVEPARNL 1405  
Qy 1155 KAAVFMIRIDSTQNSHLKDESFOTLNSVTPRLOAEDCSIAICLPRNHDKNRMDMLPPDR 1214

Db 1406 YAYIKLQITQIETGNTVGMELFKPLAS--SKAHTSRFISANLPCNFKNRLVNIMPYES 1463  
Qy 1215 CLPLIITIDG-ESSNYINAAALMDSYRQPAAFIVTQYPLPNTVKDFWRLVVDYDGTCTSIWML 1273  
Db 1464 GRVCLQPIRGVEGSDYINASFLOGYRQOKKAYIATQGPLAETTEDFWRLMWEHNSTIVVML 1523  
Qy 1274 NEVDL--SQCCPOVWPEEGLRYGPIOVECMSCMDCDVINRIFRICNLTRPQSGYLMVQ 1331  
Db 1524 TKUREMGREKCHQWPAERSARYQYFVDDPMA---EYNMPOYILREPKVTDARQDSRTVR 1580  
Qy 1332 QFOYLGWASHREVPGSKRSFLKLILQVEKWQOEKKEGERTIIHCLNGGSGRMFCFCAIGI 1391  
Db 1581 QFQTDW-PGQVPKSGEGFIDFIOVHKTKQEQFGQ-DGPISVHCSAGVGRGTGVTITLSI 1638  
Qy 1392 VVMVKQNVVDVPHAVKTVLNRKSNKPNMVEAPEQRYPCYDVVALEYLES 1438  
Db 1639 VLERMRVEGVVDIQTVMRLRTQRPAMVQTEDEQYQFCVRAALEYLG 1685

RESULT 14  
C54689  
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor  
N;Alternate names: MTP delta type B/C  
N;Contains: protein tyrosine phosphatase, receptor type delta, splice form C  
C;Species: Mus musculus (house mouse)  
C;Date: 25-Apr-1995 #sequence\_revision 19-May-1995 #text\_change 09-Jul-2004  
C;Accession: C54689; B54689  
R;Misuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.  
Mol. Cell. Biol. 13, 5513-5523, 1993  
A;Title: MTP delta, a putative murine homolog of HPTP delta, is expressed in specialize  
A;Reference number: A54689; MUID:93360986; PMID:8355697  
A;Accession: C54689  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1894 <MI2>  
A;Cross-references: UNIPROT:Q64487  
A;Experimental source: brain; splice form B  
A;Note: sequence inconsistent with nucleotide translation  
A;Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIP:137487)  
A;Accession: B54689  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <MI2>  
A;Experimental source: brain; splice form C  
A;Note: sequence inconsistent with nucleotide translation  
A;Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIP:136530)  
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
C;Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd  
F;45-107/Domain: immunoglobulin homology <IMM1>  
F;245-299/Domain: immunoglobulin homology <IMM2>  
F;317-399/Domain: fibronectin type III repeat homology <FN3A>  
F;1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F;1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F;1536/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1542/Binding site: substrate phosphate (Arg) #status predicted  
F;1826/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1832/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.2%; Score 1483; DB 2; Length 1894;  
Best Local Similarity 29.3%; Pred. No. 5.2e-92;  
Matches 418; Conservative 205; Mismatches 460; Indels 344; Gaps 43;

Qy 254 SFRLOEVTKTDQDLRYRCVTSQSRGSGVSNFAQLIVREPPRIAPPQLLGV---GPTYLLI 310  
Db 564 SYRLOGLKPNLSLYFRLSATSPQGLGAST-AEISARTWQKPSAPPQDISCTSPSSITLV 622  
Qy 311 QLNANSIIGDGPFIILK-EVEYRMTSGSWTETHAV-----NAPTYKLWHLDPDTEYIRVL 364  
Db 623 SWQPPVPEKQNGIITEYSLKVAADVGEDYKPEHEIIGNSSDTTKYLLEQLEKWTY--RIT 680  
Qy 365 LTRPGEGETGLPPLIIRTKCAEPMRTPKTLKIAEIOARRIADWES-----LG 414

Db 681 VTAHTDVGWPESLSVLRTDDEDVPSGPPRKVEVEAVNATAVKVSWSRSPVKNKHQGIQ 740  
QY 415 YNTRCHTFNVTICYHYFRGHN-ESK-----ADCLDM----- 445  
Db 741 YQV-----HYVKNENGEPKSAMLKDVMLADAQDMIIISGLQPETSYSLTVTAYT 788  
QY 446 -----DPKAPQHVNVHLPPVTVNSLKMILLNPE-----G 474  
Db 789 TKDGARKPKLVSTTSGVPGKPLVNH-----TOMTALIQHPVVDTFGLQYRLKFG 844  
QY 475 RK-----ESETIIQTD-----EDVPGPV 493  
Db 845 RKOMEPLTLTLEFSEKEDHETATDIHKGASVYFRLSARNKVGPGEMVKEISVPEEITPGF 904  
QY 494 PVKSQGTSTENKIFLNKLEPL--DPNGIITQYEISYSSIRSDPDPAVPVAG--PPQTVS 548  
Db 905 PQLHSEGTSTSVLSQSWQPVLAERNGVITKVTLLYRDINV--PLLPMELHIVPADTSM 962  
QY 549 NLWNSTHVPMLHLPHTTYQFFIRASTVKGFGPATAINVTNISAPLDPYEGVDASL-- 606  
Db 963 TLTG-----LKSDTTYDVKVRHAKTSKRRGP-----YSPSQVQFRTL--VDQSMFA 1005  
QY 607 -----NETATTITVLLR---PAQAKGAPISAYOI-----VVEELHPHRTKR---EAGAMEC 651  
Db 1006 KNFHVRAVKMTSVLLSWEIENYNPALSKFFMMMDGKMYEVDGRATQKLIYNLHPEKS 1065  
QY 652 YQVPVTVQNMAGGAPYFAELPPG-----NLPE----- 681  
Db 1066 YSFVLNTRGNSAGGLQHRVTAKTAPDLVTRKPAFIGTKNLDGMITVQLPDVPANENIKGY 1125  
QY 682 -----P 682  
Db 1126 YIIIVPLKSRGFIKPWESPDEMDDELKEISRKRSTRYGREVELKPYIAAHFDVLP 1185  
QY 683 APFTVGDNRTYQGFNPPPLAPRGYNIYFOAMSVKEKTKTQCVRATKAATREPEVIP- 741  
Db 1186 TEFTLGDGKHGYFTNKQLOGQGY-VFFVLAVMDHAEK-----MYATSPYDPVVSMD 1239  
QY 742 -DPAKOTDRVVKIAGISAGIL--VFILLLVLLIIVKSKL-AKRKRDMNGNTRQEMTHM 797  
Db 1240 LDPQITDEEGLIWWGVLAVVFIICVIAILLKRAESESRRKSLPNSKEVPSH- 1298  
QY 798 VNAMDRSYADQSTLHAEDPLSITFMDOHNSPRYENHISATAESRLLDVPRYLCEGTESP 857  
Db 1299 -----HPTDPELRLN----- 1310  
QY 858 YQTGQL--HPAIRVADLLQHINLMKTSDSYGKEEYESFEFGOSASNDVAKDONRAKOR 915  
Db 1311 FQTPGNASHPPPILELADHIERLKANDNLKFSQYESIDPGQOFTWEHNSLNVNKPKNR 1370  
QY 916 YGNIIAYDHSRVILQPVEDDPSSDIYINANYIDGYQRPISHYIATQGPVHETVYDFWRMIQ 975  
Db 1371 YANVIAVDSHRSVLSALEGIPGSDYVNAVYIDGYRKONAVIATQGSIPETFGDFWMIW- 1429  
QY 976 EQSACIYVWNLVEGRVKCYKWPD-DTEVYGDVKVCTVEMEPLABYVVRFTFLBERRY 1034  
Db 1430 EQEATVVMTKLEERSRVKCDQWPSRGTEHGLVQVTLDTVELT-YCVRTPEALYNGS 1488  
QY 1035 NEIREVKQHFHTGCPDHPGYPYHATGLLSFIRRVKLSNPPSAGPIVHSCSAGRTCCYIV 1094  
Db 1489 SEKKVRQOQFTAMPDHPGHEHTPFLAFLLRVKTCNPPDAGPMVHSCSAGVGTCCFIV 1548  
QY 1095 IDIMLMAEREGVVDIYNCKALRSRRINNVQEEQYIFTHDAILEACLCGETAIPVCEF 1154  
Db 1549 IDAMLERIKHEKTVDIYGHVTLNRAQRYNVQVEDQYIFHDLALLEAVTCGNTVEPARNL 1608  
QY 1155 KAAFYDMIRIDSGTNSHLKDEFTQLNSVTPRLQAECDSCIACLPNRHDKNRNFMDFLPPDR 1214  
Db 1609 YAVIQKLTQIETGENTVGMELFKLAS--SKAHTSRFISANLPCNFKNRLNIMPYES 1666  
QY 1215 CLPFLITIDG-ESSNVIINALMDSYQOPAFIVTQYPLNTVKDFWRLVYDYCTSIWML 1273  
Db 1667 GRVCLQPIRGVEGSDYINASFLDGYQKAYIATOGFLAETTEDFWRMLWEHNSSTIVVML 1726

QY 1274 NEVDL--SQGCPQWPEEGMLRYGPIQVECMSCMDCDVINRIFRINLNRPOBQYLMVQ 1331  
Db 1727 TKLREMGREKCHQYWAERSARYQYFVVDPM---EYNPOYILREFKVTDAEQSRTVR 1783  
QY 1332 QFOYLGWASHREVPKSKRSLKLLILOVEKWOEKEGEGRTIHLCLNGSGRSNMFCAIGI 1391  
Db 1784 QFOFTDW-PEQGVKSGEGFIDFQGHVKTKQFQG-DGPISVHCSAGVGTGVTITLSI 1841  
QY 1392 VVMVVKRQNVVDVFAVHTKTLRNSKPNVVEAPEQVRCFYCDVALEYLES 1438  
Db 1842 VLERMRYGVVDIFQIVTKMLRTQRPANVQVEDQYQFCYRAALEYLG 1888

## RESULT 15

A56493

Leucocyte common antigen-related protein (LAR) - rat (fragment)

N;Alternate names: LAR receptor-linked tyrosine phosphatase

N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: A56493; I55393

R;Zhang, J.S.; Longo, F.M.

J. Cell Biol. 128, 415-431, 1995

A;Title: LAR tyrosine phosphatase receptor: alternative splicing is preferential to the

A;Reference number: A56493; MUID:95146548; PMID:7844155

A;Accession: A56493

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1290 &lt;RES&gt;

A;Cross-references: UNIPROT:Q62917; EMBL:X83505; NID:g732918; PIDN:CAAS8495.1; PID:g7329

R;Longo, F.M.; Martignetti, J.A.; Le Beau, J.M.; Zhang, J.S.; Barnes, J.P.; Brosius, J.

J. Biol. Chem. 268, 26503-26511, 1993

A;Title: Leukocyte common antigen-related receptor-linked tyrosine phosphatase. Regulati

A;Reference number: I55393; MUID:94075340; PMID:8253779

A;Accession: I55393

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 831-1290 &lt;RES&gt;

A;Cross-references: EMBL:U00477; NID:g392565; PIDN:AAC04306.1; PID:g392566

C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas

F;80-166/Domain: fibronectin type III repeat homology &lt;3FR&gt;

F;667-1290/Domain: leukocyte common antigen cytosolic domain homology &lt;LAC&gt;

F;1047-1270/Domain: protein-tyrosine-phosphatase homology &lt;PTP2&gt;

F;931/Active site: Cys (phosphocysteine intermediate) #status predicted

F;937/Binding site: substrate phosphate (Arg) #status predicted

F;1222/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1228/Binding site: substrate phosphate (Arg) #status predicted

## Query Match

Best Local Similarity 19.1%; Score 1470.5; DB 2; Length 1290;

Matches 402; Conservative 221; Mismatches 465; Indels 247; Gaps 42;

QY 230 LQRRNGEDIPVATKININRRFAASFRLOEVTTKDQLYRCVTSQSERGSGVNSFAQLIVR 289

Db 71 VRAATGEQAPSSPPRRVQARMLASATMLVQWEPE-----EPNGLVRGVRYTTP 120

QY 290 EPPRIAP-----PQLLGVTYLLIOLNANSIIGDGP----- 322

Db 121 DSRRLPSAHKHTDAGLLTTLVGSLL-PGITYSL-RVLAFTAVGDGPPSPPTIQVKTOQGV 178

QY 323 -----LILKEVEMTSGSWTETHAVNAPT--YKLWH 352

Db 179 PAQAPDQAKAEDTRTIQLSWLLPPQERIIVKELVYVAAEDEGQHKVTFDPTSSYTL 238

QY 353 LQPDTEYERVLLTRPGEGLPGPPLTRTKCAEPMRTPTKTKIAEIQARRIADVW-- 410

Db 239 LKPDITLYHQ--LAARSDLVGVGVTVEARTAAQSNGSPGPRKVEPLNSTAVHWSKL 296

QY 411 -----BSLGNVITRCHTFNVTICYHYFRGHN-ESKADCLDMD-----PKAPQH 452



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2005, 13:32:43 ; Search time 166.956 Seconds  
(without alignments)  
4413.635 Million cell updates/sec

Title: US-09-887-669-2

Perfect score: 7709

Sequence: 1 MDTTAAALPAFVALLLLSP.....EAPQYRFCYDVALLYLESS 1439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	7688	99.7	1439	1	PTPK_HUMAN	Q15262 homo sapien
2	7673.5	99.5	1440	2	Q86WJ2	Q86WJ2 homo sapien
3	7670.5	99.5	1440	2	Q68DT8	Q68dt8 homo sapien
4	7571	98.2	1457	1	PTPK_MOUSE	P35822 mus musculus
5	4807	62.4	1452	1	PTPM_HUMAN	P28827 homo sapien
6	4791	62.1	1452	1	PTPM_MOUSE	P28828 mus musculus
7	4784	62.1	1486	2	Q68FM4	Q68fm4 mus musculus
8	4726	61.3	1390	2	Q86V60	Q86v60 homo sapien
9	4697.5	60.9	1434	2	Q6YI48	Q6yi48 gallus gall
10	4632	60.1	1436	2	Q00197	Q00197 homo sapien
11	4623	60.0	1436	2	Q92850	Q92850 homo sapien
12	4608.5	59.8	1436	2	Q35564	Q35564 mus musculus
13	4602.5	59.7	1436	2	P70125	P70125 mus musculus
14	4588.5	59.5	1454	1	PTPT_MOUSE	Q99m80 mus musculus
15	4581.5	59.4	1439	2	P78399	P78399 homo sapien
16	4564	59.2	1463	1	PTPT_HUMAN	O14522 homo sapien
17	4520	58.6	1434	2	Q6E5N7	Q6e5n7 brachydanio
18	4374.5	56.7	1442	2	Q92735	Q92735 homo sapien
19	4352	56.5	1430	1	PTPU_HUMAN	Q92739 homo sapien
20	4343	56.3	844	2	Q8CA62	Q8ca62 mus musculus
21	3481	45.2	1195	2	Q9PUM2	Q9pum2 xenopus lae
22	2651	34.4	492	2	Q8IV94	Q8iv94 homo sapien
23	2615	33.9	990	2	Q6PDN0	Q6pdn0 mus musculus
24	2518.5	32.7	502	2	Q9WUL3	Q9wul3 rattus norv
25	2255	29.3	465	2	Q9IB99	Q9ib99 potamostrygo
26	1913	24.8	617	2	Q66JV9	Q66jv9 mus musculus
27	1706	22.1	542	2	P70643	P70643 rattus norv
28	1539	20.0	1788	2	Q9IAJ0	Q9iaj0 xenopus lae
29	1534.5	19.9	1502	2	Q9UM81	Q9um81 homo sapien
30	1533.5	19.9	1529	2	Q6PG86	Q6pg86 mus musculus
31	1529.5	19.8	1501	2	Q9QW00	Q9qw00 rattus sp.

32	1527.5	19.8	1501	2	Q7TTI7	Q7tti7 mus musculus
33	1526.5	19.8	1887	2	Q9QW67	Q9qw67 rattus sp.
34	1519.5	19.7	1898	2	Q9EQ17	Q9eq17 mus musculus
35	1517.5	19.7	1898	2	Q64604	Q64604 x protein-t
36	1513	19.6	1254	2	Q8VBV0	Q8vbv0 mus musculus
37	1509	19.6	1897	1	PTPF_HUMAN	P10586 homo sapien
38	1508.5	19.6	1499	2	Q908I5	Q908i5 gallus gall
39	1505.5	19.5	1912	1	PTPD_HUMAN	P23468 homo sapien
40	1498	19.4	1948	1	PTNS_HUMAN	Q13332 homo sapien
41	1497	19.4	1898	2	Q86W50	Q86w50 homo sapien
42	1494.5	19.4	1191	2	Q7Z3X4	Q7z3x4 homo sapien
43	1485	19.3	278	2	Q8C819	Q8c819 mus musculus
44	1476.5	19.2	1889	2	Q7QXK2	Q7qxk2 anopheles g
45	1476	19.1	1896	2	Q9IAJ1	Q9iaj1 xenopus lae

#### ALIGNMENTS

##### RESULT 1

ID	PTPK_HUMAN	STANDARD	PRT	1439 AA.
AC	Q15262	Q14763		
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	05-JUL-2004	(Rel. 44, Last annotation update)		
DE	Receptor-type protein-tyrosine phosphatase kappa precursor			
DE	(EC 3.1.3.48) (R-PTP-kappa)			
GN	Name=PTPRK; Synonyms=PTPK;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96279245; PubMed=8663237; DOI=10.1074/jbc.271.28.16712;			
RA	Fuchs M., Mueller T., Lerch M., Ullrich A.;			
RT	"Association of human protein-tyrosine phosphatase kappa with members of the armadillo family."			
RL	J. Biol. Chem. 271:16712-16719(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=ForeSkin;			
RX	MEDLINE=97199372; PubMed=9047348; DOI=10.1016/S0378-1119(96)00684-1;			
RA	Yang Y., Gil M.C., Choi E.Y., Park S.H., Pyun K.H., Ha H.;			
RT	"Molecular cloning and chromosomal localization of a human gene homologous to the murine R-PTP-kappa, a receptor-type protein tyrosine phosphatase."			
RL	Gene 186:77-82(1997).			
CC	-I- FUNCTION: Regulation of processes involving cell contact and adhesion such as growth control, tumor invasion, and metastasis. Forms complexes with beta-catenin and gamma-catenin/plakoglobin. Beta-catenin may be a substrate for the catalytic activity of PTP-kappa.			
CC	-I- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein tyrosine + phosphate.			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein; at adherens junctions.			
CC	-I- TISSUE SPECIFICITY: High levels in lung, brain and colon; less in liver, pancreas, stomach, kidney, placenta and mammary carcinoma.			
CC	-I- PTM: This protein undergoes proteolytic processing.			
CC	-I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Receptor class 2B subfamily.			
CC	-I- SIMILARITY: Contains 4 fibronectin type III domains.			
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.			
CC	-I- SIMILARITY: Contains 1 MAM domain.			
CC	-I- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial			



Db 1021 EYVVRITLERRGNEIREVKQHFHTGWDHGVPHYHATGLLSFTRRVKLSNPPSAGIVV 1080  
Qy 1081 HCSAGAGRTGCIYIDIMLMDAEREGVVDIYNCVKALRRINNVOETEEOYIFTHDAILE 1140  
Db 1081 HCSAGAGRTGCIYIDIMLMDAEREGVVDIYNCVKALRRINNVOETEEOYIFTHDAILE 1140  
Qy 1141 ACLGGETAIPVCBFAAYFMIRIDSTQNSHKLKDEFTQTLNSVTPRLOAEDCSIACLPRN 1200  
Db 1141 ACLGGETAIPVCBFAAYFMIRIDSTQNSHKLKDEFTQTLNSVTPRLOAEDCSIACLPRN 1200  
Qy 1201 HDKRRFMDLPPDRCLPFLITIDGESSNYINAALMDSYROPAAFIYQYPLNVTXDFWR 1260  
Db 1201 HDKRRFMDLPPDRCLPFLITIDGESSNYINAALMDSYROPAAFIYQYPLNVTXDFWR 1260  
Qy 1261 LVYDYGCTSVMLNEVDLSGCGQYWPPEEGMLRYGPIQVECMSCMDVDINIFRICNL 1320  
Db 1261 LVYDYGCTSVMLNEVDLSGCGQYWPPEEGMLRYGPIQVECMSCMDVDINIFRICNL 1320  
Qy 1321 TRPOEGYLMVQQOYQLGWASHREVPVGSKRSLKLILQVEKWQBEWKEGEGRTIHCINGG 1380  
Db 1321 TRPOEGYLMVQQOYQLGWASHREVPVGSKRSLKLILQVEKWQBEWKEGEGRTIHCINGG 1380  
Qy 1381 GRSGMFCAGIVVEMVKRONVDFHAKVTLRNSKPNMVAPQYRRCYDVALEYLESS 1439  
Db 1381 GRSGMFCAGIVVEMVKRONVDFHAKVTLRNSKPNMVAPQYRRCYDVALEYLESS 1439

RESULT 2

Q86WJ2 PRELIMINARY; PRT; 1440 AA.  
ID Q86WJ2  
AC Q86WJ2;  
DT 01-JUN-2003 (T-EMBLrel. 24, Created)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
DE Mutant receptor type protein tyrosine phosphatase K (EC 3.1.3.48).  
GN Name=PTRPK;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Melanoma;  
RX MEDLINE=22679345; PubMed=12794170;  
RA Novellino L., Renkvist N., Rini F., Mazzocchi A., Rivoltini L.,  
RA Greco A., Deho P., Squarcina P., Robbins P.F., Parmiani G.,  
RA Castelli C.;  
RT "Identification of a mutated receptor-like protein tyrosine  
RT phosphatase 'kappa as a novel, class II HLA-restricted melanoma  
RT antigen.";  
RL J. Immunol. 170:6363-6370(2003).  
DR EMBL; AF533875; AA049502.1; -;  
DR HSSP; P28827; IRPM.  
DR CG; GO:0016020; C:membrane; IEA.  
DR CG; GO:0016787; F:hydrolase activity; IEA.  
DR CG; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
DR CG; GO:0004872; F:receptor activity; IEA.  
DR CG; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008979; FN III-like.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR000998; MAM.  
DR InterPro; IPR000387; Tyr\_phosphatase.  
DR Pfam; PF00041; fn3\_2.  
DR Pfam; PF00047; ig; 1.  
DR Pfam; PF00629; MAM; 1.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00020; MAMDOMAIN.

DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00137; MAM; 1.  
DR SMART; SM00194; PTPc; 2.  
DR PROSITE; PS00853; FN3; 3.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR PROSITE; PS00740; MAM\_1; 1.  
DR PROSITE; PS00060; MAM\_2; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
KW Glycoprotein; Hydrolase; Receptor.  
SQ SSQUENCE 1440 AA; 162271 MW; B140BC621878586A CRC64;  
Query Match 99.5%; Score 7673.5; DB 2; Length 1440;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1436; Conservative 1; Mismatches 2; Indels 1; Gaps 1;  
Qy 1 MDTTAAALPAFVALLLLSPWLLGSAQGFSAAGCTFDDGPGACDYHQDLYDDFEVHV 60  
Db 1 MDTTAAALPAFVALLLLSPWLLGSAQGFSAAGCTFDDGPGACDYHQDLYDDFEVHV 60  
Qy 61 SAQEPHYLPPEMPQGSYMIYDSSDHPDGEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 120  
Db 61 SAQEPHYLPPEMPQGSYMIYDSSDHPDGEKARLQLPTMKENDTHCIDFSYLLYSQKGLNP 120  
Qy 121 GTLNILVRNKGPLANPINVTGTRDMLRSLAVSTFWPNEVQVIFAEVSGGRSGYI 180  
Db 121 GTLNILVRNKGPLANPINVTGTRDMLRSLAVSTFWPNEVQVIFAEVSGGRSGYI 180  
Qy 181 AIDDIQVLSYPCDKSPHFLRLGDEVEVNAGONATFQCIATGRDAVHNKLMQRRNGEDIPV 240  
Db 181 AIDDIQVLSYPCDKSPHFLRLGDEVEVNAGONATFQCIATGRDAVHNKLMQRRNGEDIPV 240  
Qy 241 AQTKNINHRRAAFSLRQEVTKTDQDLRYCVTOSERGSGVSNFAQLIVRPPPIAPQL 300  
Db 241 AQTKNINHRRAAFSLRQEVTKTDQDLRYCVTOSERGSGVSNFAQLIVRPPPIAPQL 300  
Qy 301 LGVGPYLLIQNLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPYKLMHLDPDTEYE 360  
Db 301 LGVGPYLLIQNLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPYKLMHLDPDTEYE 360  
Qy 361 IRVLLTRPGEGGTGLPGPPLITRTKCAEPMRTKTLKIAEIQARRIADVWESLGYNITRC 420  
Db 361 IRVLLTRPGEGGTGLPGPPLITRTKCAEPMRTKTLKIAEIQARRIADVWESLGYNITRC 420  
Qy 421 HTFNVTICVHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLTNPGRKESEE 480  
Db 421 HTFNVTICVHYFRGHNESKADCLMDPKAPQHVVNHLPPYTNVSLKMLTNPGRKESEE 480  
Qy 481 TIIOTDEDVPGVPVKSLQGSTFENKIFLNWKEPLDNGIITQYEISYSSIRSFDPAPV 540  
Db 481 TIIOTDEDVPGVPVKSLQGSTFENKIFLNWKEPLDNGIITQYEISYSSIRSFDPAPV 540  
Qy 541 AGPQTVSNLWNSTHVFMHLHPTTYQPIRATSVKGFGPATAINVTNISAPTLPDYE 600  
Db 541 AGPQTVSNLWNSTHVFMHLHPTTYQPIRATSVKGFGPATAINVTNISAPTLPDYE 600  
Qy 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTYQN 660  
Db 601 GVDASLNETATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTYQN 660  
Qy 661 AMSGGAPYFAAELPPGNLPEPAPFTVGNRTYQGFNPPPLAPRKGNYIFQAMSSYEKE 720  
Db 661 AMSGGAPYFAAELPPGNLPEPAPFTVGNRTYQGFNPPPLAPRKGNYIFQAMSSYEKE 720  
Qy 721 TKTQCVRIATK-AATEPEVIDPAKOTDRVVKIAGISAGILVFILLVILVKKSL 779  
Db 721 TKTQCVRIATK-AATEPEVIDPAKOTDRVVKIAGISAGILVFILLVILVKKSL 780  
Qy 780 AKRKDAMGNTRQEMTHVMVNMDSYADOSTLHAEDPLSITTFMDQHNFSRYENHSATAE 839

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Db 781 AKRKGAMGNTRQSBWTHVMNADMSYADQSTLHAEDPLSITFMDQHNFSRYENHSATAE 840
Qy 840 SSRLLDVPRLCEGTESPYQGLHPAIRVADILQHINLMKTSYGFKEEYESFFPGQS 899
Db 841 SSRLLDVPRLCEGTESPYQGLHPAIRVADILQHINLMKTSYGFKEEYESFFPGQS 900
Qy 900 ASWDVAKKQNRKRNRYNIAYDHSRVLQPVDEDDSSDYINANYIDGVRPQSHYIATQ 959
Db 901 ASWDVAKKQNRKRNRYNIAYDHSRVLQPVDEDDSSDYINANYIDGVRPQSHYIATQ 960
Qy 960 GPVHETVDFWRMIWQEQSACIVMTNLVLEGRVKCYKYPDDTEVYGFVKTCVMEPL 1019
Db 961 GPVHETVDFWRMIWQEQSACIVMTNLVLEGRVKCYKYPDDTEVYGFVKTCVMEPL 1020
Qy 1020 AEYVVRFTLRRRGYNEIREVKQHFHFGWPDHGVYHATGLLSFIRRVKLSNPPSAGPIV 1079
Db 1021 AEYVVRFTLRRRGYNEIREVKQHFHFGWPDHGVYHATGLLSFIRRVKLSNPPSAGPIV 1080
Qy 1080 VHCSAGAGRTGCIYIVDILMDAREGVVDIYNCVKALRSRRINNVOTEEQYIFIHDAI 1139
Db 1081 VHCSAGAGRTGCIYIVDILMDAREGVVDIYNCVKALRSRRINNVOTEEQYIFIHDAI 1140
Qy 1140 EACLGETAIPVCEFKAAFYDMIRIDSQTNSSHLKDEFQTLNSVTPRLQAEDECSIACLPR 1199
Db 1141 EACLGETAIPVCEFKAAFYDMIRIDSQTNSSHLKDEFQTLNSVTPRLQAEDECSIACLPR 1200
Qy 1200 NHDKNRFMDMLPPDRCLPFLITIDGESSNYINAAIMDSYRQPAFIVTQYPLNTVKDPW 1259
Db 1201 NHDKNRFMDMLPPDRCLPFLITIDGESSNYINAAIMDSYRQPAFIVTQYPLNTVKDPW 1260
Qy 1260 RLVDYDGTCTSVMLNEVDLSQGCQYQPEEGMLRGPIQVECMSCMDVDINRIFRICN 1319
Db 1261 RLVDYDGTCTSVMLNEVDLSQGCQYQPEEGMLRGPIQVECMSCMDVDINRIFRICN 1320
Qy 1320 LTRPQEGYLMVQOQYLGWASHREVPVGSKRFLKLILQVEKQBEWKEGEGRTIIHCLNG 1379
Db 1321 LTRPQEGYLMVQOQYLGWASHREVPVGSKRFLKLILQVEKQBEWKEGEGRTIIHCLNG 1380
Qy 1380 GGRGMFCAIGIVEMVRQNVVDVFAVKTLRNSKPNVBAPOYRQYCVDALEYLESS 1439
Db 1381 GGRGMFCAIGIVEMVRQNVVDVFAVKTLRNSKPNVBAPOYRQYCVDALEYLESS 1440

RESULT 3
Q68DT8
ID Q68DT8 PRELIMINARY; PRT; 1440 AA.
AC Q68DT8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686C2268.
GN Name=DKFZp686C2268;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Endometrium carcinoma cell line;
RG The German cDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaiipp A.,
RA Mewes H.-W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749277; CAH18132.1; -.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR003595; PTPc_motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 2.
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DR Pfam; PF00629; MAM; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPc; 2.
DR SMART; SM00404; PTPc_motif; 2.
DR PROSITE; PSS0835; IG_Like; 1.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PSS0060; MAM_2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PSS0005; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Hypothetical protein.
SQ SEQUENCE 1440 AA; 162129 MW; 41BA5B4D6E0C0359 CRC64;

Query Match 99.5%; Score 7670.5; DB 2; Length 1440;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1435; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 MDTAAALPAFVALLLSWPVLLGSAQGSAGGCTFDDPGACDYHQDLYDDFEVHV 60
Db 1 MDTAAALPAFVALLLSWPVLLGSAQGSAGGCTFDDPGACDYHQDLYDDFEVHV 60

Qy 61 SAQEPHYLPPEMFGSVMIVDSSDHDGEGKARLQPTMKENDTHCIDFSYLLYSQKGLNP 120
Db 61 SAQEPHYLPPEMFGSVMIVDSSDHDGEGKARLQPTMKENDTHCIDFSYLLYSQKGLNP 120

Qy 121 GTNLILVRVKNGLPANIWNVTGTGRDLWRAELAVSTFWPNEYQVIFEAESVSGRSGYI 180
Db 121 GTNLILVRVKNGLPANIWNVTGTGRDLWRAELAVSTFWPNEYQVIFEAESVSGRSGYI 180

Qy 181 AIDDIQVLSYPCDKSPHFLRGVENVNAGQATFQCIATGRDAVHNKLWLQRRNGEDIPV 240
Db 181 AIDDIQVLSYPCDKSPHFLRGVENVNAGQATFQCIATGRDAVHNKLWLQRRNGEDIPV 240

Qy 241 AQTKNINHRPFAASFRLOEVTKTDDLYRCVTQSGRSGVSNFAQLIVRPPRIAPQOL 300
Db 241 AQTKNINHRPFAASFRLOEVTKTDDLYRCVTQSGRSGVSNFAQLIVRPPRIAPQOL 300

Qy 301 LGVGPTVLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPYTKLWHLDPDTEYE 360
Db 301 LGVGPTVLLIQLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPYTKLWHLDPDTEYE 360

Qy 361 IRVLLTRPGEGETGLPGPPLITRTKCAEPMRTPKTLKIAEIQAARRIAVDWESLGYNITRC 420
Db 361 IRVLLTRPGEGETGLPGPPLITRTKCAEPMRTPKTLKIAEIQAARRIAVDWESLGYNITRC 420

Qy 421 HTFNVTTCYHYFRGHNESKADCLMDPKAQHVHVNHLPPYTNVSLKMLTNPGEKKSSEE 480
Db 421 HTFNVTTCYHYFRGHNESKADCLMDPKAQHVHVNHLPPYTNVSLKMLTNPGEKKSSEE 480

Qy 481 TIIQTDEDVPGVPVKSLQGTSPENKIFLWKEPLDPNGIITQVEISYSSIRSFDPAVPV 540
Db 481 TIIQTDEDVPGVPVKSLQGTSPENKIFLWKEPLDPNGIITQVEISYSSIRSFDPAVPV 540

Qy 541 AGPQTQVSNLWNSHTHFVFMHLPGTTYQFFTRASTVKGFGPATAINVTNISAFTLPDYE 600
Db 541 AGPQTQVSNLWNSHTHFVFMHLPGTTYQFFTRASTVKGFGPATAINVTNISAFTLPDYE 600

Qy 601 GVDASLNETATTTIVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTYQN 660
Db 601 GVDASLNETATTTIVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPVTYQN 660

Qy 661 AMSGGAPYFAAELPPGNLPEPAPFTVGDNRQYOGFWNPPLAPRKGYNIYFQAMSSVEKE 720
Db 661 AMSGGAPYFAAELPPGNLPEPAPFTVGDNRQYOGFWNPPLAPRKGYNIYFQAMSSVEKE 720

Qy 721 TKTCQVRIATK-AATEEPEVIPPAPKQTDNRVVKIAGISAGILVFILLVILVKKSKL 779
Db 721 TKTCQVRIATKAAATEEPEVIPPAPKQTDNRVVKIAGISAGILVFILLVILVKKSKL 780
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QY 780 AKGKQDANGNTRQEMTHWVNDMSYADQSTLHAEDPLSITFMQHNFSRYENHSATAE 839  
 DB 781 AKGKQDANGNTRQEMTHWVNDMSYADQSTLHAEDPLSITFMQHNFSRYENHSATAE 840  
 QY 840 SSRLLDVPRLCEGTESPYOTGQLHPAIRVADLLQHLNLMKTSYSGFKEYESFFEGQS 899  
 DB 841 SSRLLDVPRLCEGTESPYOTGQLHPAIRVADLLQHLNLMKTSYSGFKEYESFFEGQS 900  
 QY 900 ASMDVAKKQDNRAKRNRYIIAYDHSRVILQPVEDDPSSDYINANYIDGQRPESHYIATQ 959  
 DB 901 ASMDVAKKQDNRAKRNRYIIAYDHSRVILQPVEDDPSSDYINANYIDGQRPESHYIATQ 960  
 QY 960 GPVHETVYDFWRIWQSQSACIVMTNLVEGRVKCYKYPDPDDTEVYGFKVTVCVMEPL 1019  
 DB 961 GPVHETVYDFWRIWQSQSACIVMTNLVEGRVKCYKYPDPDDTEVYGFKVTVCVMEPL 1020  
 QY 1020 AEYVVRTFTLERRGYNEIREVKQPHFTGWPDPHGVPHYATGLLSPIRVKLSNPPSAGPIV 1079  
 DB 1021 AEYVVRTFTLERRGYNEIREVKQPHFTGWPDPHGVPHYATGLLSPIRVKLSNPPSAGPIV 1080  
 QY 1080 VHSAGAGRTGCYIVDIDMLDMAEREGVVDIYNCVKALRRRINMVQTEQYIFIHDAIL 1139  
 DB 1081 VHSAGAGRTGCYIVDIDMLDMAEREGVVDIYNCVKALRRRINMVQTEQYIFIHDAIL 1140  
 QY 1140 EACLGBETAIPVCEFKAAAYFDMIRIDSQTNSSHLKDEFTQNSVTPRLQAEDCSIACLP 1199  
 DB 1141 EACLGBETAIPVCEFKAAAYFDMIRIDSQTNSSHLKDEFTQNSVTPRLQAEDCSIACLP 1200  
 QY 1200 NHDKNRMDMLPPDRCLPLITIDGESSNYINAAALMDSYRQPAFIVTQYPLNTVKDFW 1259  
 DB 1201 NHDKNRMDMLPPDRCLPLITIDGESSNYINAAALMDSYRQPAFIVTQYPLNTVKDFW 1260  
 QY 1260 RLVDYDGTCTSIVMNLNEVDLSQGCQPYWPEEGMLRYGPIQVECSMDCDVINRIFRICH 1319  
 DB 1261 RLVDYDGTCTSIVMNLNEVDLSQGCQPYWPEEGMLRYGPIQVECSMDCDVINRIFRICH 1320  
 QY 1320 LTRPQEGYLVVQFQYILGWASHREVPGSKRSFLKLIQVEKQWBEKGEGRITIIHCLNG 1379  
 DB 1321 LTRPQEGYLVVQFQYILGWASHREVPGSKRSFLKLIQVEKQWBEKGEGRITIIHCLNG 1380  
 QY 1380 GGRSGMFCATGIIVEMVKRONVVDVPHAVKTLRNSKKNVYEAQRFCDVDALEYLESS 1439  
 DB 1381 GGRSGMFCATGIIVEMVKRONVVDVPHAVKTLRNSKKNVYEAQRFCDVDALEYLESS 1440

RESULT 4  
 PTPK\_MOUSE  
 ID PTPK\_MOUSE STANDARD; PRT; 1457 AA.  
 AC P35822;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Receptor-type protein-tyrosine phosphatase kappa precursor  
 DE (EC 3.1.3.48) (R-PTP-kappa).  
 GN Name=Ptpkr; Synonyms=Ptpk;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=RI; TISSUE=Brain;  
 RX MEDLINE=93233655; PubMed=8474452;  
 RA Jiang Y.P., Wang H., D'Eustachio P., Musacchio J.M., Schlessinger J.,  
 RA Sep J.;  
 RT "Cloning and characterization of R-PTP-kappa, a new member of the  
 RT receptor protein tyrosine phosphatase family with a proteolytically  
 RT cleaved cellular adhesion molecule-like extracellular region.";  
 RL Mol. Cell. Biol. 13:2942-2951(1993).  
 CC -1- FUNCTION: Regulation of processes involving cell contact and  
 CC adhesion such as growth control, tumor invasion, and metastasis.  
 CC Forms complexes with beta-catenin and gamma-catenin/plakoglobin.

Beta-catenin may be a substrate for the catalytic activity of PTP-kappa.  
 -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.  
 -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 -1- TISSUE SPECIFICITY: High levels in liver and kidney. Lower levels in lung, brain and heart. Not seen in spleen and testis.  
 -1- DEVELOPMENTAL STAGE: Developmentally regulated with highest expression found in developing areas or in areas capable of developmental plasticity.  
 -1- PTM: This protein undergoes proteolytic processing.  
 -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Receptor class 2B subfamily.  
 -1- SIMILARITY: Contains 4 fibronectin type III domains.  
 -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 -1- SIMILARITY: Contains 1 MAM domain.  
 -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
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 -----  
 CC EMBL: L10106; AAA40021.1; -.  
 DR PIR: A48066; A48066.  
 DR HSP: P28827; IRPM.  
 DR MGD: MGI:103310; Ptpkr.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR008957; FN\_III-like.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR000998; MAM.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00041; fn3; 2.  
 DR Pfam: PF00047; Ig; 1.  
 DR Pfam: PF00629; MAM; 1.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00020; MAMDOMAIN.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00060; FN3; 3.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00137; MAM; 1.  
 DR SMART: SM00194; PTPC; 2.  
 DR PROSITE: PS00853; FN3; 4.  
 DR PROSITE: PS00835; IG\_LIKE; 1.  
 DR PROSITE: PS00740; MAM\_1; 1.  
 DR PROSITE: PS00660; MAM\_2; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS00506; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS00555; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Glycoprotein; Hydrolase; Immunoglobulin domain; Protein phosphatase;  
 KW Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 25 Potential  
 FT CHAIN 26 1457 Receptor-type protein-tyrosine  
 FT phosphatase kappa.  
 FT Extracellular (Potential).  
 FT Potential.  
 FT Cytoplasmic (Potential).  
 FT MAM.  
 FT Ig-like C2-type.  
 FT Fibronectin type-III 1.  
 FT Fibronectin type-III 2.  
 FT Fibronectin type-III 3.  
 FT Fibronectin type-III 4.  
 FT Protein-tyrosine phosphatase 1.  
 FT Protein-tyrosine phosphatase 2.  
 FT Phosphocysteine intermediate (By similarity).  
 FT Phosphocysteine intermediate (By similarity).  
 FT ACT\_SITE 1100 1100  
 FT ACT\_SITE 1394 1394

FT	DISULFID	215	269	similarity).	
FT	CARBOHYD	100	100	Potential	
FT	CARBOHYD	139	139	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	210	210	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	415	415	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	423	423	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	435	435	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	461	461	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	551	551	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	585	585	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	589	589	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	606	606	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	689	689	N-linked (GlcNAc. . .)	(Potential).
SQ	SEQUENCE	1457 AA;	164185 MM;	1904B9987E3E8605	CRC64;
Query Match					98.2%; Score 7571; DB 1; Length 1457;
Best Local Similarity					97.3%; Pred. No. 0;
Matches 1419; Conservative					13; Mismatches 6; Indels 20; Gaps 4;
Qy	1	MDTAAALPAFVALLLSPLLSGSAQGSAGCTPDDGPGACDYHQDLYDDFEVHVH	60		
Db	1	MD-VAAALPAFVALLLPWLLSGSALGQFSAGCTPDDGPGACDYHQDLYDDFEVHVH	59		
Qy	61	SAQEPHYLPPEMPOGSYMIVDSSDHPDCEKARLQLPTWKENDTHCIDFSYLLYSOKGLNP	120		
Db	60	SAQEPHYLPPEMPOGSYMIVDSSDHPDCEKARLQLPTWKENDTHCIDFSYLLYSOKGLNP	119		
Qy	121	GTNLVRVNGKPLANPIVNTGTGRDLRAELAVSTFWNEVQVIFPEAEVSGRSGYI	180		
Db	120	GTNLVRVNGKPLANPIVNTGTGRDLRAELAVSTFWNEVQVIFPEAEVSGRSGYI	179		
Qy	181	AIDDIQVLSYPCDKSPHPLRLGDEVVEVNAQONATQCIATGRDAVHNLWLQRRNGEDIPV	240		
Db	180	AIDDIQVLSYPCDKSPHPLRLGDEVVEVNAQONATQCIATGRDAVHNLWLQRRNGEDIPV	239		
Qy	241	AQTNKINHRRFAASFRLOEVTKTDODLYRCVTOSESGSVNFAQLIVREPRPIAPPOL	300		
Db	240	AQTNKINHRRFAASFRLOEVTKTDODLYRCVTOSESGSVNFAQLIVREPRPIAPPOL	299		
Qy	301	LGVGPTYLIIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMHLPDTEYE	360		
Db	300	LGVGPTYLIIQLNANSIIGDGPILKEVEYRMTSGSWTETHAVNAPTYKLMHLPDTEYE	359		
Qy	361	IRVLLTRPGEGETGLPGPLITRTKCAEPMPTKTLKIAEIOARRIAVDWESLGNITRC	420		
Db	360	IRVLLTRPGEGETGLPGPLITRTKCAEPMPTKTLKIAEIOARRIAVDWESLGNITRC	419		
Qy	421	HTFNVTICYHYFRGHNESKADCLMDPKAPOHVNVNHLPPYTNVSLKMLTNPGEKSESE	480		
Db	420	HTFNVTICYHYFRGHNESKADCLMDPKAPOHVNVNHLPPYTNVSLKMLTNPGEKSESE	479		
Qy	481	TIIOQDEDPGVPVVKSLQGSFENKIFLNKKEPLDNGIITQVEISYSSIRSFDPAPVP	540		
Db	480	TIIOQDEDPGVPVVKSLQGSFENKIFLNKKEPLDNGIITQVEISYSSIRSFDPAPVP	539		
Qy	541	AGPPTQVNLWNSTHVFVHMLHPGTTYQFFIRASTVKFGFPATAINVTNISAPSLPDYE	600		
Db	540	AGPPTQVNLWNSTHVFVHMLHPGTTYQFFIRASTVKFGFPATAINVTNISAPSLPDYE	599		
Qy	601	GVDSASLNATATITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTVQN	660		
Db	600	GVDSASLNATATITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTVQN	659		
Qy	661	AMSGAPYFAELPPGNLPPAPFTVGDNRTYQGFVWNPPLAPKRGYNIYFOAMSSVBEKE	720		
Db	660	ALSGAPYFAELPPGNLPPAPFTVGDNRTYQGFVWNPPLAPKRGYNIYFOAMSSVBEKE	719		
Qy	721	TKTQCVRIATK-AAATEPEVIPPDAKQDTRVVVKIAGISAGILVFILLVILVIVKSKL	779		
Db	720	TKTQCVRIATKAAATEPEVIPPDAKQDTRVVVKIAGISAGILVFILLVILVIVKSKL	779		
Qy	780	AKRKDAMGNTRQEMTHVMNAMDRSYADQSTLHAEDPLSLTFMDQHNFS	831		

Db	780	AKRKDAMGNTRQEMTHVMNAMDRSYADQSTLHAEDPLSLTFMDQHNFS	839		
Qy	832	----ENHSATAESRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHINLMKTSDSYGF	887		
Db	840	AVLDENHSATAESRLLDVPRYLCEGTESPYQTQLHPAIRVADLLQHINLMKTSDSYGF	899		
Qy	888	KEEYESPEGOSASWDAKDONAKRKNRYNIITAYDHSRVILQPVDEDDSSDYNANYI-	946		
Db	900	KBEYESPEGOSASWDAKDONAKRKNRYNIITAYDHSRVILQPVDEDDSSDYNANYID	959		
Qy	947	----DGYQRPSPHYATQGPVHETVDFWRMIWQESACIWMVTNLVEVGRVKCYKWPD	1001		
Db	960	IWLRYDGYQRPSPHYATQGPVHETVDFWRMIWQESACIWMVTNLVEVGRVKCYKWPD	1019		
Qy	1002	DTEVYGDVKVTCVEMEPLAEYVVRTFTLRRGNYNEIREVKQFHFTGMPDHGVPVHATGLL	1061		
Db	1020	DTEVYGDVKVTCVEMEPLAEYVVRTFTLRRGNYNEIREVKQFHFTGMPDHGVPVHATGLL	1079		
Qy	1062	SFIRRVKLSNPPSAGPIVHCSAGAGRTGCIYIVIDIMLDAEREGVVDIYNCVKALSR	1121		
Db	1080	SFIRRVKLSNPPSAGPIVHCSAGAGRTGCIYIVIDIMLDAEREGVVDIYNCVKALSR	1139		
Qy	1122	INNVQTEEQYIFTHDAILEACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEFO	1181		
Db	1140	INNVQTEEQYIFTHDAILEACLCGETAIPVCEFAAYFDMIRIDSQTNSSHLKDEFO	1199		
Qy	1182	SVTPRLOAEDCSIACLPRNHDKNRMDLPDCLPFLITIDGESSNYINAAALMDSYRQ	1241		
Db	1200	SVTPRLOAEDCSIACLPRNHDKNRMDLPDCLPFLITIDGESSNYINAAALMDSYRQ	1259		
Qy	1242	AAFIVTQYPLNTVKDFWRLVYDYGCTSIUMLNEVDLSQCPQYWPBEGMLRYGPIQ	1301		
Db	1260	AAFIVTQYPLNTVKDFWRLVYDYGCTSIUMLNEVDLSQCPQYWPBEGMLRYGPIQ	1319		
Qy	1302	MSCSMDCDVINRIFRICNLTRPOEGLVMVOQFOYLGWASHREVPGRSKRFLKLQVEK	1361		
Db	1320	MSCSMDCDVINRIFRICNLTRPOEGLVMVOQFOYLGWASHREVPGRSKRFLKLQVEK	1379		
Qy	1362	QEBWKEGEGRTIICHLNGGGRSGMFCAGIIVEMVKRQNVVDVFAVKTLSKNPMVEA	1421		
Db	1380	QEBWKEGEGRTIICHLNGGGRSGMFCAGIIVEMVKRQNVVDVFAVKTLSKNPMVEA	1439		
Qy	1422	PEQYRFDYVALEYLESS	1439		
Db	1440	PEQYRFDYVALEYLESS	1457		
RESULT 5					
PTPM HUMAN					
ID	PTPM HUMAN	STANDARD;	PRT;	1452 AA.	
AC	P28827;				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-DEC-1992 (Rel. 24, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48) (R-PTP-mu).				
GN	Name=PTPRM; Synonyms=PTPRL1;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OK	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=92008644; PubMed=1655529; DOI=10.1016/0014-5793(91)81241-Y;				
RA	Gebink M.F.B.G., van Eften I., Hateboer G., Suijkerbuijk R.,				
RA	Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.;				
RT	"Cloning, expression and chromosomal localization of a new putative				
RL	receptor-like protein tyrosine phosphatase.";				
RN	FEBS Lett. 290:123-130(1991).				
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 879-1156.				
RX	MEDLINE=98010572; PubMed=9346878; DOI=10.1074/jbc.272.44.27505;				

FT	ACT_SITE	1095	1095	Phosphocysteine intermediate (By similarity).
FT	ACT_SITE	1389	1389	Phosphocysteine intermediate (By similarity).
FT	DISULFID	206	260	Potential
FT	CARBOHYD	72	72	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	92	92	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	131	131	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	249	249	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	406	406	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	414	414	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	454	454	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	534	534	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	544	544	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	598	598	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	651	651	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	681	681	N-linked (GlcNAc. . .) (Potential).
FT	STRAND	880	881	
FT	TURN	882	884	
FT	HELIX	885	905	
FT	TURN	906	906	
FT	TURN	916	919	
FT	HELIX	921	926	
FT	TURN	930	931	
FT	HELIX	936	938	
FT	STRAND	939	941	
FT	TURN	946	947	
FT	TURN	949	952	
FT	STRAND	953	961	
FT	TURN	962	963	
FT	STRAND	964	971	
FT	HELIX	976	978	
FT	HELIX	979	988	
FT	TURN	989	990	
FT	STRAND	993	996	
FT	STRAND	1001	1002	
FT	TURN	1003	1004	
FT	STRAND	1005	1006	
FT	STRAND	1016	1019	
FT	TURN	1020	1021	
FT	STRAND	1022	1032	
FT	TURN	1033	1034	
FT	STRAND	1035	1044	
FT	TURN	1045	1046	
FT	STRAND	1051	1058	
FT	HELIX	1071	1083	
ET	TURN	1086	1087	
FT	STRAND	1091	1094	
FT	HELIX	1100	1118	
FT	STRAND	1120	1121	
FT	HELIX	1123	1133	
FT	TURN	1135	1136	
FT	HELIX	1141	1155	
SQ	SEQUENCE	1452 AA;	163633 MW; 08175D3595A6C7E0 CRC64;	
Query Match				62.4%; Score 4807; DB 1; Length 1452;
Best Local Similarity				60.8%; Pred. No. 6.8e-313;
Matches 889;				Conservative 206; Mismatches 326; Indels 42; Gaps 8;
Qy	4	TAAALPAPFVALLLLSPWPLLSAQGFSAAGCTTDDPGACADYHQDLYDDPFWHVHSAQ	63	
Db	3	TLGTCLATLAGLLL-----TAAGETFSGGCLFDEPYSTCGYSQSEGGDFNWEQVNTL	54	
Qy	64	EPHYLPPEMQGSMIVDSSDHPDGEKARLQLPMTKENDTHCIDPSVLLYSOKGLNPGTL	123	
Db	55	TKPTSDPMPWPGSLMLVNASGRPEGQRAHLLLPOLKENDTHCIDPHYFVSSKNSPPGLL	114	
Qy	124	NILRVNKGPLANPIWNVTGTCGRDMLRAELAVSTFWPNEYQVIFAEVSGGRSGYIAID	183	
Db	115	NVYKVNNGPLGNPIWNISGDPTRTNRAELAVSTFWPNEYQVIFEV-ITSHGQGYLAID	173	
Qy	184	DIQVLSYPCDKSPHFLRLGDEVNAGQNAFTQCIAATGRDAVHNKMLQRENGEDIPVAQT	243	

Db 174 EVKVLGHPCTRTPHFLRIQNVENVAGQATPQCASIGRTVAGDRLMLQGLDVRDAPLKEI 233  
Qy 244 KNIHRRPAASRLQEVTKTDQDLRYCVTQSERGSVSNFAQLIVRPPRIAPQLLGV 303  
Db 234 KVTSSRRFIASFNVTNTKRDAGRYCIRTEGGVGISNAELVVRKEPVPVIAAPQLASV 293  
Qy 304 GPTVLLIQLNANSIIGDGPITLKEVYRMTSGSTETHAVNPATYKLMHLDPDTEYELRV 363  
Db 294 GATVLMQLNANSINGDGPVAREVEYCTAGSNDQRPVDSSTYKIGHLDPDTEYELSV 353  
Qy 364 LLTRPGEGETGLPGPPLITRTKCAEPMRPTKTLKIAEIQAARRIAVDMESLGYNITRCHTF 423  
Db 354 LLTRPGEGETGPGALRTRTKADPMRGPRLKEVVEVKSQITIRWEPPGYNVTRCHSY 413  
Qy 424 NVTICYHYFRGHNESKAD--CLMDPDKAPQHVHNPPLPYTVNSUKMLITNPEGRKSEET 481  
Db 414 NLTVHYCYVQGGQEQVREBEVSDTNSHPQHTITNLSPTVTVSVKLIIMNPEGRKSEQL 473  
Qy 482 IIOETDEDVPGVPVKSLQGTSPFNKIPLNWKPELDPNGIITQYEISYSSIRSFDPAPVPA 541  
Db 474 IVQETDEDLFGAVPTESIQGSTFEKIFLOWREPTQTYGVITLYEITYKAVSSDFPEIDL 533  
Qy 542 GPPQTVSNLMSNTHRVFMHLPGTITYQFFIRASTVKGFGPATINVTNISAPTLDPYEG 601  
Db 534 NOSGRVSKLGNETHFLFGLYPGTITYFTIRASTAKGFPATNQFTTKISAPMPAYE- 592  
Qy 602 VDASLNETHATTIVLLRPAQAKGAPISAYQIVVELHPHRTKRBAGAMECYQVPTVQNA 661  
Db 593 LETPLNQDNTVTVMLKPAHSGAPSVYQIVWBEERPRRTKKTTEILKCYVPPIHFQNA 652  
Qy 662 MSGGAPYFAELPGLNPELAPFTVGNRTYQGFNPPPLAPRGYNILYFOAMSSVEKET 721  
Db 653 SLNLSQYFAEFPAFDDSLQAQPTTIGDNKTYNGVNTPLPYKSYRIYFOAASRANGET 712  
Qy 722 KTCQVRIATKAATEPEVIPPAPKOTDRVWKIAGISAGILVPIILLVILVVKSKLAK 781  
Db 713 KIDCQVATKGA--TPKVPPEPEKQTDHTVKIAGIAGILVFIIFLGVLVVKKRLAK 771  
Qy 782 KRKAMGNTRQEMTHVMNDRSYADQSTLHAEDPLSTTFMDQHNFSRY----- 831  
Db 772 KRKETMSSTRQEMTVNWSMDKSYAEQGTNDE--AFSPMDTNLNGRSVSSPSFTMK 828  
Qy 832 -----ENHSATAESRLDLVRY-LCEGTESPYOTGOLHPAIRVADLLQH 875  
Db 829 TNLSTSVNSYYPDETHMTASDSSLVQSHTYKKREPADVPYQGLHPAIRVADLLQH 888  
Qy 876 INLMTSDSYGFKEEYEFEGQASWDVAKQDNRAKNRYGNIIAYDHSRVILQPVBD 935  
Db 889 ITQMKASGYGFKEEYEFEGQASAPDSAKDENEMENRYGNIIAYDHSRVRLQTIBGD 948  
Qy 936 PSSDYINANYIDGYORPSHYIATQGVNHTVYDFWRMTWQBSACIVMVTNLVEGRVKC 995  
Db 949 TNSDYINGNYIDGYHRPNHYIATQGMQETTYDFWRVWVENTASIIWVTNLVEGRVKC 1008  
Qy 996 KYKPPDDTVEYDGFVTCVEMEPLAEYVVRFTLERRGYNEIREVKQHFHTGWDHGVY 1055  
Db 1009 CKYKPPDDTEIYKDIKTIETELLAEYVIRFAVEKRGVHEIREIRQHFHTGWDHGVY 1068  
Qy 1056 HATGLLSFTRRVKLSNPPSAGPIVHVCAGAGRTGCIYIDIMLDMASREGVVDIYNVCV 1115  
Db 1069 HATGLLGFVRQVKSPPSAGPLVHVCAGAGRTGCFIVIDIMLDMASREGVVDIYNVCR 1128  
Qy 1116 ALRSRRINNVQTEQYIFTHDAILEACLCGETAIPVCEFFKAYFDMIRIDSQTNSSHLK 1175  
Db 1129 ELRSRRVNVQTEQYVIFTHDAILEACLCGDSVPASQVRSLSYDMNKLDPQTNSSQIKE 1188  
Qy 1176 EPQTLSNVTPLQAEDECSITACLRNHDKNRPMMLPPDRCLPFLTITIDGESSNYNAALM 1235  
Db 1189 EFRTLNMTVPTLRVEDCSIALPRNHNKXNCRMDILPPDRCLPFLTITIDGESSNYNAALM 1248  
Qy 1236 DSYRQPAAFIVTQYPLNPTVKDFWRLVYDYGCTSIWMLNEVDLSQCQCPQYWPCEGLRYG 1295  
Db 1249 DSYKQPSAFIVTQHPLENTVKDFWRLVLDYHCTSVVMLNDVDPAQLCPQYWPENGVRHGG 1308

Qy 1296 PIVOECMSCMDCDVINRIENLTPORGYLMVQOFOYLGWASHREVPGSKESFLKLI 1355  
Db 1309 PIQVEFVSADLEEDIIISRIFRINARPDQYRNQVQOQFLGWPMYRDTDPVSKRSFLKLI 1368  
Qy 1356 LQVEKMEQBEKKEGEGRTIIHCLNGGGRSGMFCAGIIVVMVKRQNVVDVFAVKTLRNSK 1415  
Db 1369 RQVDKQEEYNGGEGPTVHCLNGGGRSGTFCALISIVCEMLRHQRTVDVFAVKTLRNK 1428  
Qy 1416 PNWVEAPEQRYPCYDVVALEYLES 1438  
Db 1429 PNWDLDDQYKFCVVALEYLNS 1451  
RESULT 6  
PTPM MOUSE  
ID PTPM MOUSE STANDARD; PRT; 1452 AA.  
AC P28828;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Receptor-type protein-tyrosine phosphatase mu precursor (EC 3.1.3.48)  
DE (R-PTP-mu).  
GN Name=Ptpm;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung.  
RX MEDLINE=52008644; PubMed=1655529; DOI=10.1016/0014-5793(91)81241-Y;  
RA Gebbink M.F.B.G., van Etten I., Hateboer G., Suijkerbuijk R.,  
RA Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.;  
RT "Cloning, expression and chromosomal localization of a new putative  
RT receptor-like protein tyrosine phosphatase.";  
RL FEBS Lett. 290:123-130(1991).  
CC -!- FUNCTION: May play a key role in signal transduction and growth  
CC control.  
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
CC tyrosine + phosphate.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Most abundant in lung, less in brain and  
CC heart.  
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
CC Receptor class 2B subfamily.  
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 MAM domain.  
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X58287; CAA41225.1; -;  
CC PIR; S17670; S17670.  
CC HSSP; P28827; IRLPM.  
CC MGD; MGI:102694; Ptpm.  
CC InterPro; IPR003961; FN\_III.  
CC InterPro; IPR008957; FN\_III-like.  
CC InterPro; IPR008979; Gal\_bind\_like.  
CC InterPro; IPR003599; Ig-like.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR000998; MAM.  
CC InterPro; IPR000387; TYR\_phosphatase.  
CC InterPro; IPR000242; Tyr\_PP.  
CC Pfam; PF00041; fn3; 3.  
CC Pfam; PF00047; ig; 1.



QY 1375 HCLNGGSGMFCAGIGIVEMVKEQNVVDVPHAVKTLRNKNPNVMAPEQVRFCDYVALE 1434  
 Db 1388 HCLNGGSGMFCAGISIVCEMLRHQRTVDVPHAVKTLRNKNPNVDLLDQKFCYEVAALE 1447  
 QY 1435 YLES 1438  
 Db 1448 YLNS 1451

RESULT 7  
 Q68FM4 PRELIMINARY; PRT; 1486 AA.

AC Q68FM4  
 DT 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Ptpm protein.  
 GN Name=Ptpm;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Director MGC Project;  
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; BC079621; AAH79621.1; -.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR000998; MAM.  
 DR InterPro; IPR003595; PTPc motif.  
 DR InterPro; IPR000387; TYR phosphatase.  
 DR InterPro; IPR000242; TYR\_PP.  
 DR Pfam; PF00041; fn3; 3.  
 DR Pfam; PF00047; IG; 1.  
 DR Pfam; PF00629; MAM; 1.  
 DR Pfam; PF0102; Y phosphatase; 2.  
 DR PRINTS; PR00020; MAMDOMAIN.  
 DR PRINTS; PR00700; PTPPHPTASE.  
 DR SMART; SM00060; FN3; 3.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00137; MAM; 1.  
 DR SMART; SM00194; PTPC; 2.  
 DR SMART; SM00404; PTPc motif; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 1.

DR PROSITE; PS00740; MAM\_1; 1.  
 DR PROSITE; PS00600; MAM\_2; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Glycoprotein.  
 SQ SEQUENCE 1486 AA; 167143 MW; 3698D67AD522D01A CRC64;

Query Match 62.1%; Score 4784; DB 2; Length 1486;  
 Best Local Similarity 60.1%; Pred. No. 2.5e-311;  
 Matches 887; Conservative 205; Mismatches 319; Indels 66; Gaps 7;

QY 23 LLGSAQGPSAGGCTPDGPGACDYHODLYDDDEWHVHSAQEPHYLPPEMQSGSYMLVDS 82  
 Db 14 LLTAAGETFGGCLDFEYSTCYSDAEDDFNWEQVNTLTKTPTSPWPGSGFMLVNT 73  
 QY 83 SDHPGGEKARLQLPTMKENDTHCICDFSLLYSQKGLNPGTILNLVRVKNKGLANPINWVT 142  
 Db 74 SGKEGQRAHLLLPQKENDTHCICDFHYFVSSKSNAAAPGLLVVYKVNNGPGLGNPINNIS 133  
 QY 143 GFTGRDWLRALAVSWFNPWEYQVIFPAEYSGRSGYIAIDDIQVLSYPCDKSPHFLRLG 202  
 Db 134 GDEPTTHRAELAISTFWPNFYQVIFEV-VTSHQGYLAIDEVKVLGHGCTRTTHFLRIQ 192  
 QY 203 DVEVNGONATFOCIATGRDAVHNKMLQRNGEDI PVAOTKNINHRHFAASPRLOEVTK 262  
 Db 193 NVEVNGQATFOCSAIGRTVAGDRLWLQIGIDVADPLKEIKVTSRRFTASFNVVNTTK 252  
 QY 263 TDQDLVRCVTVSGRGSVSNFAQLIVREPPRIAPOLLGVGPTTYLLIQLNANSIIGDGP 322  
 Db 253 RDAGKYRCMCTEGGVGISNVAELVKEPPVPIAPPOLASVGATYLIQLNANSINGDGP 312  
 QY 323 ILKVEYRMTSGSWTETHAVNAPTYKMLHLDPTDEYIEIRVLLTRPGEGETGLPGPLIT 382  
 Db 313 IVAREVEYCTASGWNDRQVDSYKIGHLDPTDEYIEISVLLTRPGEGETGSGPALRT 372  
 QY 383 RTKCAEPMRTKTLKIAEIOABRIADVDSISGYNITRCHTNFTVTCIHYPRGHESKAD- 441  
 Db 373 RTKCADPMRGLKLEVVVEVSKRQITIRWEPFNVNTRCHSYNLTVHYGYVGGEQVREE 432  
 QY 442 -CLDMDPKAPQHVNVHLPVTVNLSKMLTNPEGRKSEETIIQTDEDVPGFVPVKSLQG 500  
 Db 433 VSWDTDNHSHQHTNLSPYTNVSVKLLANPEGRKESQELTVQTDDELPGAVTESIQG 492  
 QY 501 TSFENKIFLNKBPDLNPGIITQYEISYSSIRSDPAVPVAGPPQTQVSNLWNSHTHFPMH 560  
 Db 493 SAFEKIFLOWREPTQYVITLYEITYKAVSSDPDEIDLNSQSGRVS KLGNETHFLPFG 552  
 QY 561 LHPGTTYQFFIRASTVKGFGPATVNTNLSAPTLPDYGVDASLNETATTITVLLRPA 620  
 Db 553 LYPTTYSFTIRASTAGFGPPATNQFTTKISAFMPAYE-FETPLQTDNTVTVMKXPA 611  
 QY 621 QAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTYQNAMSGAPYFAELPPGNLP 680  
 Db 612 QSRGAPSVVQIVVEERPRRTKTKTEILKCPVPIHFQNASILNSQYVFAAEFPADSLQ 671  
 QY 681 EPAPFTVGDNRTYOGFWNPPLAPRKGNIIYFOAMSSVEKETKTCVRIATKAA----- 733  
 Db 672 AAQPFTIGDNKTYNGYWNTPLLPHKSYRIYQAAASRANGETKIDCVRVATKAAIIVTOLT 731  
 QY 734 -----TESPEVTPDAKOTDRVVVKIAGISAGILVFTILLVLIIVKK 776  
 Db 732 TPYIRIAPAGDGGTGAIVTPKVPPEPEKQTDHTVTKIAGTAGIAGLFLVIIIFLGVLVWKK 791  
 QY 777 SKLAKKKDAMGNTRQSMTHVMNAMDYSADQSTLHAEADPLSITFMDQHNFSRY----- 831  
 Db 792 RKLAKKKETMSSTRQETVMVNSMDKSYAEQGTNCDE---AFSEFMGTHNLNGRSVSSPS 848  
 QY 832 -----ENHSATAESSRLLDVRY-LCEGTESPYQTG 861  
 Db 849 SFTMTKNTLSTSPVNSYYPDPFVPTAILDETHTWASDTSSLAQPHTYKKREAADVPYQTG 908  
 QY 862 QLHPAIRVADLLQHLINLMKTSDSYGFKEEYESPFEGQSASWDVAKDQNRKRYGIIIA 921

Db 909 QLHFAIRVADLLOHITQMKCAEGYGFKEEYSEFFEGSQAPWDSAKDENRMKNRYGNIIA 968  
 Qy 922 YDHSRVLQPVEDDPSSDIYINANTIDYQRPSPHYATQGPVHETVYDFWIMWEOASACI 981  
 Db 969 YDHSRVLQMLEGDNNSDYINGNYIDYGRPNHYIATQGPQETIYDFWFWHENTASI 1028  
 Qy 982 VMVNTLVYGVKCYKWPDDTEVYGFDPKTCVEMEPLEAEVYVTFYLLERGVNEIREVK 1041  
 Db 1029 IMVNTLVYGVKCYKWPDDTEVYGFDPKTCVEMEPLEAEVYVTFYLLERGVNEIREVK 1088  
 Qy 1042 QFHTGPDGVPVHATGLLSFTIRRVKLSNPPSAGPIVHCSAGAGTGCYIVIDIMLDM 1101  
 Db 1089 QFHTGPDGVPVHATGLLGFRVQVSKSPPNAGPLVHCSAGAGTGCYIVIDIMLDM 1148  
 Qy 1102 ABREGVVDIYVNCVKALESRRINMVQTEEQYIFHDAILEACLCGETAIPVCEFAAYFDM 1161  
 Db 1149 ABREGVVDIYVNCVKALESRRINMVQTEEQYIFHDAILEACLCGETAIPVCEFAAYFDM 1208  
 Qy 1162 IRDSQTNHSLKDEFOTLNSVTPRLQAECDSCIACLPRNHDKNRFDMLPPDRCLPLIT 1221  
 Db 1209 NKLDPTQNSSQIKKEEFTLNVTPTLVEVDCSIALPRNHEKKNRCDMLPPDRCLPLIT 1268  
 Qy 1222 IDGESSNYINAAALWDSYRQPAFTVTOYPLNTPVKDFWRLVYDYGCTSIYMLNEVDLSQ 1281  
 Db 1269 IDGESSNYINAAALWDSYRQPAFTVTOYPLNTPVKDFWRLVYDYGCTSIYMLNEVDLSQ 1328  
 Qy 1282 CPQYWPBEGMLYGPQVEQWCSMDVDINRIFRINLTPQBOGYLWVQFOVGLGWASH 1341  
 Db 1329 CPQYWPBEGMLYGPQVEQWCSMDVDINRIFRINLTPQBOGYLWVQFOVGLGWASH 1388  
 Qy 1342 REVPGSKRSLKILQVKEWKEBEGRTIHLNGGGRSGMFCAGIVEMVQRQNV 1401  
 Db 1389 RDTFVSKRSLKILQVKEWKEBEGRTIHLNGGGRSGMFCAGIVEMVQRQNV 1448  
 Qy 1402 VDVFHAVKTLNRKNPNVRAPEQYRCYDVALEYLES 1438  
 Db 1449 VDVFHAVKTLNRKNPNVRAPEQYRCYDVALEYLES 1485

## RESULT 8

Q86V60 PRELIMINARY; PRT; 1390 AA.  
 AC Q86V60  
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE PTPRM protein  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hoeh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vailion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.W., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywicki M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;

Query Match 61.3%; Score 4726; DB 2; Length 1390;  
 Best Local Similarity 62.2%; Pred. No. 1.7e-307;  
 Matches 867; Conservative 202; Mismatches 292; Indels 34; Gaps 7;  
 Qy 72 MPOGSMYIVDSDHDPGEKARLQPTMKENDTHCIDPSYLLYSQKGLNPGCTLAILVRVKN 131  
 Db 1 MPSSGFMVLVNASGRPEGRAHLLLPQKENDTHCIDFHYFVSSKSNPPGLLNVYKVN 60  
 Qy 132 GPLANPIWNTGFTGRDWRALAVSTFWPNEYQVIFAEVSGSGSGYIAIDDIQVLSYP 191  
 Db 61 GPLGNPIWNTGFTGRDWRALAVSTFWPNEYQVIFAEVSGSGSGYIAIDDIQVLSYP 119  
 Qy 192 CDKSPHFLRLGDEVNAGQATPQCTATGRDAVHKNLWQRRNGEDIPVATQKNINRRF 251  
 Db 120 CTRTFPLRIQNVNAGQATPQCTATGRDAVHKNLWQRRNGEDIPVATQKNINRRF 179  
 Qy 252 AASFLQEVTKTDODLYRCVQSGSGVSNFAQLVREPPRIAPQLLVGPTVLLIQ 311  
 Db 180 IASFNVTNTKRDAGKYRCMIRTEGGVGSINVAELVKKPPVPIAPQLLVGPTVLLIQ 239  
 Qy 312 LNANSIIGDPITLKEVEYRMVSGSWTEVHVNAPYKLMWHLDPDTEYERILLTRPGE 371  
 Db 240 LNANSINGDPVAREVEVCTAGSNDQPDVSTSYKLGHLDPDTEYERILLTRPGE 299  
 Qy 372 GTGLPGPPLITRTKCAEMRTPKTKIARIADWESLGYNTTRCHTFNVTICHY 431  
 Db 300 GTGSPGALRTKCAEMRTPKTKIARIADWESLGYNTTRCHTFNVTICHY 359  
 Qy 432 FRGHNSKAD--CLMDPKAPQHVHNLPPYTNVSLKMLTNPGEKSEBETIOTDEDV 489  
 Db 360 QVGGQGVREEVSWDTEHNSHPQHTITNLSPYTNVSKLILMNPGEKSEBETIOTDEDV 419

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]  
 SEQUENCE FROM N.A.  
 TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC051651; AAH51651.1; -;  
 DR HSSP; P28827; IRPM.

DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0016787; F-hydrolase activity; IEA.  
 DR GO; GO:0004725; P-protein tyrosine phosphatase activity; IEA.  
 DR GO; GO:0006470; P-protein amino acid dephosphorylation; IEA.

DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR000998; MAM.  
 DR InterPro; IPR000387; TYR\_phosphatase.  
 DR InterPro; IPR000242; Tyr\_PP.

DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00047; ig; 1.  
 DR Pfam; PF00629; MAM; 1.  
 DR Pfam; PF00102; Y\_phosphatase; 2.  
 DR PRINTS; PR00020; MAMDOMAIN.

DR PRINTS; PR00700; PRTYPHPTASE.  
 DR SMART; SM00060; FN3; 3.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00194; PTPC; 2.

DR PROSITE; PS00853; FN3; 3.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR PROSITE; PS00740; MAM 1; 1.

DR PROSITE; PS00660; MAM 2; 1.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 2.  
 DR PROSITE; PS00056; TYR\_PHOSPHATASE 2; 2.

DR PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Glycoprotein; Hydrolase.  
 SQ SEQUENCE 1390 AA; 156936 MW; D8173543CDD9F79 CRC64;



Db 264 VTQSSRGSGVSNPAELIVKBPPTPIAPPQLLRAGSTVLIILQNTNSIIGDGPVIRKEIEY 323  
Qy 331 RMTSGSWTETHAVNAPYKILWHLDPDTEYERVLLTRPGEGTGLPGPPLITRTKCAEPM 390  
Db 324 RMTSGPSEVHVNMQYKILWHLDPDTEYERVLLTRPGEGTGLPGPPLISRTKCAEPM 383  
Qy 391 RTPKTLKIAEIOARRIADVESIGYNTTRCTFTNTVTCIHYFP--RGHNSKACLDMDPK 448  
Db 384 RAPKGLAFSIOGRQLTQWEPGLYNLTRCHTSVSLCYRYLVGSLGNQTFRECAKERN 443  
Qy 449 APQHVNNHLPYNTVNSLMLITNPEGRKESEETIIQDDEVPGPVPVKLSQGSFENKIF 508  
Db 444 ANRYTIKNLPLPYRNHVKLILSNPEGRKEKEVTFTQDEVDVPGIASESTFTPLEDMIF 503  
Qy 509 LNKWELDPNGIITQVEISYSSIRSDPAPVAVPGPQTVSNLWNSTHVMFHLHPGTYQ 568  
Db 504 LKWEPEVPEPLITQVEISYQSISSDPAVNVPPRTVSKLRNETHVPSNLHPGTYL 563  
Qy 569 FPIRASTVKGFGPATAINVTNITASPLTPDYEGVDASLNETATITVLLRPAQAKGAPIS 628  
Db 564 FSVRAETGKFGQTALTETITNISAPTF-DYGDMPSPLGSESESTITVLLRPAQGRGAPIS 622  
Qy 629 AYQIVVEELHPHTKREAGAMECVQVPTVYQNASGGAPVYEAELPPGNLPPAPPTVG 688  
Db 623 TYQIVVEEDRPKRIKELGQECFPVPLTFDDHMSRGSVHYFGAELPASPASTEAKPTVG 682  
Qy 689 DNRTYQGFWMNPPLAPRKGNYIFQAMSSVEKETKTCVRIATKAATEEPPEVIPPDAKQTD 748  
Db 683 DNQYSGYWNPPLEPKKAYLIFYQAMSLNAGETRLNCIRIARKAACKESKRPLEVSQHS 742  
Qy 749 RVVKIAGISA-GILVFIILLVILVIVKSKLAKRKDANGNTRQEMTHMNVNMDRSYAD 807  
Db 743 EMGLILGICAGGLWLLILGAIIVIRKGPVNMTK-ATINYRHEKTHMMSIDRSFTD 801  
Qy 808 QSTLHADPLSITFMDQHNPSRYENHSATA-BSSRL-L-DVRYLCBGTSPYOTGOLHP 865  
Db 802 QSTLQEDERLCGLFMDTHNYSNGQRSSVNVSSLLGSPRQCCKGSPYHTGOLHP 861  
Qy 866 AIRVADLLQHINLMKTSDSYGFKEEYESFFEGOSASWDVAKQDNRAKNRYGNIAYDHS 925  
Db 862 AVRVDLLQHINQMKAEGYGFQKYESFFEG---WDASK-KDKTKGRQDHVSYDRH 916  
Qy 926 RVTLQVEDDPSDYINANYIDYQRPVSHVYIATQGPVHETVYDFWFMWQEQSACIVMT 985  
Db 917 RVKLHLLGDPNSDYINANYIDYGRSHNHFIAQGPQKQENVYDFWFMWQEHCCSVMIT 976  
Qy 986 NLVEGVRVKYKWPDDTEVYGFVKTCVMEPLAEYVVTPTLERGYNEIREVKQFHF 1045  
Db 977 KLVEGVRVKSKYWPDDSEMYGDIKITLVKSEMLAEYAVVTFALERRGYSSARHEVQFHF 1036  
Qy 1046 TGWPDHGVPHATGLLSFIRRVKLSNPPSAGPIVWHCSAGARTGCYIVIDIMLDMARE 1105  
Db 1037 TSWPEHGVPHATGLLAFIRVKAFTPPDAGPIVHCSAGTGTGYIVLDMVMDMAECE 1096  
Qy 1106 GVVDIYNVCKALSSRNINMQTEQYIFIHDAILEACLCGETAIPVCEFKAAFYDMIRID 1165  
Db 1097 GVVDIYNVCKTLCSSRNIMQTEQYIFIHDAILEACLCGETSIPASEPKPTVKEMVRIE 1156  
Qy 1166 SQTNSSHLKDEFTLNSVTRLOAEDCSIACLPRNHDKNRPFMDLPDRCLPLIITIDGE 1225  
Db 1157 PQSNSSQLREFTLNSVTRPHLDECSIALLPNERNRNDVLPDRCLPLISVDGD 1216  
Qy 1226 SSNYINAAIMDSYRQPAFTVTOYPLNPTVKDFWRLVYDYGCTSIIVMLNEVDLSQG--C 1282  
Db 1217 SSNYINAAITDSTYKSAFIVTLHPLQNTTDFWRLVYDYGCTSIIVMLNQNSGAWPC 1276  
Qy 1283 PQYWPEGLMYGP1QVECMSCMDCDVINRIFRICNLTRPQRYGLMWQOYQYLWASHR 1342  
Db 1277 LQWPEPGLQHYGMEVEYVSGAEDIVSRLEFRVQNTITLQEGHLMVHRFQYLRWSAYR 1336  
Qy 1343 EYDGSKRSFLKILQVEKQWEEKBEGRTHIICLANGGSGSMFCAGIIVEMVKQNVV 1402  
Db 1337 DTPDSKSKSFHLHQAQVERWQKE--SGDGRTVVHCLNGGSGSGTGYCASTMILEMIKCHNWA 1394

Qy 1403 DVHAVKTLRNSKNPVWEAPEQYRFCYDVALEYLES 1438  
Db 1395 DIFAAKTLRNPKNVETLEQYHFCYDIALEYLES 1430  
RESULT 10  
000197  
ID 000197 PRELIMINARY; PRT; 1436 AA.  
AC 000197;  
DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Receptor protein tyrosine phosphatase hPTP-J precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SEQUENCE FROM N.A.  
RP TISSUE=Skeletal muscle;  
RC MEDLINE=97223402; PubMed=9070223; DOI=10.1006/bbrc.1997.6004;  
RX Wang B., Kishihara K., Zhang D., Hara H., Nomoto K.;  
RT "Molecular cloning and characterization of a novel human receptor  
RT protein tyrosine phosphatase gene, hPTP-J: down-regulation of gene  
RL expression by PMA and calcium ionophore in Jurkat T lymphoma cells.";  
RL Biochem. Biophys. Res. Commun. 231:77-81(1997).  
DR EMBL; U73727; AAB51343.1; -;  
DR PIR; JCS290; JCS290.  
DR HSSP; P28827; IRPM.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR003962; FNIII\_subd.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR000998; MAM.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00041; fn3; 3.  
DR Pfam; PF00629; MAM; 1.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00014; FNTYPEIII.  
DR PRINTS; PR00020; MAMDOMAIN.  
DR PRINTS; PR00700; PRTYPHPTASE.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00137; MAM; 1.  
DR SMART; SM00194; PTPC; 2.  
DR PROSITE; PS00853; FN3; 3.  
DR PROSITE; PS00740; MAM\_1; 1.  
DR PROSITE; PS00660; MAM\_2; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
DR PROSITE; PS00356; TYR\_PHOSPHATASE\_2; 2.  
DR PROSITE; PS00055; TYR\_PHOSPHATASE\_FTP; 2.  
KW Glycoprotein; Hydrolase; Receptor; Signal.  
FT SIGNAL 1 18 Potential.  
FT CHAIN 19 1436 receptor protein tyrosine phosphatase  
FT hPTP-J.  
SQ SEQUENCE 1436 AA; 161092 MW; C05B86FF7A9412D9 CRC64;

Query Match 60.1%; Score 4632; DB 2; Length 1436;  
Best Local Similarity 60.1%; Pred. No. 3.6e-301;  
Matches 867; Conservative 211; Mismatches 339; Indels 26; Gaps 10;

Qy 6 AALPAFVALLLSLWPLIGSAQGSAGCTPD---DGFACDHYQDLDDFEWVHVA 62  
Db 4 AQAFLVALLTFLQCAP-----ETETFAAGCTFEASDPVPCYSQAQYDDEQVRI 56



Db 4 AQAALVLAITFQLCAP-----ETETPAAGCTFEASDPAVPCYCSAQYDDFQWQVRI 56  
QY 63 QBEHYLPPEMQSGYIMVDSDDHDPGEKARLQLPPTMKENDTHCIDFSYLYSQKGNPGT 122  
Db 57 HPGTRAPADLPHGSGYLMVNTSQAPQORAHVIFQSLSENTHCQVFSYFLYSDGHSPT 116  
QY 123 LNTILVRNKGPLANPTVNTVGTFRDGLWRAELAVSTFWPNEYOVIFEAESGGRSGVIAI 182  
Db 117 LGVYVRVNGGPLGSAVNMGTSGHROHQAELAVSTFWPNEYQVLFALISPDRRYMG 176  
QY 183 DDIQVLSYPCDKSPHFLRLGDVEVNAQONATFOCIATGRDAVHNKWLQORNGEDIPVAQ 242  
Db 177 DDILLSPYCAKAPHESRLGDEVEVNAQONAFQMAAGRAAEAEERFLQROSGALVPAAG 236  
QY 243 TKMINHRFAASRLQEVTKTDQOLYRCVTVQSRGSGVSNFAQLIVRPPRPPIAPQLLG 302  
Db 237 VRHISHRFLATPPLAAVSAEQLYRCVSAQPRGAGVSNFAELIVKEPPTPIAPQLLR 296  
QY 303 VGPYLLIOLNANSIIGDGPILLKEVEYRMTSGSWTETHAVNAPTLYKLWHLDPDTEY 362  
Db 297 AGPTYLIQIOWNTSIIIGDGPVIRKEIERYMARGFAEVAHVSLOTYKLWHLDPDTEY 356  
QY 363 VLLTRPGEGETGLPGPLITRTKCAEPMRTPKTKIAEIQARRIAVDWESLGYNITRCHT 422  
Db 357 VLLTRPDGSGTGRPGPLISRTKCAEPMRAPKGLAFIAEQARQLTQWEPFLGYNITRCHT 416  
QY 423 FNTVICYHPRG--HNESKADCLMDPKAPQHVNVNHLPPYTNVSLXKMLTNPGRKES 480  
Db 417 YTVSLCVHYTLGSSHNQITRECVKTEQGVSRYTINKLLPYRNVHVRVLVLTNPGRKEG 476  
QY 481 TIOTDEVDGPPVVKSLQTSFENKIFLNKPELDPNGIITQYEISYSIRSFDPAVPV 540  
Db 477 VTQTDDEVPSGIAAESLTFPLEDMIFLKWEPEQFNGLITQYEISYQSISSDPAVNV 536  
QY 541 AGPPQVSNLWNTTHVFMHLPGTTVOPPIRASTVKGFGPATAINVNTNISAPTLPDYE 600  
Db 537 PGPRTIISKLRNTYVFSMLHGTTLTFLSVARTKGFQQAALTEITNISAPSP-DYA 595  
QY 601 GVDASLNATATTITVLLRPAQAKGAPISAYQIVVEELHPHRTKREAGAMECYQVPTYQN 660  
Db 596 DMPSPGSESENTITVLLRPAQAGRAPISVYQVIVEERARLRAREPGQDCFPVPLTFF 655  
QY 661 AMSGGAPYPAELPQNLPEPAPFTVGDNRRTVQGFVWNPPLAPRKGNVYFQAMSSVEKE 720  
Db 656 ALARGLVHFGABLAASLPEAMPFTVGDNQTYRGFWNPPLPRKAYLIYFQAASHLKG 715  
QY 721 TKTCQVRIATKAATEPEVTPDPAKQTDVVVKIAGISA-GILYFIALLLVILVVKSKL 779  
Db 716 TRUNCIRIARAKACKSRPLEVSQRSEEMGLIIGICAGGLAVLILLGAIIVILIRKGP 775  
QY 780 AKKRKAMGNTRQEMTHVNMADRSYADQSTLHAEDPLSITFMDQHNFSPRYENHS--AT 837  
Db 776 VNMTK-ATVNYROEKTHMSAVDRSPDQSTLQEDERLGLSFMDTHGYSTRGQORSGVT 834  
QY 838 AESRLLDVPRYLCEGTESPYQGLHPAIRVADLLOHINMKTSDSYGFKBYESFFEG 897  
Db 835 EASSLLGSGSPRRCGRKGSPYHTQGLHPAVRVADLLOHINOMKTAEGYGFQBYESFFEG 894  
QY 898 QASASDVAKQDNRAKNRYGNIITAYDHSRVLQPEVDDPSDDYNANYIDQYORPHYIA 957  
Db 895 ----WDATKKDKVKSGRQBPMPAYDRHRVKLHPLMGDPNADYNANYIDGYHRSNHFA 950  
QY 958 TQGPVHTVYDFWRMLWQESACTVMVNLVVEGRVKCYKVPDDTEVYGDGPKVTCVEME 1017  
Db 951 TQGPKEVYVDFWRVWVWQEHCSISVITKLVEGRVKCSRYWEDSDTYGDIKIMLVKTE 1010  
QY 1018 PLAEYVVRTFLERRGYNEIREVKQHFHTGPDGHPYHATGLLSFIRRVKLSNPPSAGP 1077  
Db 1011 TLAEYVVRTFALERGYSARHEVRQFHTTAWPEHGVYPYHATGLLAFIRRVKASTPPDAGP 1070  
QY 1078 IVVHCSAGAGRTGCIYVIDIMLMDAREGVVDIYNCVKALRSRRINWQTEQYIIFHDA 1137  
Db 1071 IVIHCSAGTGTGCIYVLDVMDMAECEGVVDIYNCVKILCSRRVNMIQTEQYIIFHDA 1130

RESULT 12  
O35564

ID O35564 PRELIMINARY; PRT; 1436 AA.  
AC O35564;  
DT 01-JAN-1998 (TREMblrel. 05, Created)  
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
DE 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
DE Ftp-1.  
GN Name=Ptptru; Synonyms=ftp-1;  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=97417493; PubMed=9272866; DOI=10.1016/S0378-1119(97)00174-1;  
RA Yoneya T., Yamada Y., Kakeda M., Osawa M., Arai E., Hayashi K.,  
RA Nishi N., Inoue H., Nishikawa M.;  
RT "Molecular cloning of a novel receptor-type protein tyrosine  
RT phosphatase from murine fetal liver.";  
RL Gene 194:241-247(1997).  
DR EMBL; D88187; BAA23475.1; -.  
DR HSSP; P28827; IRPM.  
DR MGD; MGI:1321151; Ptptru.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR InterPro; IPR003962; FnlIII\_subd.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR000998; MAM.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR InterPro; IPR000242; Tyr\_PP.  
DR Pfam; PF00041; fn3; 3.  
DR Pfam; PF00629; MAM; 1.  
DR Pfam; PF00102; Y\_phosphatase; 2.  
DR PRINTS; PR00014; FNTYPEIII.  
DR PRINTS; PR00020; MAMDOMAIN.  
DR PRINTS; PR00700; PRTPHPTASE.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00137; MAM; 1.  
DR SMART; SM00194; PTPC; 2.  
DR PROSITE; PS00853; FN3; 3.



DR	PRINTS; PR00700; PRTYDPHPTASE.	
DR	SMART; SM00060; FN3; 3.	
DR	SMART; SM00409; IG; 1.	
DR	SMART; SM00137; MAM; 1.	
DR	SMART; SM00194; PTEC; 2.	
DR	PROSITE; PS00853; FN3; 2.	
DR	PROSITE; PS00080; MAM; 2; 1.	
DR	PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.	
DR	PROSITE; PS50056; TYR_PHOSPHATASE 2; 2.	
DR	PROSITE; PS50055; TYR_PHOSPHATASE PTP; 2.	
KW	Glycoprotein; Hydrolase; Receptor	
SQ	SEQUENCE 1436 AA; 161199 MW; EFPAAE52C6903F02 CRC64;	
Query Match		
Best Local Similarity 60.3%; Pred. No. 3.5e-299;		
Matches 855; Conservative 214; Mismatches 329; Indels 19; Gaps 9;		
QY	33 AGCTTDDGPG--ACDYHQDLVDDDEWHVHSQAEPHYLPPEMPQGSYMIYVDSDDHDPGE 89	
DB	24 AAGCTFEASDPVVPCEFSQAQYDDFQWEQVRIPHGTRTPEDLPHGAYLVNVAQSHTPGQ 83	
QY	90 KARLQLPTMKENDTHCIDFSYLLYSQKGLNPGLTILNLRVKNKGLPANIWNVTGFTGRDW 149	
DB	84 RAHLIIFQTLSENTHCVQFSYFLYSRDGSPGLGVYRVNCGPLGSAVNMVMTGSHGRQW 143	
QY	150 LRALAVSTFWPNEYQVIFEAHSVGGSGSYAIAIDDIQVLSYPCDKSPHFLRLGDEVYNAG 209	
DB	144 HQELAVSTFWPNEFQVLFALISPDHKYVIGLDDILLFSYPCAKAPHFSLRGDEVYNAG 203	
QY	210 QNATFOCIATGRAVHNKMLWRNGEDIPVAQTKNINHRPFAASFLRQLBQVTKDQOLYR 269	
DB	204 QNASFCMAAGRAAEABHFLQSQGLVPAAGVRHISHRRFLATPPLASVGRSEQDLYR 263	
QY	270 CVTQSERGSGVNSFAOLIVREPRPTAPOLLGVGPTYLLIQNLNANSIIGDGPILKEVE 329	
DB	264 CVSQAPRGAGVNSFAELIVKEPTPIAPPQLLAGPTYLLIQNLNANSIIGDGPILVKEIE 323	
QY	330 YRMTSGSWTETHAVNAPTYKMLHLDPDTEYIEIRVLLTRPGEGLTGPPLIIRTKCAEP 389	
DB	324 YRMARGPWAEBHAVNLQTYKMLHLDPDTEYIEISVLLTRPGDGGTGRGPPLISRTKCAEP 383	
QY	390 MRPYKILKTAIEQARIADVWESLGNITRCHTFNVTICVHYFRG--HNESKADCLDMDP 447	
DB	384 TRAPKGLAFAEIOARQLTQWEPLGVNVTCHTYAVSLCYRYTLGGSHNQITRECVKMER 443	
QY	448 KAPQVNVHLPPVTNYSKMLNPEGRKESEETIQTDEDVPGVPVKSLQGTSPENKI 507	
DB	444 GABRYTIKNLPPRNHVRLLTNPEGRKEGKEVTFQTDDEDVPGGIAASLSLTFPLEDMI 503	
QY	508 FLNWKBPDLNGIITQVEISYSIRGFPDPAVPVAGPPQTVSNLWNSHVRHFMHLHPGTTY 567	
DB	504 FLKWEFPQENGLITQVEISYQIESDDPAVNVPGPRRTISKLRNETHYVFSNLHPGTTY 563	
QY	568 QFFIRASTVKGFGPATAINVTNNISAPLTPDYEGVDASLNETHATTITVLLRPAQAGAPI 627	
DB	564 LFSVRARTSGFGQAALTEITNNISAPSF-DYADMPSPGSESENTITVLLRPAQAGAPI 622	
QY	628 SAYQIVVEELHPRTHKEAGAMECYQVPVYQYQAMSGAPYFAAELPGNLEPAPFTV 687	
DB	623 SVYQVVEEERPRRLRREPGAQCFSPVLTFETALARGLVHYFGAELAASSLLEAPFTV 682	
QY	688 GDNRTYQGFVNPLAPRKGNVYFQAMSSVEKETKTQCVRATKAATESEPEVDPDAKOT 747	
DB	683 GDNQTVRGFWNPFLERPAKALVIFQAASHLKGTRLCNIRIARAKACKSKRPLEVSQRS 742	
QY	748 DRVVKIAGISA-GILVPIFILLVVLIVKRSKLAKRKDAMGNTRQEMTHMNMAMDRSYA 806	
DB	743 EEMGLILGICAGGLAVILLGLGAILVIIRKGPVNMWK-ATVNVYRQEKTHMMSAVDRSFT 801	
QY	807 DQSTLHAEDPLSTFMDQHNFSRYENHS--ATAESRLLDVRYLCEGTESYQTGOLH 864	
DB	802 DQSTLOEDERGLGSFMDAPGYSRQGRSGVTVASLSLLGSGSPRRRCGRKGSYPHTGOLH 861	
QY	865 PAIRVADLLQHINLMKTSDSYGFKEYESFFEQSASWDAKQDNRAKRYNMIAYDH 924	
DB	862 PAVRVADLLQHINQMKTAEYGFKEYESFFEQSASWDAKQDNRAKRYNMIAYDH 917	
QY	925 SRVILQVEDDDSSDYINANYIDGYQSPSHYATQGVHETVDFWRMIHQEQSACIMV 984	
DB	918 HHVKLHPLADPDADYISANYIDGYSRHSNHFATQGPKEMIYDFWRMVMWQEQSACIMV 977	
QY	985 TNLVVEGRVKCYKYPDDTEVYGDFTKVTCEMEMEPLAEYVVRTTFLERRRGYNEIREVKQFH 1044	
DB	978 TKLVEVGRVKCSRYWEDSDMYGDIKITLVKTETLAEYVVRTTFLERRRGYNSARHEVRQFH 1037	
QY	1045 FTQWPHGVPPYHATGLLSFIRRVKLSNPPSAGPIVHCSAGARTGCIYIVIDIMLMAER 1104	
DB	1038 FTAWPEHGVPPYHATGLLAFIRRVKASTPPDAGPIVHCSAGRTGCIYIVIDIMLMAEC 1097	
QY	1105 EGVVDIYNCVKALRSRINNVQTEEQYIFTHDAILEACLCGETAIPVCEPKAAYFDMIRI 1164	
DB	1098 EGVVDIYNCVKLSRRVNMVQTEEQYIFTHDAILEACLCGETTIPVNEFRATYREMIRI 1157	
QY	1165 DSQTNSSHLKDFQTLNSVTPLQABDCSIACLPNRHDKNRMDMLPPDRCLPFLITIDG 1224	
DB	1158 DPQSSSQLREBFQTLNSVTPLDVCECSIALLPNRDNKNSMDVLPDPDCLPFLISSDG 1217	
QY	1225 ESSNYINAALMDSYROPAAFIYQYPLPNTVKDFWRLVYDYGCTSIUMLNEVDLSQG--- 1281	
DB	1218 DPNYINAALTDSTYRSAAFIYTLHPLQSTTPDFWRLVYDYGCTSIUMLNQLNQSNAWP 1277	
QY	1282 CQYWEEEGMLRVGPIQVECMSCMDCDVINRIFRINLTPQEGVYLMVQOQFYLWASH 1341	
DB	1278 CQYWEEEGMLRVGPIQVECMSCMDCDVINRIFRINLTPQEGVYLMVQOQFYLWASH 1337	
QY	1342 REVPGSKRFLKILQVEKQWQEWKEGEGRTIHLCLNGGSGRSMFCAGIYVWEMVKRQNV 1401	
DB	1338 RUTPDGRKAFHLHLAEVDKQAB--SGDGRVTVHCLNGGSGRSTFCACATVLEMRCHSL 1395	
QY	1402 VDVFHAKVTLRNSKPNMVEAPEQYFCYDVALEYLES 1438	
DB	1396 VDVFHAKVTLRNSKPNMVEAPEQYFCYDVALEYLES 1432	
RESULT 14		
PTPT	MOUSE	
ID	STANDARD; PRT; 1454 AA.	
AC	Q99M80; Q99M81; Q99M82; Q9JIZ1; Q9JIZ2; Q9JKC2; Q9JLP0;	
DT	10-OCT-2003 (Rel. 42, Created)	
DT	10-OCT-2003 (Rel. 42, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	Receptor-type protein-tyrosine phosphatase T precursor (EC 3.1.3.48)	
DE	(R-PTP-T) (RPTP-rho) (mRPTPrho) (RPTPmam4).	
GN	Name=Ptptr;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A. (ISOFORMS 2 AND 5), AND ALTERNATIVE SPLICING.	
RC	STRAIN=C57BL/6J;	
RX	MEDLINE=22730707; PubMed=11423001;	
RA	Besco J.A., Frostholt A., Popesco M.C., Burghes A.H.M., Rotter A.;	
RT	"Genomic organization and alternative splicing of the human and mouse	
RT	RPTPrho genes.";	
RL	BMC Genomics 2:1-1(2001).	
RN	[2]	
RP	ERRATUM.	
RX	MEDLINE=22730717; PubMed=11814386;	
RA	Besco J.A., Frostholt A., Popesco M.C., Burghes A.H.M., Rotter A.;	
RL	BMC Genomics 2:5-5(2001).	
RN	[3]	
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).	
RA	Buchli A.D., Zimmermann D.R., Pfister F., Vaughan L.;	
RT	"RPTPmam4: a fourth member of the NAM family of receptor protein	
RT	tyrosine phosphatases expressed in adult brain.";	

Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[4]  
SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).  
Mizuta M., Bergman B., Miki T., Hutton J.C.;  
"Molecular cloning and functional characterization on mouse receptor-  
like protein tyrosine phosphatase, mbrprho, which mediates cell-cell  
adhesion of pancreatic beta cells,"  
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

[5]  
TISSUE SPECIFICITY.  
MEDLINE=98146229; PubMed=9486824;  
DOI=10.1002/(SICI)1096-9861(19980222)391:4<444::AID-CNE3>3.0.CO;2-0;  
McAndrew P.E., Frotscholtz A., Evans J.E., Zillar D., Goldowitz D.,  
Chiu I.-M., Burghes A.H.M., Rotter A.;  
"Novel receptor protein tyrosine phosphatase (RPTPrho) and acidic  
fibroblast growth factor (FGF-1) transcripts delineate a rostrocaudal  
boundary in the granule cell layer of the murine cerebellar cortex,"  
J. Comp. Neurol. 391:444-455(1998).

-!- FUNCTION: May be involved in both signal transduction and cellular  
adhesion in the CNS. May have specific signaling roles in the  
tyrosine phosphorylation/dephosphorylation pathway in the anterior  
compartment of the adult cerebellar cortex.

-!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
tyrosine + phosphate.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=5;  
Name=1;  
IsoId=Q99M80-1; Sequence=Displayed;  
Name=2;  
IsoId=Q99M80-2; Sequence=VSP\_007803, VSP\_007806;  
Name=3; Synonyms=RPTPrho2;  
IsoId=Q99M80-3; Sequence=VSP\_007803, VSP\_007804;  
Name=4; Synonyms=RPTPrho1;  
IsoId=Q99M80-4; Sequence=VSP\_007803;  
Name=5;  
IsoId=Q99M80-5; Sequence=VSP\_007803, VSP\_007805;

-!- TISSUE SPECIFICITY: Expression is restricted to the CNS.  
Distributed throughout the brain and spinal cord.

-!- DEVELOPMENTAL STAGE: Exceptionally high levels found in the cortex  
and olfactory bulbs during perinatal development and are down-  
regulated during postnatal week 2. Expression in the cerebellar  
cortex is restricted to the granule cell layer of lobules 1-6.  
Anterior and posterior compartments become discernible only during  
postnatal weeks 2 and 6.

-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.  
Receptor class 2B subfamily.

-!- SIMILARITY: Contains 4 fibronectin type III domains.

-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

-!- SIMILARITY: Contains 1 MAM domain.

-!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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EMBL; AF152556; AAD34158.4; -;  
EMBL; AY026861; AAK18741.1; -;  
EMBL; AY026862; AAK18742.1; -;  
EMBL; AY026863; AAK18743.1; -;  
EMBL; AF244125; AAF44712.1; -;  
EMBL; AF162856; AAF82400.2; -;  
EMBL; AF162857; AAF82401.1; -;  
HSP; F10586; ILAR.  
MGD; MGI:1321152; Ptptr.  
InterPro; IPR003961; FN\_III.  
InterPro; IPR008957; FN\_III-like.  
InterPro; IPR003599; Ig\_  
InterPro; IPR007110; Ig-like.

InterPro; IPR000998; MAM.  
InterPro; IPR000387; TYR\_phosphatase.  
InterPro; IPR000242; Tyr\_PP.  
Pfam; PF00041; fn3; 3.  
Pfam; PF00629; MAM; 1.  
Pfam; PF00102; Y\_phosphatase; 2.  
PRINTS; PR00020; MAMDOMAIN.  
PRINTS; PR00700; PRTYPHPHTASE.  
SMART; SM00060; FN3; 3.  
SMART; SM00409; IG; 1.  
SMART; SM00137; MAM; 1.  
SMART; SM00194; PTPc; 2.  
PROSITE; PS0853; FN3; 4.  
PROSITE; PS0835; IG LIKE; 1.  
PROSITE; PS00740; MAM\_1; 1.  
PROSITE; PS00660; MAM\_2; 1.  
PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
PROSITE; PS00056; TYR\_PHOSPHATASE\_2; 2.  
PROSITE; PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
KW Alternative splicing; Glycoprotein; Hydrolase; Immunoglobulin domain;  
KW Protein phosphatase; Receptor; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 29 Potential.  
FT CHAIN 30 1454 Receptor-type protein-tyrosine  
phosphatase T.  
FT DOMAIN 30 770 Extracellular (Potential).  
FT TRANSMEM 771 791 Potential.  
FT DOMAIN 792 1454 Cytoplasmic (Potential).  
FT DOMAIN 34 195 MAM.  
FT DOMAIN 197 288 Ig-like C2-type.  
FT DOMAIN 292 383 Fibronectin type-III 1.  
FT DOMAIN 390 484 Fibronectin type-III 2.  
FT DOMAIN 485 588 Fibronectin type-III 3.  
FT DOMAIN 670 767 Fibronectin type-III 4.  
FT DOMAIN 902 1156 Protein-tyrosine phosphatase 1.  
FT DOMAIN 1188 1450 Protein-tyrosine phosphatase 2.  
FT ACT\_SITE 1097 1097 Phosphocysteine intermediate (By  
similarity).  
FT ACT\_SITE 1391 1391 Phosphocysteine intermediate (By  
similarity).  
FT DISULFID 217 271 Potential.  
FT CARBOHYD 82 82 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 102 102 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 141 141 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 212 212 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 425 425 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 514 514 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 551 551 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 605 605 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 658 658 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 688 688 N-linked (GlcNAc... ) (Potential).  
FT VARSPPLIC 731 749 Missing (in isoform 2, isoform 3, isoform  
4 and isoform 5).  
FT FTID=VSP\_007803.  
FT FTID=VSP\_007803.  
FT FTID=VSP\_007804.  
FT FTID=VSP\_007805.  
FT FTID=VSP\_007805.  
FT R -> RHPAHTVGTATLGRAASPCM (in isoform  
2).  
FT FTID=VSP\_007806.  
FT Missing (in Ref. 1).  
FT R -> P (in Ref. 1).  
FT GCSC -> RGVF (in Ref. 1).  
FT A -> T (in Ref. 4; AAF82401).  
FT A -> S (in Ref. 4; AAF82401).  
FT I -> V (in Ref. 4; AAF82401).  
FT T -> S (in Ref. 4; AAF82401).  
FT A -> T (in Ref. 4; AAF82401).  
FT G -> S (in Ref. 4; AAF82401).  
FT TD -> N (in Ref. 4; AAF82401).  
FT D -> A (in Ref. 4; AAF82401).  
FT Y -> H (in Ref. 1).  
FT H -> N (in Ref. 4; AAF82401).



```
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000998; MAM.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00020; MAMDOMAIN.
DR PRINTS; PR00700; PRTPHPHTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 1.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00853; FN3; 3.
DR PROSITE; PS00740; MAM; 1; 1.
DR PROSITE; PS00060; MAM; 2; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Hydrolase; Receptor.
SQ SEQUENCE 1439 AA; 161655 MW; 99E8E8D14D7C965D CRC64;

Query Match          59.4%; Score 4581.5; DB 2; Length 1439;
Best Local Similarity 59.6%; Pred. No. 8.9e-298;
Matches 863; Conservative 212; Mismatches 339; Indels 35; Gaps 13;

QY 6 AAALPAFVALLLSFWLLLSAQGQAGGCTFD---DGPACDHYHQDLYDDFEWVHSA 62
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 QEPHYLPMPGCGSMIVSDSDHPDGEKARQLPTMKENDTHCTDFSVLLYSQGLNPGT 122
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 57 HPGTRAPADLPHGSYLMVNTSQHAPGORAHVIFQSLSENDDHCYQSFYLSRDSGSPGT 116
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 LNLIVRVNKGPIANPIWNTGFTGRDLWRLAEAVSTFWPNQYVITFEAEVSGSGXIAT 182
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 LGVYRVNNGPLGSAVWNTGSHGQWHAELAVSTFWPNQYVITFEALISPDRRGYNGL 176
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 183 DDIVLSYPCDKSPHFLRLGDEVNAGQATFQCIGTGRDAVHNKMLQRENGEDIPVAQ 242
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 DDILLSYCAKAPHFSLGDEVNAGQASFCQMAAGRAAEERFLQROSGALVPAAG 236
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 243 TKNINHRFAASFRLOEVTKTDQDLYRCVTSQSGSGVSNFAQLIVRPPRPPIAPPQLLG 302
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 237 VRHISHRFLATFPLAAVSRAEQDLYRCVSOAPRGAGVSNFAELIVKEPPTPIAPPQLLR 296
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 303 VGPVTLILQLNANSIIGDPIILKEVEYRMTSGSWTETHAVNAPTYKLWHLDPDTEYR 362
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 297 AGPTVLIILQNTNSIIGDPIVRKEIEYRMARGPWAHVLSQTYKLWHLDPDTEYRIS 356
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 363 VLLTRPGEGLPGPLPITRTKCAEPMRTPKTKIAIEIOARRIADVWESLGYNITRCHT 422
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 357 V-LSRPGDGGTGRPGPLISRTKCAEPMRAPKGLAFABEIQARQALQWEPLGYNVTRCHT 415
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 423 FNVITCYHYFRG--HNESKADCLMDPKAPQHVNHLPYTNVSLKMLTNPGEKESSE 480
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 416 YTVSLCYHYTLGSSHNQITRECVKTEQGVSYRTIKNLLPYRNHVHVLNTPGEKKEG 475
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 481 TTIQTDENVPGVPVKSLOGTSFENKIFLNKKEPLDPNGIITQVEISYSSIRSDPAVPV 540
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 476 VTFQDDEVPSGIAAESLTFPLEDMIFLKWEPEQEPNGLITQVEISYQSIESSDPAVNV 535
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 541 AGPQTVSNLMNSTHVVHMLHPGTYQFFIRASTVKGFGPATAINVTNINISAPTLPDYE 600
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 536 PGPRETISKLRNETHYVSNLHPGTYLFSVRARTGKGFGQAALTEITINISAPSF-DYA 594
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 601 GVDASINETATITVLLRPAQAKGAPISAYQIVBELHPHRTKREAGAMECYQVPVTVQN 660
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 595 DMPSPLGSESENTITVLLRPAQGRGAPISYQIVIVEERARRLRREPQGGDCFPVPLTPEA 654
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 661 AMSGAPYVFAELPFGNLPPEAPPTVGDNRTYQGFWNPPPLAPRKGYNIFYQAMSSVEKE 720
DB   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

655 ALARGLVHYFGAELAAASSLPEAMPFTVGDNQTYRGFWNPPEPRKAYLIYFQAASHLKGE 714
721 TKTCQVRIATKAATERPEVIPPDAKQTDVRVKIAGISA-GILVFIILLVILLVIVKSKL 779
715 TRLNCIRIARKAACKESKRPLEVSQRSEEMGLIGICAGGLAVLILGLAIIVIRKGP 774
780 AKKRDAMGNTRQBMTHVNMADRSVADQSTLHAEDPLSITFMDQHNFSRYENH--SAT 837
775 VNMTK-ATVNYRQEKTHMSAVDRSFTDQSTQEDERLGLSFMDFTHGYSTRGDORGXVT 833
838 AESSRLIDVPRYLCEGTESPYQQLHPAIRVADLLOHINLMKTSDSYGKKEYESPFEG 897
834 EASSLLGSPRRPCGRKGSFYHTGQLHPAVRVADLLOHINQMKTAEYGFQKEYESPFEG 893
898 QSASWDVAKDQNRKAKRYNIIITAYDHSRVILQVEDDPSDDIYNIYID-----GYOR 951
894 ---WDATKKKOKVKSGRSQRPMPAYDRHRVKLHPMLGDPNADYINANYIIDIRINREGYHR 949
952 PSYIATQGPVHETVDFWMIWQEQSACIWMVTNLVEVGRVKCYKVPDDTEVYGFVKV 1011
950 SNHFATQGPKEPVYDFWRWVWQEHCSIIWMIKLVVEVGRVKCSRWPEDSDYIGIKI 1009
1012 TCVEMEPLAEYVYVTRFTFLERRGYNEIREVKQFHTGPDHGVPHYATGLLSFIRRVKLSN 1071
1010 MLVKTETLAEVVVRTFALERRGYSARHEVQFHTAMPEHGVPHYATGLLAFIRRVKAST 1069
1072 PPSAGPIVHCSAGAGRTGCIIVIDIMLMAEREGVVDIYNCVKALSRINNMVQTEQY 1131
1070 PPOAGPIVHCSAGTGTGCIYVLDVMDLMAECEGVVDIYNCVKTLCSRRVNMVQTEQY 1129
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1192 CSTACLPNRHDKRFDMLPPDRCLPFLITIDGESSNYINAAALMSYRQPAAFIVTQYPL 1251
1190 CSTALLPRNDRKNSMDVLPDRCLPFLITDGDSSNNYINAAALDTSYTRSPAFIVTLHPL 1249
1252 PNTVKDFWRLVYDYGCTSIIVMLNEVDLSQG---CPQWPEBGMURYGPQIQCCHSCSMD 1308
1250 QSTTPDFWRLVYDYGCTSIIVMLNQLNQSNSAWPCQYWPPEPGRQQYGLMEVEFMSGTA 1309
1309 DVINRIERI CNLTPQSGYLMVQOFOYLGWASHREVPGSKESFLKLILQVEKWQOEK 1368
1310 DLVARVPRVQNISR--EGHLLVRHFQFLRSAYRDTDPDSKAKAFUHLAEVDKQAE--SG 1365
1369 EGRTIIHCLNGGGRSGMFCFCAIGIVEMVKRQNVVDVFAVKTLRNSKPNMVEAPEQYRFC 1428
1366 DGRITVHCLNGGGRSGTFCACATVLEIRCHNLVDVFFAAKTLRNYPKNMVEVTDQYHFC 1425
1429 YDVALEYL 1437
1426 YDVALEYL 1434

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Job time : 173.956 secs
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